

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 19:23:49 ; Search time 90.7435 seconds  
(without alignments)  
8672.640 Million cell updates/sec

Title: US-09-918-568-46

Perfect score: 1783  
Sequence: 1 CGCGTACGCAAGACAGGGGT.....ACCCCTGTCTCTGCTAGCCG 1783

Scoring table: IDENTITY NUC  
Gapop 10.0 ; Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 10%  
Listing first 45 summaries

Database : Issued\_Patents\_NA.\*

1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq.\*  
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3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCFUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1783	100.0	1783	1 US-08-229-781-46	Sequence 46, Appl
2	1783	100.0	1783	1 US-08-630-918-46	Sequence 46, Appl
3	1783	100.0	1783	4 US-09-004-422-46	Sequence 46, Appl
4	1606.4	90.1	1728	1 US-08-229-781-28	Sequence 28, Appl
5	1606.4	90.1	1728	1 US-08-630-918-28	Sequence 28, Appl
6	1606.4	90.1	1728	4 US-09-004-422-28	Sequence 28, Appl
7	908.8	51.0	1135	1 US-08-229-781-49	Sequence 49, Appl
8	908.8	51.0	1135	1 US-08-630-918-49	Sequence 49, Appl
9	908.8	51.0	1135	4 US-09-004-422-49	Sequence 49, Appl
10	734	41.2	1701	3 US-09-232-468A-13	Sequence 13, Appl
11	734	41.2	1701	4 US-09-784-984B-11	Sequence 11, Appl
12	707.4	39.7	1721	3 US-08-686-968C-226	Sequence 226, Appl
13	706.2	39.6	1766	2 US-08-453-848-8	Sequence 8, Appl
14	706.2	39.6	1766	3 US-09-169-027-8	Sequence 8, Appl
15	696.4	39.1	1724	3 US-09-197-679A-1	Sequence 1, Appl
16	695.6	39.0	1754	1 US-08-229-781-27	Sequence 27, Appl
17	695.6	39.0	1754	1 US-08-630-918-27	Sequence 27, Appl
18	695.6	39.0	1754	4 US-09-004-422-27	Sequence 27, Appl
19	400	22.4	400	1 US-08-229-781-33	Sequence 33, Appl
20	400	22.4	400	1 US-08-630-918-33	Sequence 33, Appl
21	400	22.4	400	4 US-09-004-422-33	Sequence 33, Appl
22	397	22.3	405	1 US-08-229-781-34	Sequence 34, Appl
23	397	22.3	405	1 US-08-630-918-34	Sequence 34, Appl
24	397	22.3	405	4 US-09-004-422-34	Sequence 34, Appl
25	382.4	21.4	410	1 US-08-229-781-35	Sequence 35, Appl
26	382.4	21.4	410	1 US-08-630-918-35	Sequence 35, Appl
27	382.4	21.4	410	4 US-09-004-422-35	Sequence 35, Appl

28	379.6	21.3	394	1 US-08-229-781-36	Sequence 36, Appl
29	379.6	21.3	394	1 US-08-630-918-36	Sequence 36, Appl
30	379.6	21.3	394	4 US-09-004-422-36	Sequence 36, Appl
31	373	20.9	924	5 PCT-US94-01149-15	Sequence 15, Appl
32	372.6	20.9	810	5 PCT-US94-01149-19	Sequence 19, Appl
33	368.2	20.7	670	5 PCT-US94-01149-5	Sequence 5, Appl
34	361.4	20.3	912	5 PCT-US94-01149-31	Sequence 31, Appl
35	318.6	17.9	1777	1 US-08-229-781-54	Sequence 54, Appl
36	318.6	17.9	1777	4 US-08-630-918-54	Sequence 54, Appl
37	318.6	17.9	1777	4 US-09-004-422-54	Sequence 54, Appl
38	309.4	17.4	1762	1 US-08-105-483-284	Sequence 284, Appl
39	309.4	17.4	1762	1 US-08-709-209-284	Sequence 284, Appl
40	309.4	17.4	1762	1 US-08-458-101-284	Sequence 284, Appl
41	309.4	17.4	1793	2 US-08-453-848-6	Sequence 6, Appl
42	309.4	17.4	1793	3 US-09-169-027-6	Sequence 6, Appl
43	307.4	17.2	1757	2 US-08-453-848-14	Sequence 14, Appl
44	307.4	17.2	1757	3 US-09-169-027-14	Sequence 14, Appl
45	302.6	17.0	1757	2 US-08-453-848-20	Sequence 20, Appl

## ALIGNMENTS

RESULT 1  
US-08-229-781-46  
Sequence 46, Application US/08229781  
Patent No. 5589174  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/229,781  
FILING DATE: April 19, 1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1783 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: A/Okuda/57  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:

HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-229-781-46

Query Match 100.0%; Score 1783; DB 1; Length 1783;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 TATCTCATCTCTCTGTTACAGCAGTGAGAGGGGACAGATATGATGGATACATGCC 120  
QY 121 AATTAATCCACAGAGAGGTCGACACAATTTCTAGAGCGGAAGCTGACTGATGCC 180  
DB 121 AATTAATCCACAGAGAGGTCGACACAATTTCTAGAGCGGAAGCTGACTGATGCC 180  
QY 181 AAGGACATCTTGAGAGAGCCCATTAACGGAAGTTATGCAACTAAACGGAATCCCTCCA 240  
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DB 1081 GCATATCTGTTTATAGAAGAGATGSCAAGAAATGTTGACGTTGATGATGATAC 1140  
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DB 1561 GAGCTTAACTAAATGAATGAATCAAGAGGCTAAATTTGACGAGCATGGGCTTTAT 1620  
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DB 1621 CAATCTCTTGCATTTATGCTACAGTACAGGTTTATGTCACCTGCAATCATGATGCT 1680







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Db 721 CCAGAAATAGCAACAGGCTTAAAGTGAATGAGCAAGAGGTGAATGSAATCTCTGG 780  
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Db 841 GAGATGTGATTTCAATATATGAGAGAGGATGTTTCAAGGATCATGAAACAGAGAGACA 900  
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Db 1261 GCTGTGGAAGATTTGCGTAACTTGAAGAAAAGATGAGAACTTGAACAAAAGATG 1320  
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Db 1321 GAAGACGGGTTTCTAGATGTGTGACATATACATCTGAGCTTTAGTTCTGATGAAAT 1380  
QY 1381 GAGAGACACTTGTACTTTTCATGATTTCTAATGTCAAGATCTGTATAGTAAAGTCAGATG 1440  
|||||  
Db 1381 GAGAGACACTTGTACTTTTCATGATTTCTAATGTCAAGATCTGTATAGTAAAGTCAGATG 1440  
QY 1441 CAGCTGAGACACAGCTCAAGAGTGAAGATGAGATGTTTGAATTTTATACAAATGT 1500  
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Db 1441 CAGCTGAGACACAGCTCAAGAGTGAAGATGAGATGTTTGAATTTTATACAAATGT 1500  
QY 1501 GATGATGAATGATGAATAGTGTGAAAAACGGACATATGATTTATCCCAATGAGAA 1560  
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Db 1501 GATGATGAATGATGAATAGTGTGAAAAACGGACATATGATTTATCCCAATGAGAA 1560  
QY 1561 GAGCTTAACCTAATTAAGAAATGAATCAAGAGGTTAAATTTGACAGCATGGGCTTAT 1620  
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Db 1561 GAGCTTAACCTAATTAAGAAATGAATCAAGAGGTTAAATTTGACAGCATGGGCTTAT 1620  
QY 1621 CAATTCCTTGCCATTTATGCTACAGTACAGTGTCTATGTCACGTGCAATCATGATGCT 1680  
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Db 1621 CAATTCCTTGCCATTTATGCTACAGTACAGTGTCTATGTCACGTGCAATCATGATGCT 1680  
QY 1681 GGGATCTCTTCTGAGTGTGCTCCCAAGGGTCTCTGACAGTGCAGAGATCTGCATATGATTA 1740  
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Db 1681 GGGATCTCTTCTGAGTGTGCTCCCAAGGGTCTCTGACAGTGCAGAGATCTGCATATGATTA 1740  
QY 1741 TAAGTCAATTTTATTAATTAATAAACCCCTGTTTCTGCTAGCCG 1783  
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Db 1741 TAAGTCAATTTTATTAATTAATAAACCCCTGTTTCTGCTAGCCG 1783  
|||||

## RESULT 4

US-08-229-781-28  
Sequence 28, Application US/08229781  
Patent No. 5589174  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/229,781  
FILING DATE: April 19, 1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1728 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

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? MOLECULE TYPE: cdna to genomic RNA
? HYPOHETICAL:
? ANTI-SENSE:
? FRAGMENT TYPE:
? ORIGINAL SOURCE:
? ORGANISM: A/1zum1/5/65
? STRAIN:
? INDIVIDUAL ISOLATE:
? DEVELOPMENTAL STAGE:
? HARLOT TYPE:
? TISSUE TYPE:
? CELL TYPE:
? CELL LINE:
? ORGANELLE:
? IMMEDIATE SOURCE:
? LIBRARY:
? CLONE:
? POSITION IN GENOME:
? CHROMOSOME/SEGMENT:
? MAP POSITION:
? UNITS:
? FEATURE:
? NAME/KEY:
? LOCATION:
? IDENTIFICATION METHOD:
? OTHER INFORMATION:
? PUBLICATION INFORMATION:
? AUTHORS:
? TITLE:
? JOURNAL:
? VOLUME:
? ISSUE:
? PAGES:
? DATE:
? DOCUMENT NUMBER:
? FILING DATE:
? PUBLICATION DATE:
? RELEVANT RESIDUES IN SEQ ID NO:
US-08-229-781-28

Query Match 90.1%; Score 1606.4; DB 1; Length 1728;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1652; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

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? 27 ATAGAAACCAAGCAAAACAATGCGCATCTTATCTCATCTCTCTGTCACAGACT 86
? 1 ATAGCAACCAAGCATATACCAATGGCCATCTATCTCATCTCTCTGTCACAGACT 60
? 87 GAGAGGGACACGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 146
? 61 GAGGGGGACGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
? 147 AATCTAGAGCGGAACGTCAGTGTGATGATGATGATGATGATGATGATGATGATGAT 206
? 121 AATCTAGAGCGGAATGTCAGTGTGATGATGATGATGATGATGATGATGATGATGAT 180
? 207 CGGAAGATTATGCAACATTAACGGAATCCCTCCACTTGAAGTGAAGGACTGTAGCAT 266
? 181 CGGAAGCTATGCAACATTAACGGAATCCCTCCACTTGAAGTGAAGGACTGTAGCAT 240
? 267 CGGATGGCTCTTGGAAATCCAAATGTATAGGGCTTCAAGTGTCCCGAAGCGGTCTTA 326
? 241 CGGATGGCTCTTGGAAATCCAAATGTATAGGGCTTCAAGTGTCCCGAAGTGTCTTA 300
? 327 TATATGGAGAAAGAAACCCGAGAGCGGTTGTATATCCAGGACGCTCAATGATTA 386
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? 567 TGCCAAAGATGCTGACAAACAATACAGCGGAGAACAAATGCTTAATTTTGGGGGTGCA 626
? 541 TGCCAAAGATGCTGACAAACAATACAGCGGAGAACAAATGCTTAATTTTGGGGATGCA 600
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? 721 GAATGACAAAGAGTGAATGGAATTCCTTGACCTCTTGATATGTGGACACCAT 780
? 807 AATTTTGAAGATGCTGATATCTAATGTGACAGAGTATGATTAATTAATTCGAAAG 866
? 781 AATTTTGAAGATGCTGATATCTAATGTGACAGAGTATGATTAATTAATTCGAAAG 840
? 867 AGGTAGTTCAGGATCATGAACAGAGACACTTGAAGACTGTGAGACCAATGCCA 926
? 841 AGGTAGTTCAGGATCATGAACAGAGACACTTGAAGACTGTGAGACCAATGCCA 900
? 927 AACTCTTTGGAGCAATTAATCAACATTTACCTTTTCAATGTCACCCACTGACAT 986
? 901 AACTCTTTGGAGCAATTAATCAACATTTACCTTTTCAATGTCACCCACTGACAT 960
? 987 AGGTAGTTCAGGATCATGAACAGAGACACTTGAAGACTGTGAGACCAATGCCA 1046
? 961 AGGTAGTTCAGGATCATGAACAGAGACACTTGAAGACTGTGAGACCAATGCCA 1020
? 1047 TGTTCGCCAGATTTGAATCAAGAGATTTGTTGGGCAATAGCTGTTTATGAGAGAG 1106
? 1021 TGTTCGCCAGATTTGAATCAAGAGATTTGTTGGGCAATAGCTGTTTATGAGAGAG 1080
? 1107 ATGCAAGAGATGCTGTGACGTTGATGATGATGATGATGATGATGATGATGATGAT 1166
? 1081 ATGCAAGAGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
? 1167 GTATGACAGAGCAAAAGATTCACCTCAAAAGCATTTGTGATGATGATGATGATGAT 1226
? 1141 GTATGACAGAGCAAAAGATTCACCTCAAAAGCATTTGTGATGATGATGATGATGAT 1200
? 1227 TTTCTGTGATTTGAAAAGATTAACACCAATTTGATGATGATGATGATGATGATGAT 1286
? 1201 TTTCTGTGATTTGAAAAGATTAACACCAATTTGATGATGATGATGATGATGATGAT 1260
? 1287 AGAGAAAGACTGAGAACTTGAACAAAAGATGAGAGCGGTTTCTAGATGTGTGAC 1346
? 1261 AGAGAAAGACTGAGAACTTGAACAAAAGATGAGAGCGGTTTCTAGATGTGTGAC 1320
? 1347 ATACAAATGCTGAGCTTTTGTCTGTGATGAGAAATGAGAGCACTTGCATGATTC 1406
? 1321 ATACAAATGCTGAGCTTTTGTCTGTGATGAGAAATGAGAGCACTTGCATGATTC 1380
? 1407 TATGTCAAGATTCGTATAGTAAAGTCAAGTGCAGTGCAGCAACGCTCAAGAACT 1466
? 1381 TATGTCAAGATTCGTATAGTAAAGTCAAGTGCAGTGCAGCAACGCTCAAGAACT 1440
? 1467 AGAGAAATGATGTTTGAATTTTATCAGAAATGATGATGATGATGATGATGATGAT 1526
? 1441 AGAGAAATGATGTTTGAATTTTATCAGAAATGATGATGATGATGATGATGATGAT 1500
? 1527 AAGCGGACATATGATTTATCCCACTATGAGAGAGAGCTTAAACTAAATAGAAAT 1586

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[illegible]

Db	61	GAAGGGGACGACGATTAATGATTTGGATTACCATTCGCAATATTTCCAGAAAGGTGACAC	120
QY	147	AATTTTACAGGGGAACGTACATGTTGACATCATGCGCAAGGACATCCTTGGAAAGACCCATTA	206
Db	121	AATTTACAGGGGAAATGTCTACGTGATCTATCTATCCCAAGGACATCCTTGAAGAACCCACAA	180
QY	207	CGGAAAGTTATGCAAACTTAACGCGAATCCCTCCACTTGAACCTAGGGGACCTGTAGCATTCG	266
Db	181	CGGAAGCTTATGCAAACTTAACGCGAATCCCTCCACTTGAACCTAGGGGACCTGTAGCATTCG	240
QY	267	CGGATGGCTCTTGGAAATTCGAAATGTGATAGGCTTTAGTGTGCCAGAACGGTCCCTA	326
Db	241	CGGATGGCTCTTGGAAATTCGAAATGTGATAGGCTTTAGTGTGCCAGAAATGGTCTCTA	300
QY	327	TATATTTGAGAAAGAAACCCGAGAGAGGTTTGGTTATTCGAGGACGCTTCATATGATTA	386
Db	301	TATATTTGAGAAAGAAACCCGAGATTAACAGTTTATGTTATCCGAGCACTTCAATATGACTA	360
QY	387	TGAACAATTTGAAACATCTCTCTAGCAGCGTGAACAATTTGAGAAAGTAAGATCTTCC	446
Db	361	TGAAGAATTTGAAACATCTCTCTAGCAGCGTGAACAATTTGAGAAAGTAAGATCTTCC	420
QY	447	CAAGATTTGATGACACAGCATATACACAACCTGAGAGTTCCAGGGCTCGCGGTCTCTCG	506
Db	421	CAAAATTTGATGAGACACAGCATATACACAACCTGAGAGTTCAAAAGGCTTCGCGATCTCAG	480
QY	507	TAAATCCATCATTTTTCAGGAACATGCTGTGGCTGCAAGAGAGATGAGATTAATCCGCT	566
Db	481	TAAACATCATTTCTTCAGGAACATGCTGTGGCTGCAAGAGAGATGAGATTAATTCGCGT	540
QY	567	TGCCAAAGGATGCTACAACAATTAACAAGCGGAGAACAAATGCTATATATTTGGGGGGTCA	626
Db	541	TGCCAAAGGATGCTACAACAATTAACAAGCGGAGAACAAATGCTATATATTTGGGGAGTCA	600
QY	627	CCATTCCTTTGATGAGACAGAAACAAGCAATTTGTCACGAATGTGGGAACCTATGTTTC	686
Db	601	CCATTCCTTTGATGAGACAGAAACAAGCAATTTGTCACGAAGAGTGGGAACCTATGTTTC	660
QY	687	CGTAGGCAATCAACATTTGAACAAAAGGTCAACCCGACAAATATGACAAAGGCTTAAAGT	746
Db	661	CGCAAGCAATCAACATTTGAACAAAAGGTCAATCCCTTAAATATGACGAAGGCTTAAAGT	720
QY	747	GAATGACAAAGAGGTAGATGAATTCCTCTTGGACCCCTTGGATATGTGGGACACCAT	806
Db	721	GAATGACAAAGAGGTAGATGAATTCCTCTTGGACCCCTTGGATATGTGGGACACCAT	780
QY	807	AAATTTTGAAGTACTGTTATCTTAATTTGACACAGAGTATGATTTCAAAATATTCGAAAG	866
Db	781	AAATTTTGAAGACTGTGTTATCTTAATTTGACACAGAGTATGATTTCAAAATATTCGAAAG	840
QY	867	AGTAGTTTCAGAGATCATGAAGAAAGAGAGAAACCTTAGAACTGTGAGACCAATGCGCA	926
Db	841	AGTAGTTTCAGAGATCATGAAGAAAGAGAGAAACCTTGTGGAACCTGTGAGACCAATGCGCA	900
QY	927	AACCTCTTTGGGACCAATTAATTAACAACATTCCTTTTACAATGTCCACCCACTGCACAT	986
Db	901	AACCTCTTTGGGACCAATTAATTAACAACATTCCTTTTACAATGTCCACCCACTGCACAT	960
QY	987	AGGTGAGTGGCCCCCAATATGTAAATTCGGAAGAGTTGGTCTTAGCAACAGCACTTAAGAA	1048
Db	961	AGGTGAGTGGCCCCCAATATGTAAATTCGGAAGAGTTGGTCTTAGCAACAGCACTTAAGAA	1020
QY	1047	TGTTTCCCAAGTTTAATCAACAGAGATTTGTTGGGCAATTAAGTGGTTTATTAAGAAAGGG	1106
Db	1021	TGTTTCCCAAGTTTAATCAACAGAGATTTGTTGGGCAATTAAGTGGCTTTATTAAGAGGGGG	1086
QY	1107	ATGCGCAAGGAATGTTGAACGGTGTGTATGATATACATCAACAGCATGACCGAGGATCAGG	1166
Db	1081	ATGCGCAAGGAATGTTGATGTTGTGTATGATATACATCAACAGCATGACCGAGGATCAGG	1140
QY	1167	GTATGCGAGCAACAAAGATTCACATAAGGCAATTTGATGGAATCACCACAAGGTAA	1226

DB 1141 GTATGACGACGACAAAGATCCACTCAAAAAGCATTTGATGGAATCCACCAAGGTAAA 1200  
QY 1227 TTCTGTGATGAAAGATTAACACCCCAATTTGAAGCTGTTGGAAAGAAATTCGTAATT 1286  
DB 1201 TTCTGTGATGAAAGATTAACACCCCAATTTGAAGCTGTTGGAAAGAAATTCATTAATT 1260  
QY 1287 AGGAAAGACTGAGAACTTGAACAAAGATGGAAGACGGGTTCTAGATGTGTGAC 1346  
DB 1261 AGGAAAGACTGAGAACTTGAACAAAGATGGAAGACGGGTTCTAGATGTGTGAC 1320  
QY 1347 ATCAATGCTGAGCTTTTACTTCTGATGAAATGAGAGGACATTCATCTTCTGATTC 1406  
DB 1321 ATCAATGCTGAGCTTCTACTTCTGATGAAATGAGAGGACATTCATCTTCTGATTC 1380  
QY 1407 TAATGTCAGAAATCTGTATAGTAAGTCAGAAATGACAGTGAACAGTCAAGAACT 1466  
DB 1381 TAATGTCAGAAATCTGTATAGTAAGTCAGAAATGACAGTGAACAGTCAAGAACT 1440  
QY 1467 AGGAAATGATGTTTGAATTTTATCACAATGTGATGATGATGATGATGATGATGATG 1526  
DB 1441 AGGAAATGATGTTTGAATTTTATCACAATGTGATGATGATGATGATGATGATGATG 1500  
QY 1527 AAACGGACATATGATTTATCCCAAGTATGAAAGAGTCTAACTAAATGAATGAAT 1586  
DB 1501 AAACGGACATATGATTTATCCCAAGTATGAAAGAGTCTAACTAAATGAATGAAT 1560  
QY 1587 CAAAGGGGTAAATTTAGAGCATGGGGTTTATCAAAATCCTTGCCATTTATGCTACAGT 1646  
DB 1561 CAAAGGGGTAAATTTAGAGCATGGGGTTTATCAAAATCCTTGCCATTTATGCTACAGT 1620  
QY 1647 AGCAGTCTGATGCTGCTGCAATCATGATGCTGGGATCTTTCTGGGTGCTCCAA 1706  
DB 1621 TCGAGTCTGCTGCTGCTGCAATCATGATGCTGGGATCTTTCTGGGTGCTCCAA 1680  
QY 1707 CGGGTCTGCTGCTGCTGCAATCATGATGCTGGGATCTTTCTGGGTGCTCCAA 1754  
DB 1681 CGGGTCTGCTGCTGCTGCAATCATGATGCTGGGATCTTTCTGGGTGCTCCAA 1728

RESULT 6  
US-09-004-422-28

; Sequence 28, Application US/09004422

; Patent No. 6337070

; GENERAL INFORMATION:

; APPLICANT: Yoshinobu OKUNO et al.

; TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING

; NUMBER OF SEQUENCES: 58

; CORRESPONDENCE ADDRESS:

; STREET: 2033 K Street, N.W., #800

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/004,422

; FILING DATE: January 8, 1998

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/443,862

; FILING DATE: May 22, 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/229,781

; FILING DATE: April 19, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/054,016

; FILING DATE: April 29, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200

TELEFAX: 202-721-8250

TELEX:

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 1728 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to genomic RNA

HYPOTHETICAL:

ANTI-SENSE:

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM: A/12um1/5/65

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE:

ORGANELLE:

IMMEDIATE SOURCE:

LIBRARY:

CLONE:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUE:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-09-004-422-28

Query Match

Best Local Similarity

Matches 1652; Conservative

90.1%; Score 1606.4; DB 4; Length 1728;

95.6%; Pred. No. 0;

0; Mismatches 76; Indels 0; Gaps 0;

QY 27 ATAGAAACCAACCAACCAACCAATGCCATCATCTTTATCTCTCTGTTACAGACAGT 86  
DB 1 ATAGAAACCAACCAACCAACCAATGCCATCATCTTTATCTCTCTGTTACAGACAGT 60  
QY 87 GAGAGGGGACGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 146  
DB 61 GAGAGGGGACGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120  
QY 147 AATCTAGAGCGGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 206  
DB 121 AATCTAGAGCGGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
QY 207 CGGAAAGTTATGCAAACTTAACGGAATCCCTCCACTTGAACCTAGGAGACTGTACATTC 266  
DB 181 CGGAAAGTTATGCAAACTTAACGGAATCCCTCCACTTGAACCTAGGAGACTGTACATTC 240

267 CGATGGCTCTTGGAAATCCAAATGATAGGCTTCTAGTGTGCGAGAGCGTCTTA 326  
241 CGGATGGCTCTTGGAAATCCAAATGATAGGCTTCTAGTGTGCGAGAGCGTCTTA 300  
327 TATATGGAGAAAGAAACCCGAGAGAGCGTGTGTATCCAGCAGCTTCAATGATTA 386  
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387 TGAAGATTTGAACATCTCTCAGCAGCTGTAACCATTTTGAGAAAGTAAAGATTGCCC 446  
361 TGAAGATTTGAACATCTCTCAGCAGCTGTAACCATTTTGAGAAAGTAAAGATTGCCC 420  
447 CAAAGATAGATGACAGCAGCATACAGCACTGAGGTTCACGGCTCGCGGCTGTGCG 506  
421 CAAAGATAGATGACAGCAGCATACAGCACTGAGGTTCACAGGCTCGCGGCTGTGCG 480  
507 TAATCCATCATTTTTCAGGAACATGTGTGCTGACAAAGAGAGATCAGATTATCCGGT 566  
481 TAAACCATCATTTTTCAGGAACATGTGTGCTGACAAAGAGAGATCAGATTATCCGGT 540  
567 TGCCTAAGAGATCGTTCACCAATACAGCGAGAAATGCTATATTTGGGGGCTGCA 626  
541 TGCCTAAGAGATCGTTCACCAATACAGCGAGAAATGCTATATTTGGGGGCTGCA 600  
627 CCATCCCATTTGATGAGCAGAGAACAAAGACATTTGACAGATGTTGGGAACCTATGTTTC 686  
601 CCATCCCATTTGATGAGCAGAGAACAAAGACATTTGACAGATGTTGGGAACCTATGTTTC 660  
687 CGTAGGACATCAACATTTGAACAAAGATCAACCCCAAGAAATAGCAACAGGCTTAAAGT 746  
661 CGTAGGACATCAACATTTGAACAAAGATCAACCCCAAGAAATAGCAACAGGCTTAAAGT 720  
747 GAATGGCAGAGAGCTGATGATGGAATCTCTTGACCTCTTGATATTTGGGACACCAT 806  
721 GAATGGCAGAGAGCTGATGATGGAATCTCTTGACCTCTTGATATTTGGGACACCAT 780  
807 AAATTTGAGAGATGATGATGATGGAATCTCTTGACCTCTTGATATTTGGGACACCAT 866  
781 AAATTTGAGAGATGATGATGATGGAATCTCTTGACCTCTTGATATTTGGGACACCAT 840  
867 AGTAGTTCAGGAGCATGTAAGAAACAGAGAACATTTGAGAACTGTGAGACCAATGCCA 926  
841 AGTAGTTCAGGAGCATGTAAGAAACAGAGAACATTTGAGAACTGTGAGACCAATGCCA 900  
927 AACTCCCTTGGGAGATTAATACATATACATTTTCCAAATGTCACCCACTGACAAAT 986  
901 AACTCCCTTGGGAGATTAATACATATACATTTTCCAAATGTCACCCACTGACAAAT 960  
987 AGTAGTTCAGGAGCATGTAAGAAACAGAGAACATTTGAGAACTGTGAGACCAATGCCA 1046  
961 AGTAGTTCAGGAGCATGTAAGAAACAGAGAACATTTGAGAACTGTGAGACCAATGCCA 1020  
1047 TGTTCCTCCAGATTTATCAAGAGATTTGTTGGGCAATAGCTGTTTATAGAAGAGG 1106  
1021 TGTTCCTCCAGATTTATCAAGAGATTTGTTGGGCAATAGCTGTTTATAGAAGAGG 1080  
1107 ATGGCAAGGAATGTTTACGGTGTGATGATACATCAAGCAATGACAGGATAGG 1166  
1081 ATGGCAAGGAATGTTTACGGTGTGATGATACATCAAGCAATGACAGGATAGG 1140  
1167 GTATGACAGAGACATAGATCCACTCAAAAGCATTTGATGAGATCCCAACAGGTAA 1226  
1141 GTATGACAGAGACATAGATCCACTCAAAAGCATTTGATGAGATCCCAACAGGTAA 1200  
1227 TTTCTGATTTGAATGATAAACCACCATTTGAGAGCTGTTGGGAAAGAAATTCGTAATCT 1286  
1201 TTTCTGATTTGAATGATAAACCACCATTTGAGAGCTGTTGGGAAAGAAATTCGTAATCT 1260  
1287 AGAGAAAGAGCTGTAAGTGAACAAAGATGGAAGAGAGGCTTTCTAATGTGTGAC 1346  
1261 AGAGAAAGAGCTGTAAGTGAACAAAGATGGAAGAGAGGCTTTCTAATGTGTGAC 1320

1347 ATACATGCTGAGCTTTAGTCTGATGAGAAATGAGAGCACTGTGATGATTC 1406  
1321 ATACATGCTGAGCTTTAGTCTGATGAGAAATGAGAGCACTGTGATGATTC 1380  
1407 TAATGTCAGAAATCTGATATAGTAAAGTCAGAAATGAGAGCACTGTGATGATTC 1466  
1381 TAATGTCAGAAATCTGATATAGTAAAGTCAGAAATGAGAGCACTGTGATGATTC 1440  
1467 AGGAATGATGATTTGATTTGATTTATCACAATGATGATGATGATGATGATGATGAT 1526  
1441 AGGAATGATGATTTGATTTGATTTATCACAATGATGATGATGATGATGATGATGAT 1500  
1527 AAACGGACATATGATTTATCCAGTATGAGAGAGCTTAACTTAAATAGAAATGAAAT 1586  
1501 AAACGGACATATGATTTATCCAGTATGAGAGAGCTTAACTTAAATAGAAATGAAAT 1560  
1587 CAAAGGGGTAAATTTGAGCAGCATGAGGCTTTATCAAAATCCCTTGCATTAATGCTACAGT 1646  
1561 CAAAGGGGTAAATTTGAGCAGCATGAGGCTTTATCAAAATCCCTTGCATTAATGCTACAGT 1620  
1647 AGCAGTTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 1706  
1621 TGCAGGTTCTGTCACCTGCGCAATCATGATGATGATGATGATGATGATGATGATGAT 1680  
1707 CGGCTCTGTCAGTGCAGATCTGATATGATTTAATAGTCAATTTTATA 1754  
1681 CGGCTCTGTCAGTGCAGATCTGATATGATTTAATTTTATTTTATA 1728

RESULT 7  
US-08-229-781-49  
Sequence 49, Application US/08229781  
Patent No. 5589174  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Menderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/229,781  
FILING DATE: April 19, 1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1135 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cdna to genomic RNA  
HYPOTHETICAL:  
ANTI-SENSE:



LENGTH: 1135 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cdna to genomic RNA  
ORIGINAL SOURCE:  
ORGANISM: A/Okuda/57  
US-08-630-918-49

Query Match 51 0% Score 908.8; DB 1; Length 1135;  
Best Local Similarity 98 7% Pred. No. 2.8e-263;  
Matches 916; Conservativ 0; Mismatches 12; Indels 0; Gaps 0;

QY 853 AAAAAATCGAAGAGGAGTACATGAGAAACAGAGAGAGACACTTGAGAACTGT 912  
DB 208 AAGTTATGCAACACAAAGGATCCGGGATCATGAAAACAGAGAGACACTTGAACTGT 267  
QY 913 GAGACCAAAATGCCAACTCCTTTGGAGCAATAAATCAACATTACCTTTTACAAATGTC 972  
DB 268 GAGACCAAAATGCCAACTCCTTTGGAGCAATAAATCAACATTACCTTTTACAAATGTC 327  
QY 973 CACCCACTGACAAATAGTAGAGTGCCTCCCAATATGTAATCGGAGAGTTGCTTAGCA 1032  
DB 328 CACCCACTGACAAATAGTAGAGTGCCTCCCAATATGTAATCGGAGAGTTGCTTAGCA 387  
QY 1033 ACAGACTAAGGAATGTTCCCAAGATTGAATCAAGAGAGATTGTTGGGCAATAGCTGCT 1092  
DB 388 ACAGACTAAGGAATGTTCCCAAGATTGAATCAAGAGAGATTGTTGGGCAATAGCTGCT 447  
QY 1093 TTTTATAGAGAGAGATGGCAAGAAATGTTGACGGTTGTATGATACCATCAGACAAT 1152  
DB 448 TTTTATAGAGAGAGATGGCAAGAAATGTTGACGGTTGTATGATACCATCAGACAAT 507  
QY 1153 GACCAAGGATCAGGTTATGACGACAGACAAGAAATCCACTCAAAAGGCAATTGATGATC 1212  
DB 508 GACCAAGGATCAGGTTATGACGACAGACAAGAAATCCACTCAAAAGGCAATTGATGATC 567  
QY 1213 ACCAACAAGGTAAATTCCTGATTTGAAAGATAAACCACCAATTTGAAGCTGTTGGGAAA 1272  
DB 568 ACCAACAAGGTAAATTCCTGATTTGAAAGATAAACCACCAATTTGAAGCTGTTGGGAAA 627  
QY 1273 GAATTCGGTAACCTTNGAGAAAAGACTGAGACACTTGAACAAAAAGATGGAAGCGGTTT 1332  
DB 628 GAATTCGGTAACCTTNGAGAAAAGACTGAGACACTTGAACAAAAAGATGGAAGCGGTTT 687  
QY 1333 CTAGATGTGGGAATATCAATGCTGACCTTTTAGTTGATGGAATGAGAGACACTT 1392  
DB 688 CTAGATGTGGGAATATCAATGCTGACCTTTTAGTTGATGGAATGAGAGACACTT 747  
QY 1393 GACTTTCATGATTCCTAATGTCAGAAATCTGATAGTAAGTCAGAAATGAGCTGAGAGAC 1452  
DB 748 GACTTTCATGATTCCTAATGTCAGAAATCTGATAGTAAGTCAGAAATGAGCTGAGAGAC 807  
QY 1453 AACGTCAAAGACTAGGAAAATGATGTTTGAATTTTATCACAATGTGATGATGAATGC 1512  
DB 808 AACGTCAAAGACTAGGAAAATGATGTTTGAATTTTATCACAATGTGATGATGAATGC 867  
QY 1513 ATGAATGTGTGAATAAAGGGAGCATATGATTATCCCAAGATGAGAAGAGCTTAAACTA 1572  
DB 868 ATGAATGTGTGAATAAAGGGAGCATATGATTATCCCAAGATGAGAAGAGCTTAAACTA 927  
QY 1573 AATGAATGAATAAACAAGGGGTAAATATGAGCAGATGGGGGTTTATCAAACTCTTCC 1632  
DB 928 AATGAATGAATAAACAAGGGGTAAATATGAGCAGATGGGGGTTTATCAAACTCTTCC 987  
QY 1633 ATTATATCTACAGTAGAGAGTTCTATGTCACCTGGCAATCATGATGCTGGATCTCTTTC 1692  
DB 988 ATTATATCTACAGTAGAGAGTTCTATGTCACCTGGCAATCATGATGCTGGATCTCTTTC 1047  
QY 1693 TGGGTGTCATCCATCGGGTCTCTGACAGTGCAGATGTCATGATGATATAGCATTTTA 1752  
DB 1048 TGGGTGTCATCCATCGGGTCTCTGACAGTGCAGATGTCATGATGATATAGCATTTTA 1107

QY 1753 TAATTAATAACACCCCTGTGTTCTGCTAG 1780  
DB 1108 TAATTAATAACACCCCTGTGTTCTGCTAG 1135

RESULT 9  
US-09-004-422-49  
Sequence 49, Application US/09004422  
Patent No. 6337070  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Menderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/004,422  
FILING DATE: January 8, 1998  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1135 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cdna to genomic RNA  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: A/Okuda/57  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
ORGANELLER:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:

UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-09-004-422-49

Query Match 51.0%; Score 908.8; DB 4; Length 1135;  
Best Local Similarity 98.7%; Pred. No. 2.8e-263;  
Matches 916; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
QY 853 AAATATCGAAAGAGGTAGTTCAGGATCATGAAACAGAGAGACACTTGAGACTGT 912  
DB 208 AAGTTATGCAAACTAAACGATCCGGATCATGAAACAGAGAGACACTTGAGACTGT 267  
QY 913 GAGACCAATGCCAACTCCTTTGGAGCAATAATCAACATTCCTTTTCAACATGTC 972  
DB 268 GAGACCAATGCCAACTCCTTTGGAGCAATAATCAACATTCCTTTTCAACATGTC 327  
QY 973 CACCCCTGACATAGTGTGATGTCGCCCAATATGTAATAATGCGAGAGAGTTGGTCTAGCA 1032  
DB 328 CACCCCTGACATAGTGTGATGTCGCCCAATATGTAATAATGCGAGAGAGTTGGTCTAGCA 387  
QY 1033 ACAGGACTAGAGATGTTCCCGAGATTGATCAAGAGAGTTGGGGCAATGCTGT 1092  
DB 388 ACAGGACTAGAGATGTTCCCGAGATTGATCAAGAGAGTTGGGGCAATGCTGT 447  
QY 1093 TTTTATGAAGAGAGATGCGAAGAGATGTTGACGGTTGTATGATACATCACAGCAAT 1152  
DB 448 TTTTATGAAGAGAGATGCGAAGAGATGTTGACGGTTGTATGATACATCACAGCAAT 507  
QY 1153 GACCGAGGATCGAGGATGTCAGAGCAAGAAATCCACTCAAAAAGCATTTGATGATC 1212  
DB 508 GACCGAGGATCGAGGATGTCAGAGCAAGAAATCCACTCAAAAAGCATTTGATGATC 567  
QY 1213 ACCAACAGGTAATCTGTGATTGAAAGATTAACACCCATTTGAGCTGTGGGAA 1272  
DB 568 ACCAACAGGTAATCTGTGATTGAAAGATTAACACCCATTTGAGCTGTGGGAA 627  
QY 1273 GAATTCGTAATCTGAGAGAAAGACTGGAACCTTGACAAAAGATGGAAGCGGTTT 1332  
DB 628 GAATTCGTAATCTGAGAGAAAGACTGGAACCTTGACAAAAGATGGAAGCGGTTT 687  
QY 1333 CTAGATGCTGACATATGATGCTGCTGCTTTAGTTAGTTCTGATGAGAAATGAGAGACATT 1392  
DB 688 CTAGATGCTGACATATGATGCTGCTGCTTTAGTTAGTTCTGATGAGAAATGAGAGACATT 747  
QY 1393 GACTTTCATGATTCTAATGTCAAGAACTGTATAGTAAAGTCAAGTGCAGCTGAGAGAC 1452  
DB 748 GACTTTCATGATTCTAATGTCAAGAACTGTATAGTAAAGTCAAGTGCAGCTGAGAGAC 807  
QY 1453 AAGCTCAAGAACTGAGAAATGATGTTTGAATTTTATCACAATGTGATGATGATGC 1512  
DB 808 AAGCTCAAGAACTGAGAAATGATGTTTGAATTTTATCACAATGTGATGATGATGC 867  
QY 1513 ATGATAGTGTGAAAAAGCGGATATGATGTTATCCCAATATGAGAGAGTCTTAACATA 1572  
DB 868 ATGATAGTGTGAAAAAGCGGATATGATGTTATCCCAATATGAGAGAGTCTTAACATA 927  
QY 1573 AATGAAATGAATCAAAAGGGGTAAATATGACAGCATGGGGTTTATCAAAATCCTTGGC 1632

DB 928 AATGAAATGAATCAAAAGGGGTAAATATGACAGCATGGGGTTTATCAAAATCCTTGGC 987  
QY 1633 ATTATGCTACAGAGAGGTTCTATGCTGCTGCACTGCATCATGATGGTGGATCTCTTC 1692  
DB 988 ATTATGCTACAGAGAGGTTCTATGCTGCTGCACTGCATCATGATGGTGGATCTCTTC 1047  
QY 1693 TGGGTGCTCCCAAGGGGTCCTCTGACAGATGATGATGATGATGATGATGATGATGAT 1752  
DB 1048 TGGGTGCTCCCAAGGGGTCCTCTGACAGATGATGATGATGATGATGATGATGATGAT 1107  
QY 1753 TAATTAACACCCCTGTTCTGCTAG 1780  
DB 1108 TAATTAACACCCCTGTTCTGCTAG 1135

RESULT 10  
US-09-232-468A-13  
Sequence 13, Application US/09232468A  
Patent No. 6207165  
GENERAL INFORMATION:  
APPLICANT: AUDONNET et al.  
TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE FORMULA AGAINST PORCINE  
FILE REFERENCE: 454313-2230  
CURRENT APPLICATION NUMBER: US/09/232.468A  
CURRENT FILING DATE: 1999-01-05  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 1701  
TYPE: DNA  
ORGANISM: Porcine Flu Virus (SIV, H1N1 "Sw" strain)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1698)  
US-09-232-468A-13

Query Match 41.2%; Score 734; DB 3; Length 1701;  
Best Local Similarity 65.5%; Pred. No. 1.3e-210;  
Matches 1092; Conservative 0; Mismatches 570; Indels 6; Gaps 1;  
QY 76 TTCACAGCAGTGTAGAGGGGACAGATATGATGATGATGATGATGATGATGATGATGAT 135  
DB 34 TTCACAGCAGTGTAGAGGGGACAGATATGATGATGATGATGATGATGATGATGATGAT 93  
QY 136 AAGTGACACATTTCTAGAGGAGAGGACGTCATGTCATGATGATGATGATGATGATGAT 195  
DB 94 ACTGTGACACATTTCTAGAGGAGAGGACGTCATGTCATGATGATGATGATGATGATGAT 153  
QY 196 AAGACCCATTAACGAAAGTTATGCAAACTAAACGGAATCCCTGCACTGAACTAGGGAGC 255  
DB 154 AAGACCCATTAACGAAAGTTATGCAAACTAAACGGAATCCCTGCACTGAACTAGGGAGC 213  
QY 256 TGTAGCATTCGCGAGATGCTCCTTGGAAATCCAAATGTGATAGGCTTTCTAGTGTCCA 315  
DB 214 TGTAGCATTCGCGAGATGCTCCTTGGAAATCCAAATGTGATAGGCTTTCTAGTGTCCA 273  
QY 316 GAAGGCTCTATATATGAGAAAGAAACCCGAGAGAGCGTTTGTATTCACAGGACGC 375  
DB 274 TCATGCTCTTACATATATGAGAACTTCAAAATGGAAGAACTGCTACCCGGAGAA 333  
QY 376 TTCATGATTAAGAAATGGAAGATGCAATCTCTCAGCAGCGTGAACATTTGAGAGAGTA 435  
DB 334 TTCATGATTAAGAAATGGAAGATGCAATCTCTCAGCAGCGTGAACATTTGAGAGAGTT 393  
QY 436 AAGATTTCTCCCAAGAGTA-----GATGACACGATATACAACTGAGAGTTCAACGG 489  
DB 394 AAGATTTCTCCCAAGAGTA-----GATGACACGATATACAACTGAGAGTTCAACGG 453  
QY 490 GCCTGGCGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 549  
DB 454 GCATGCTCTTACTGTGAAACCCCGAGTTTATGAGAAATTTGATGATGATGATGATGATGAT 513



QY 550 GATCAGATATATCCGTTGGCCAAAGATCGTACAAATACAGCGGAGAAACAATGCTA 609  
DB 514 GAAATATTCATCTCTAACTCAGCAATTCATACCAACAACAAGGAAAGAAAGTCTT 573  
QY 610 ATAAATTTGGGGGGTGCACCATCCCATTTGATGAGACAGACAAAGAACATTTGTACCAAT 669  
DB 574 ATATCTTGGGGAGTGCACCAACCCCTCAACTACCAATGACCAAAACCTCTATACGAAT 633  
QY 670 GTGGAGACCTATGTTCCGTAGGACATCAACATTTGAACAAAGTCAACCCCAAGATA 729  
DB 634 GCTGATCATATATGTTTGTAGTTGGTCTCATCAAAATACACGGAAGTTTCACACGAAGATA 693  
QY 730 GCAACAGGCTTAATATGATGAGAGAGTGAATGGAATCTCTTGACCCCTTGT 789  
DB 694 GCAGCTGACCTTAATATCAAGAGACAGACGAGATGATTAATTTTGTGACATTTGTA 753  
QY 790 GATATGTGGACACCATTAATTTTGAAGATGATGTAATCTAATTTGCACAGATATGA 849  
DB 754 GATCAAGAGACACCATTAAGCTTTGAAGCCATGGAATTAATAGCACCATGATGAGCC 813  
QY 850 TTCAAAATATCGAATAGATGATTCAGGATCATGAAAACAGAGAACACTTGAAC 909  
DB 814 TTGCAATGTAATAGGCTCTGTGTTGGAATTAACGTCGATCTCGGTTCAAT 873  
QY 910 TGTGAGACCAAAATGCCAACTCCTTTGGGAGCAATTAATCAACATTAATTTTCAAT 969  
DB 874 TGTGATGCAAAATGTCAAACCCCTCATGGGGCTTGAACGATGCTCTCTTTTCAACAC 933  
QY 970 GTCCACCCACTGACATAGTGTAGTGTGAGTGTGATTAATGAGAGAAATGCTGCTTA 1029  
DB 934 GTTCAATCCCATCTACTTTGAGAGATGCCCAATATGTTAAAGACCAACATCGAATG 993  
QY 1030 GCAACAGGACTAAGGATGTTCCCAAGATGATCAAGAGAGATGTTGGGGCAATAGCT 1089  
DB 994 GCACAGGACTAAGGAGACGTCCTCTATTCATTCACAGAGACTTTTGCAGCAATGCT 1053  
QY 1090 GGTTTTATAGAGGTCGATGAGCAAGAAATGTTGAGTGTGATGATTCATCAGAC 1149  
DB 1054 GGAATTCATTAAGGTCGATGAGCAAGAAATGATGATGATGATGATGATGATGATGATG 1113  
QY 1150 AATGACAGGATCTGAGTGTGACAGACAAAGAAATCACTCAAAAGCAATTTGATGA 1209  
DB 1114 AATGAGCAGGATCTGAGTGTGACAGACAAAGAAATCACTCAAAAGCAATTTGATGA 1173  
QY 1210 ATACCAACAAGGTAAATCTGTGATGTAAGAAATACCAACCAATTTGAAGCTGTGG 1269  
DB 1174 ATGAGCAACAAGGTAAATCTGTGATGTAAGAAATACCAACCAATTTGATGAAGCTGTGG 1233  
QY 1270 AAGAAATTCGATTAATGAGAAAGAAAGCTGAGAACTTGAACAAAAGATGGAAGAGGG 1329  
DB 1234 AAGAAATTCATTAATGAGAAAGAAAGATGAGAAATTTGAATTAAGAAAGCTGATGAGGG 1293  
QY 1330 TTTCTGATGATGTCACATCAATGCTGAGCTTTTGAATGATGAGAAATGAGAGACA 1389  
DB 1294 TTTTGTGATGTTGTCATTAATGCTGAGTGTGCTGTCGAGAAAGCAAGTGTG 1353  
QY 1390 CTGACCTTATGATGTCATTAATGCTGATGATGATGATGATGATGATGATGATGATG 1449  
DB 1354 CTGATATTTCCATGCTTTTAAGCTAAGAAATTTAATGAAGGTCAGTCAATGATGAGA 1413  
QY 1450 GACACGCTCAAGAACTGAGAAATGATGTTTGAATTTTATCAAAATTTGATGATGAA 1509  
DB 1414 AACAAATGCCAAAGATACGGGAATGTTGTTGAGTCTATCACAAAATTTGATGAGAA 1473  
QY 1510 TGCATGATATGTTGTAAGAAAGGAGACATGATTAATCCCAAGATGAGAGAGTCTAAA 1569  
DB 1474 TGCATGAGAGGCTTAAGAAATGACATTAATTAATCCCAAAATTTGAGAGATGAGAA 1533  
QY 1570 CTAAATAGAAATGATCAAAAGGAGTAAATGAGACGATGAGGAGTGTTCATTAATCTT 1629  
DB 1534 TTGAATAGAGAGATAGAGGAGTGTAACTGATGATCAATGAGGAGTGTACAGATTTTG 1593

QY 1630 GCCATTTATGCTACAGTAGCAGGTTCTATGTCATCGCAATCATGATGAGGCTGATCT 1689  
DB 1594 GCGATTAATGCTACAGTAGCAGGAGTTCCTGCTGTTAGTCTCCGGGGCAATGAGC 1653  
QY 1690 TTCTGGGTGTCTCCAAAGGCTCTCTGACAGTGCAGGATTCGATATGA 1737  
DB 1654 TTCTGATGCTGCTTAATGAGTGTATGTCATGCAATGCAAGATATGCAATTTAA 1701

RESULT 11  
US-09-784-984B-11  
; Sequence 11, Application US/09784984B  
; Patent No. 6576243  
; GENERAL INFORMATION:  
; APPLICANT: Merital Ltd.  
; APPLICANT: Audomnet, Jean-Christophe  
; APPLICANT: Bouchardon, Annabelle  
; APPLICANT: Baudou, Philippe  
; APPLICANT: Riviere, Michael  
; TITLE OF INVENTION: Polynucleotide Vaccine Formula Against Porcine Reproductive an  
; TITLE OF INVENTION: Respiratory Pathologies  
; FILE REFERENCE: 454313-2230.1  
; CURRENT APPLICATION NUMBER: US/09/784,984B  
; PRIOR FILING DATE: 2001-02-16  
; PRIOR APPLICATION NUMBER: FR 96/09338  
; PRIOR FILING DATE: 1996-07-19  
; PRIOR APPLICATION NUMBER: PCT/FR97/01313  
; PRIOR FILING DATE: 1997-07-15  
; PRIOR APPLICATION NUMBER: US 6,207,165  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 1701  
; TYPE: DNA  
; ORGANISM: Porcine Flu Virus (SIV, HINI "SW" Strain  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1698)  
; OTHER INFORMATION:  
US-09-784-984B-11

Query Match 41.2%; Score 734; DB 4; Length 1701;  
Best Local Similarity 65.5%; Pred. No. 1.3e-210;  
Matches 1092; Conservative 0; Mismatches 570; Indels 6; Gaps 1;

QY 76 TTCACAGCAGTGAAGGGGACCAAGATATGATGATGATGATGATGATGATGATGATGATGAT 135  
DB 34 TTCACGCTGCTGAAGCTGACACCATCTGTGATGATGATGATGATGATGATGATGATGATGAT 93  
QY 136 AAGTGTGACCAATTTCTAGAGCGGAACGTGACGTGATGATGATGATGATGATGATGATGATGAT 195  
DB 94 ACTGTGACCAATTAATCTGAGAGAAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 153  
QY 196 AAGACCATTAACGGAAGTATGCAAACTAAAGGAATCCCTCCTCACTTGAAGTGAAGGAG 255  
DB 154 AACAGTCATATATGAGAAACCTGACAGCTGAATGATGATGATGATGATGATGATGATGATGATG 213  
QY 256 TGTAGCAATTCGCGAGTGTCTTGAATATCAAAATGATGATGATGATGATGATGATGATGATG 315  
DB 214 TGCACGCTAGCAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 273  
QY 316 GAAAGGTCCTATATTTGAGAGAAAGAAACCCGAGAGAGGTTGTTGATTCAGAGCAGC 375  
DB 274 TCATGCTCTTCAATATAGAGACTTCAATATTCAGAAATGGAACATGCTACCCCGAGAA 333  
QY 376 TTCAATGATTAAGATATGAAACATCTCTCAGCAGCAGCTGAACATTTTCGAGAAAGTA 435  
DB 334 TTCAATGATTAATGAGATTAAGAGAGCAGCAGCTGATGATGATGATGATGATGATGATGATG 393  
QY 436 AAGATTCCTGCCAAAGATA-----GATGACACACAGCATCAACAACACTGAGGTTCAAGC 489  
DB 394 GAAATTTTCCCAAAAGCAACTGATGAGCCAAATCATGATGAGCAACAAGGATATTAACAGCT 453



Db 523 GGAATTCATACCCAAAGCTCAGCAAAATCCATATATTAACAAATAGAGAAAGAGTCCCTC 582  
QY 610 ATATTTGGGGGGTCCACCATCCATGATGAGACAGCAAAACAAATTTTACCAGAT 669  
Db 583 GTGCTATGGGGCATTCACCATCCACCTACAGTACTGCTACCAACAAAGTCTCTACAGAT 642  
QY 670 GTGGGAACCTATGTTCCGTAGGACATCAACATTTGAACAAAGTCAACCCCAAAATA 729  
Db 643 GCAATGCTCTATGTTTGTGGGGTCAATCAAAATACAAAGAAATTCAGCCAGAAATA 702  
QY 730 GCAACAAGGCTTAATGTGAATGCAAGAAGAGTGAATGAATTCCTTTGGACCCCTCTG 789  
Db 703 GCAACAGAGCCCAAGTGAAGAGTCAAGCAGAGAGAAATGAATCTTACTGAGCCCTAGTA 762  
QY 790 GATATGGGACAGATTAATTTGAGAGTACTGTGTAATCTTAATTCACCCAGATTAAGA 849  
Db 763 AAGCTTGAGACACATACATTAATTCAGCAACTGGAATCTAGGGTTCAGAAATATGCC 822  
QY 850 TTCAAAATATCGAAAGAGGTAGTTCAGGGATCATGAACAGAGAGACACTTGAGAAC 909  
Db 823 TTCCCATGAAAGAGGTTCGATCTGATTTATTCATTTTCAGATACACCACTCCAGAT 882  
QY 910 TGTGAGACCAATATCAACTCTTTGGGAGCAATTAATACACATTACTTTTCAAT 969  
Db 883 TGTATATGAGCTTGCACACACCCAAAGGTCTATTAACACACCCTTCCATTCAGAAAT 942  
QY 970 GTCCACCACCTGACAAATAGGTGAGTGGCCCCAAATATGTAAATGCGAAGTTGGTCTTA 1029  
Db 943 ATACATCCAGTACATATTTGGAATGTCCAAATATGTCAAAACACAAATTTAGATG 1002  
QY 1030 GCAACAGGACTAGAAATGTTCCCAATTTGGAATCAAGAGATGTTTGGGGCAATAGCT 1089  
Db 1003 GCTACAGAGATTAAGAAATATCCCTATTCATCTAGAGCCGCTTTGGAGCCATTTGCT 1062  
QY 1090 GGTTTATAGAGAGAGTGCAGAGATGTTACGTTGCTTGTGATACATCAACAGC 1149  
Db 1063 GGGCTTTATGAGGGTGAAGTGCAGAGATGATGATGCTGGTATACCATCAG 1122  
QY 1150 AATGACAGGAGATGAGGTATGACAGACAAAGATCCACTCAAAAGGCAATTTGATGGA 1209  
Db 1123 AATAGAGAGGATGAGATATGACGCCAGCCAGAAAGACACAAATGCAATTTGACGGC 1182  
QY 1210 ATCAACAAGATGTAATTTCTGTGATTTGAAGAATAACCCCAATTTGAAGTGTGGG 1269  
Db 1183 ATCACTAACAAGTAATCTGTGATTTGAAGAATAACACACATTCACAGCAGTGGGT 1242  
QY 1270 AAAAATTCGGTAATCTTAGAGAAAAGCTGAGACATTTGAACAAAAGATGGAAGCGG 1329  
Db 1243 AAAAATTCACCCCTGGAAGAAAAGATGAGAAATTTAAACAAAAGGTTGATGATGCT 1302  
QY 1330 TTTCTAGATGTTGACATACATGCTGAGCTTTAGTCTGATGGAAGAAATGAGAGACA 1389  
Db 1303 TTTCTGATGTTTGSACTTACATATGCCGAATGTTGGTCTGATTTGAAAGAAAGAACT 1362  
QY 1390 CTTCAGCTTTCATGTTCTAATGTCAGAAATCTGTATAGTAAGTCAGAAATGCACCTGAGA 1449  
Db 1363 TTGGATTTATCAGCTTCAAAATGTGAAGACCTATATGAGAAAGTAAGAGACACTAAA 1422  
QY 1450 GACAACTCAAAAGTACTAGAGAAATGATGTTTAAATTTATCAAAATGTGATGAGAA 1509  
Db 1423 AACATGCCAAGGAATTTGAAATGGCTGCTTGAATTTTACCCAATGTGATGAGACGC 1482  
QY 1510 TGCATGATAGTGTGAAGAAAGGACATATGATTTCCCAAGTATGAAGAAAGATCTAAA 1569  
Db 1483 TGCATGAGAGCGCTCAAAATGGAGCTTATGATTAACCCAAATATCTAGAGAGAAAGAAA 1542  
QY 1570 CTAATATGAATGTAATCAAGGGGTAAATTTGAGACAGATGGGGGTTTATCAAAATCCTT 1629  
Db 1543 CTAACAGAGAGGATGATGATGGGTAAGCTGGAATCAACAGATTTTACCAATTTTG 1602  
QY 1630 GCCATTTATGCTAATAGTAGAGGTTCTATGCTCATGCGCAATCATGATGGCTGAGTCTCT 1689  
Db 1603 GCGATTTATCAATTTGCGCAGATTCTCATTTGCTACTGTTAGTCTCCCTGGGGGCAATCAGT 1662

QY 1690 TTCTGGGTGCTCCCAAGGGTCTCTGCACTGAGAGATCTCATATGATTATAG 1744  
Db 1663 TTCTGATGTGCTCAATGGGTCTTTACAGTGCAGAAATGTATTTAAATTAG 1717

RESULT 13  
US-08-453-848-8  
Sequence 8, Application US/08453848  
Patent No. 5853368  
GENERAL INFORMATION:  
APPLICANT: Smith, Gale Eugene  
APPLICANT: Volovitz, Franklin  
APPLICANT: Wilkinson, Bethanie Elident  
APPLICANT: Voznesensky, Andrei I.  
APPLICANT: Hackett, Craig Stanway  
TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/453,848  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/120,607  
FILING DATE: 13-SEPT-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: MGS101CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-873-8794  
TELEFAX: (404)-873-8795  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1766 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Influenza virus  
INDIVIDUAL ISOLATE: A/Texas/36/91 rHA  
FEATURE:  
NAME/KEY: polyhedrin mRNA leader (partial)  
LOCATION: 1 to 18  
FEATURE:  
NAME/KEY: coding region for AcNPV 61k protein signal  
NAME/KEY: peptide  
LOCATION: 19 to 72  
FEATURE:  
NAME/KEY: SmaI restriction site  
LOCATION: 76 to 81  
FEATURE:  
NAME/KEY: KpnI restriction site  
LOCATION: 82 to 87  
FEATURE:



1	CORRESPONDENCE ADDRESS:	
2	ADDRESSEE: Patricia L. Pabst	
3	STREET: 2800 One Atlantic Center	
4	STREET: 1201 West Peachtree Street	
5	CITY: Atlanta	
6	STATE: GA	
7	COUNTRY: USA	
8	ZIP: 30309-3450	
9	COMPUTER READABLE FORM:	
10	MEDIUM TYPE: Floppy disk	
11	COMPUTER: IBM PC compatible	
12	OPERATING SYSTEM: PC-DOS/MS-DOS	
13	SOFTWARE: Patentin Release #1.0, Version #1.25	
14	CURRENT APPLICATION DATA:	
15	APPLICATION NUMBER: US/09/169,027	
16	FILING DATE:	
17	CLASSIFICATION:	
18	PRIOR APPLICATION DATA:	
19	APPLICATION NUMBER: US/08/453,848	
20	FILING DATE: 30-MAY-1995	
21	APPLICATION NUMBER: 08/120,607	
22	FILING DATE: 13-SEPT-1993	
23	ATTORNEY/AGENT INFORMATION:	
24	NAME: Pabst, Patricia L.	
25	REGISTRATION NUMBER: 31,284	
26	REFERENCE/DOCKET NUMBER: MGS101CIP	
27	TELECOMMUNICATION INFORMATION:	
28	TELEPHONE: (404)-873-8794	
29	TELEFAX: (404)-873-8795	
30	INFORMATION FOR SEO ID NO: 8:	
31	SEQUENCE CHARACTERISTICS:	
32	LENGTH: 1766 base pairs	
33	TYPE: nucleic acid	
34	STRANDEDNESS: single	
35	TOPOLOGY: linear	
36	MOLECULE TYPE: DNA (genomic)	
37	HYPOTHETICAL: NO	
38	ANTI-SENSE: NO	
39	ORIGINAL SOURCE:	
40	ORGANISM: Influenza Virus	
41	INDIVIDUAL ISOLATE: A/Texas/36/91 rHA	
42	FEATURE:	
43	NAME/KEY: polyhedrin mRNA leader (partial)	
44	LOCATION: 1 to 18	
45	FEATURE:	
46	NAME/KEY: coding region for AcNPV 61k protein signal	
47	NAME/KEY: peptide	
48	LOCATION: 19 to 72	
49	FEATURE:	
50	NAME/KEY: SmaI restriction site	
51	LOCATION: 76 to 81	
52	FEATURE:	
53	NAME/KEY: KpnI restriction site	
54	LOCATION: 82 to 87	
55	FEATURE:	
56	NAME/KEY: SmaI restriction site	
57	LOCATION: 88 to 93	
58	FEATURE:	
59	NAME/KEY: coding region for mature rHA	
60	LOCATION: 73 to 1734	
61	FEATURE:	
62	NAME/KEY: KpnI restriction site	
63	LOCATION: 1744 to 1749	
64	FEATURE:	
65	NAME/KEY: BglII restriction site	
66	LOCATION: 1750 to 1755	
67	FEATURE:	
68	NAME/KEY: universal translation termination signal	
69	LOCATION: 1756 to 1765	
70	US-09-169-027-8	

	Matches	1069:	Conservative	0:	Mismatches	578:	Indels	6:	Gaps	1:
QY	91	GGGACCAAGATATG	ATG	CGATTGGAT	ACC	ATG	CCCAATTAATTC	ACAGAGAGAGAG	GTGCACACAAT	150
Db	91	GGGACCAAGATATG	ATG	ATGAGCGCT	ACC	ATG	CCCAATTAATTC	ACAGAGAGAGAG	GTGCACACAAT	150
QY	151	CTGAGGGGAAGCTG	AC	TGCTGCTCAT	CGCAAG	GCATCT	CTTGAGACAC	CCATTAAGCGA		210
Db	151	CTTGAGAGAAAGT	AC	GTGACAGT	CAAC	CTGCTT	GTGAGAGAC	GTGACACGGA		210
QY	211	AAGTTAAACAAC	CT	TAACGGAAT	CCCT	CTCACTT	GTAGCA	TAGGGGAGAT	GTAGCATTTGCCGGA	270
Db	211	AAACATATGCGAT	CT	TAAGGGAAT	ACC	CCCACT	ACATATG	GGGTAAT	TGCAAGCTTCCCGGA	270
QY	271	TGGCTCTTGGAA	AT	CCAAATGT	AGCCT	CTTAAGT	GTGCCGAAG	AGCGTCTTATATTA		330
Db	271	TGGATCTTGGAA	AT	CCAAATGT	AGCCT	CTTAAGT	GTGCCGAAG	AGCGTCTTATATTA		330
QY	331	TTGAGGAAGAA	AA	ACCCGAGAG	ACG	GTGTGTTAT	TCAGCAG	CGCTTCAATGATATATGA		390
Db	331	GCAGAAACCA	AA	ACCCGAGAG	ATG	GAACATGT	TATACCA	CGGATATTTGCGCGACATATAG		390
QY	391	GAATTGAACA	AT	CTCTCAG	ACG	CTGTAACA	ATTTGCGAA	AGTAATTAATCTCGCCAAA		450
Db	391	GAACGTAGAGG	AG	CAATTTAG	ATG	ATCATCAT	TTGCGAG	AGATTTGGAATATATTC	CCCAAA	450
QY	451	GATAGAT-----		GGACACAG	CA	TACAACA	CTGAG	AGGTTCACGGGCGCTCGCGGTCTCT		504
Db	451	GAACACTCAT	GG	CCCAAC	CA	CCGTAACCA	AGAGTA	ACAGAGATCATGCTCCCATATAT		510
QY	505	GGTATTCATCAT	TT	TTTTCAG	AGACAT	GTGTGCTG	ACAAAGGA	AGAGATTCAGATATATTCG		564
Db	511	GGGAAAGAC	AG	ATTTTAC	AGAAATTTG	CTATG	GTGCGAG	AGAGAAATAGCTGTGTACCCA		570
QY	565	GTGGCCAAAG	AG	TGCTTAC	ACA	AAATTC	CAAGCGAG	ACAATTCATATTTGGGGGGTG		624
Db	571	AATCTGACAA	AG	TCTTATG	TAAAC	CACAAAGAA	AGAAATG	CTTGTACTATGGGGTGT		630
QY	625	CACCATCCCAT	T	GATGAG	ACAGACA	MAAGAACAT	TGTACCA	GAATGTGGAACCATATGTT		684
Db	631	CATCACCCGT	T	TAACAT	TAAGG	GACCA	CCATCAT	CTATACAGAAATAGCTTATGTC		690
QY	665	TCCGTAGG	CA	CATCA	CACTTGA	CAACAAAG	GTCAACCC	CGAATATGCAACAAGGCTTAA		744
Db	691	TCTGTAGT	GT	CTTCA	CTTATAG	CGAGAA	GAATTCACCC	CGAATATGCAACAAGGCTTAA		750
QY	745	GTAATGGA	CA	AGG	GTGAAT	GAATTC	CTGAGAC	CCCTTGGAATATGTGGAGACCC		804
Db	751	GTAAAGAT	CA	TCAAGAG	GAATTA	TACTACT	GTGCTG	GAACCCGGGGACCA		810
QY	805	ATAAATTTG	AG	AGTACT	GTAAAT	CTAATTC	TACACAG	ATATGATTCGAATATATCGAA		864
Db	811	ATAAATTTG	AG	CAATAT	GAATAT	CTAATTC	TACACAG	ATATGATTCGAATATATCGAA		870
QY	865	AGAGTACT	TA	AGGATCAT	GA	AAACAG	AGAACTTG	GAACCTGTGAGACCAATATGC		924
Db	871	GGCTTTGGGT	CA	GCAGAT	CATCA	CTCAAC	CCATCAAT	GTGATGTGACGCAAGCTGT		930
QY	925	CAACCTCT	TT	GGGAGCA	ATAAT	AACA	CATTACT	CTTTCACAAATGCCACCCACTGCA		984
Db	931	CAAAACAC	CC	CAAGGG	GTAT	TAACAG	TAATGCT	CTTCTTCCAGAAATGTAACCCAGTCA		990
QY	985	ATAGTGAG	TG	ATGCTT	GAATAT	TAATAT	CGAGAGA	AGTTGGTCTTACAGCAACGAGACTAAG		1044
Db	991	ATAGAGAG	GT	ATGCTT	GAATAT	TAATAT	CGAGAGA	AGTTGGTCTTACAGCAACGAGACTAAG		1050
QY	1045	AATGTTCCCA	CA	GATTTGA	ATCAAG	AGATGTT	TTGGGGCA	ATATGCTGTTTATATGAACA		1104
Db	1051	AAACATCC	CA	TCATTCAT	CCAGAG	GGTTGTT	TGGAGC	CAATGGCCGGTTTCATGTGAAGG		1110
QY	1105	GGATGGCA	AG	GAATG	GTTCAG	CGTGTG	ATATAC	ATCAACAGCAATGACAGAGGATCA		1164
Db	1111	GGGTGAG	CA	TGAAT	GAATG	ATGATG	TTATAT	CAATCAATGAAGCAAGCAATCT		1170



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Db 874 TGTAAATACGACCTGTCAAAACCCCAAGGTCCTATAAACACCGACCTCCCATTTTCAGAAAT 933
QY 970 GTCCACCCACTGACAAATAGTAGTAGTGCCTCCCAATATGTAAATCGAGACGTGGTCTTA 1029
Db 934 ATACATCCAGTACAAATTTGGAGAAATGTCCAAATATGTCAAAAGTACAAATTTGAGAAATG 993
QY 1030 GCAACGAGTAAAGCAATGTTCCCGAGATTAATCAAGAGATGTTGGGGCAATAGCT 1089
Db 994 GCTACAGAGATTAAGCAATATCCCGTATCAATCTAGGGGCTGTTTGGAGCCATTGCT 1053
QY 1090 GGTTTTATAGAGAAATGATGGCAGAGAAATGTTGACGTTGGTATGATACCATCACAGC 1149
Db 1054 GGGTTTATGAGAGAGAGGTTGGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1113
QY 1150 AATGACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1209
Db 1114 AATGACGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1173
QY 1210 ATCAACCAAGGATTAATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1269
Db 1174 ATCACTAAACAAAGTAACTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1233
QY 1270 AAAGATTCGCTACTAGAGAAAGAGCTGAGAACTTGAACAAAGAGATGAGAGACGGG 1329
Db 1234 AAAGATTCGCTACTAGAGAAAGAGCTGAGAACTTGAACAAAGAGATGAGAGATGATGATGAT 1293
QY 1330 TTTCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1389
Db 1294 TTTCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1353
QY 1390 CTGACCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1449
Db 1354 TTGATTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1413
QY 1450 GACACGTCGAAAGAGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1509
Db 1414 AACATGCGCAAGGAAATTTGGAATGCTGCTTGAATTTTACCAAAATGATGATGATGATGAT 1473
QY 1510 TGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1569
Db 1474 TGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1533
QY 1570 CTAATATGAAATGAAATCAAAAGGGTAAATTTGAGACGATGAGGGGTTTATCAAAATCCTT 1629
Db 1534 CTAACACAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1593
QY 1630 GCCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1688
Db 1594 GCCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1653
QY 1689 TTTCTGGGTGCTCCATGAGGGTCTGACAGTGCAGAGATGATGATGATGATGATGATGATGATGAT 1744
Db 1654 TTTCTGGGTGCTCCATGAGGGTCTGACAGTGCAGAGATGATGATGATGATGATGATGATGATGAT 1709
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Search completed: August 10, 2003, 16:15:36  
Job time : 95.7435.secs

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/\*tag= e  
/product= Stem region of C-terminal domain

EP621339-A2.  
26-OCT-1994.  
20-APR-1994; 94EP-0302819.  
20-APR-1993; 93JP-0115216.  
16-MAR-1994; 94JP-0070194.  
(TAKI ) TAKARA SHUZO CO LTD.  
Isegawa Y, Okuno Y, Sasao F, Ueda S;  
WPI: 1994-325949/41.  
P-PSDB: AAR63588.  
Human influenza-A virus haemagglutinin polypeptide(s) - useful in  
Influenza-A vaccine composition  
Example 1; Page 45-49; 68pp; English.  
This sequence was amplified using the primer sequences given in  
AA072845-47 and it encodes the hemagglutinin (HA) gene of the H2N2  
subtype of human influenza A virus from A/Okuda/57. The protein encoded  
by the amplified cDNA contains two conserved regions, the A region, TGLRN  
and the B region, GTRNVNVIETK. These regions are close to each other in  
the stem of the HA molecule and they represent epitopes which are  
recognised by the antibody C179. C179 binds to the stem region of the HA  
molecule and thus inhibits the membrane fusion action of the HA molecule  
and neutralises the virus. Polypeptide molecules which contain the  
conserved peptide regions, A and B, esp. HA molecules lacking the  
globular head region, are antigenically equivalent to the stem region  
of the HA molecule of influenza A virus. These artificial peptides may  
be used as vaccines for prophylaxis of influenza A virus infection.  
(Updated on 25-MAR-2003 to correct PN field.)  
Sequence 1783 BP; 610 A; 323 C; 424 G; 426 T; 0 other;

Query Match 100.0%; Score 1783; DB 15; Length 1783;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGGCTGACAAAGAGGAGGTTATACATAGAAAACCAAGCAAAACCAATGCCATCAT 60  
1 CGGCTGACAAAGAGGAGGTTATACATAGAAAACCAAGCAAAACCAATGCCATCAT 60  
61 TATCTCATCTCTCTGTTACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120  
61 TATCTCATCTCTCTGTTACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120  
121 TATCTCATCTCTCTGTTACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120  
121 TATCTCATCTCTCTGTTACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120  
121 AATTAATTCACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
121 AATTAATTCACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
181 AAGGACATCTCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240  
181 AAGGACATCTCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240  
181 AAGGACATCTCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240  
241 CTTGAACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300  
241 CTTGAACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300  
301 CTTGAACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
301 CTTGAACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
361 TGTATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
361 TGTATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420

421 CATTTGAGAAAGTAAGATTCTGCCAAAGATAGATGAGACAGCATACAACTGGA 480  
421 CATTTGAGAAAGTAAGATTCTGCCAAAGATAGATGAGACAGCATACAACTGGA 480  
481 GGTTCACGGGCGCTGGCGGGTGTCTGTAATCATCATTTTTCAGGAACATGTCGCTG 540  
481 GGTTCACGGGCGCTGGCGGGTGTCTGTAATCATCATTTTTCAGGAACATGTCGCTG 540  
541 ACAAGGAGAGATCATGATTTATCCGGTTCGCAAGAGATGTCACCAATACAGCGGGA 600  
541 ACAAGGAGAGATCATGATTTATCCGGTTCGCAAGAGATGTCACCAATACAGCGGGA 600  
601 CAATGCTAATTAATTTGGGGGGTCCACCATTCATATGAGACAGAAACAAATG 660  
601 CAATGCTAATTAATTTGGGGGGTCCACCATTCATATGAGACAGAAACAAATG 660  
661 TACCAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
661 TACCAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
721 CCAGAAATAGCAAGAGGCTAAAGTGAATGAGACAGAGGAGGAGGAGGAGGAGGAGGAG 780  
721 CCAGAAATAGCAAGAGGCTAAAGTGAATGAGACAGAGGAGGAGGAGGAGGAGGAGGAG 780  
781 ACCCTCTTGATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
781 ACCCTCTTGATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
841 GAGTATGATTCATTAATATGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900  
841 GAGTATGATTCATTAATATGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900  
901 CTTGAGAACTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960  
901 CTTGAGAACTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960  
961 TTTGACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020  
961 TTTGACATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020  
1021 TTTGCTTTAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
1021 TTTGCTTTAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
1081 GCAATGATGCTGTTTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140  
1081 GCAATGATGCTGTTTATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140  
1141 CATCAGAGCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200  
1141 CATCAGAGCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200  
1201 TTTGATGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260  
1201 TTTGATGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260  
1261 GCTGTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320  
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1321 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380  
1321 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380  
1381 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440  
1381 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440  
1441 CAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500  
1441 CAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500  
1501 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560

|||||  
Db 1501 GATGATGAATGCAATGATAGTGTGAAAAACGGACGATATGATATATCCAGTATGAGAA 1560  
QY 1561 GAGCTAACTAAATGAATGAATCAAGGGGTAAATTTGAGCGATGGGGTTTAT 1620  
Db 1561 GAGCTAACTAAATGAATGAATCAAGGGGTAAATTTGAGCGATGGGGTTTAT 1620  
QY 1621 CAAATCCTTGCCTATTTATGCTACAGTAGCAGGTTCTATGCTACATGCAATCATGAGCT 1680  
Db 1621 CAAATCCTTGCCTATTTATGCTACAGTAGCAGGTTCTATGCTACATGCAATCATGAGCT 1680  
QY 1681 GGGATCTCTTCTGCTGCTGCTCAACGGGCTCTCTGCAATGCAATGATTA 1740  
Db 1681 GGGATCTCTTCTGCTGCTGCTCAACGGGCTCTCTGCAATGCAATGATTA 1740  
QY 1741 TAAATCTTTTATATTAATAAACAACCCCTGTTCTGCTAGCCG 1783  
Db 1741 TAAATCTTTTATATTAATAAACAACCCCTGTTCTGCTAGCCG 1783

## RESULT 2

AAD37057 standard; cDNA; 1773 BP.

AAD37057;  
21-AUG-2002 (first entry)

Influenza A virus/singapore/1/57/ca HA mutant cDNA.

Attenuated influenza vaccine; prophylactic; therapeutic; infection;  
virulence; gene; HA protein; mutant; ss.Influenza A virus.  
Synthetic.Key Location/Qualifiers  
CDS 44..1732  
FT /\*lag-2  
FT /product= "HA mutant protein"

W0200224876-A2.

28-MAR-2002.

25-SEP-2001; 2001MO-EP11087.

25-SEP-2000; 2000EP-0126896.

(POLY-) POLYMN SCI IMMLNOBIOLOGISCHE FORSCHUNG.

Katlinger H, Egorov A, Ferko B, Romanova J, Katlinger D;

WPI; 2002-416282/44.

P-PDB; AAE23111.

Manufacturing live vaccine, by infecting Vero cells with virus.  
PT combining cells with serum-free cell culture medium, incubating cells  
PT in presence of protease and nuclease, harvesting virus and preparing  
PT vaccine

Example 4; Page 41-42; 50pp; English.

The present invention relates to a method for isolating viruses from  
CC various sources and for producing live attenuated influenza vaccines from  
XX in a serum-free African green monkey kidney (Vero) cell culture under  
CC conditions where alterations in the surface antigens of the virus due  
CC to adaptive selection are minimised or prevented. The method is useful  
CC for the manufacture of whole-virus vaccine, preferably attenuated live  
CC vaccine. It is useful for prophylactic or therapeutic administration  
CC against viral infection, preferably influenza virus infections. The  
CC present sequence is Influenza A virus/singapore/1/57/ca (cold adapted)  
CC HA mutant cDNA. This sequence is used in the exemplification of the

CC Invention.

SQ Sequence 1773 BP; 611 A; 321 C; 417 G; 424 T; 0 other;

Query Match 96.7%; Score 1725; DB 24; Length 1773;

Best Local Similarity 98.3%; Pred. No. 0;

Matches 1743; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 6 AGCAAAAGCAGGGGTTATACATAGAAACCAAGCAAAACATGGCCATCTTTTCT 65  
Db 1 AGCAAAAGCAGGGGTTATACATAGACACACAGCAAAACATGGCCATCTTTTCT 60  
QY 66 CATTCCTCTTGCACAGCAGTAGAGGGGACAGATATGATTCATTCATGACATTA 125  
Db 61 CATTCCTCTTGCACAGCAGTAGAGGGGACAGATATGATTCATTCATGACATTA 120  
QY 126 TTCACACAGAGAGGTGCACAAATTTCTAGAGCGGACGTCAGTGTGATGCCAAGA 185  
Db 121 TTCACACAGAGAGGTGCACAAATTTCTAGAGCGGACGTCAGTGTGATGCCAAGA 180  
QY 186 CATCTCTGAGAGACCCATTAAGCGAAAGTATGCAAACTAAAGGAATCCCTCAGTTGA 245  
Db 181 CATCTCTGAGAGACCCATTAAGCGAAAGTATGCAAACTAAAGGAATCCCTCAGTTGA 240  
QY 246 ACTAGGGAGCTGTAGCATTTGCCGATGGCTCTTGGAAATCCAAATGTATAGGCTTCT 305  
Db 241 ACTAGGGAGCTGTAGCATTTGCCGATGGCTCTTGGAAATCCAAATGTATAGGCTTCT 300  
QY 306 AAGTGTGCCAAGACGCTCTATATATTGGAAGAAAGAAACCCGAGAGCGGTTGTGTTA 365  
Db 301 AAGTGTGCCAAGACGCTCTATATATTGGAAGAAAGAAACCCGAGAGCGGTTGTGTTA 360  
QY 366 TTCAGGAGCTTGAATGATATGAGAAATGGAACATCTCTGACAGCGCTGAAACATTT 425  
Db 361 TTCAGGAGCTTGAATGATATGAGAAATGGAACATCTCTGACAGCGCTGAAACATTT 420  
QY 426 CGAGAAAGTAAAGATTCCTGCCCAAGATAGATGAGACACACATCAACAATGGAGTTTC 485  
Db 421 CGAGAAAGTAAAGATTCCTGCCCAAGATAGATGAGACACACATCAACAATGGAGTTTC 480  
QY 486 ACGGGCGCTGGCGGTGTCTGTGTAATCCATATTTTCAGAGACATGCTGTGCTGACAAA 545  
Db 481 ACGGGCGCTGGCGGTGTCTGTGTAATCCATATTTTCAGAGACATGCTGTGCTGACAAA 540  
QY 546 GGAAGGATCGATATTCCTGCCCAAGATGATGTCACAAATCAACAGGGAGACAAAT 605  
Db 541 GGAAGGATCGATATTCCTGCCCAAGATGATGTCACAAATCAACAGGGAGACAAAT 600  
QY 606 GCTAATATTTGGGGGTGCACCATTCATTTGATGAGACAGAACAAACATTTGTACCA 665  
Db 601 GCTAATATTTGGGGGTGCACCATTCATTTGATGAGACAGAACAAACATTTGTACCA 660  
QY 666 GAATGTGGGAACCTATGTTTCCGTAGGACATCAACATTTGACAAAGGTCACCCAGCA 725  
Db 661 GAATGTGGGAACCTATGTTTCCGTAGGACATCAACATTTGACAAAGGTCACCCAGCA 720  
QY 726 AATAGCAACAGGCGCTAAGTGAATGAGAAAGAGAGATGAATGATTCCTTGAGCCCT 785  
Db 721 AATAGCAACAGGCGCTAAGTGAATGAGAAAGAGAGATGAATGATTCCTTGAGCCCT 780  
QY 786 CTGTGATATGTGGGACACCAATAATTTTGGAGTACTGTGAATCTAATTTGACACAGATGA 845  
Db 781 ATTGATATGTGGGACACCAATAATTTTGGAGTACTGTGAATCTAATTTGACACAGATGA 840  
QY 846 TGGATTCAAATATTCGAAAAGAGGTGTTCAGGATCATGAAAACAGAGAACTGTGA 905  
Db 841 TGGATTCAAATATTCGAAAAGAGGTGTTCAGGATCATGAAAACAGAGAACTGTGA 900  
QY 906 GAACGTGAGACCAAAATGCGCAACCTCTTGGAGAGCAATTAATCAACATTTACTCTTTCA 965  
Db 901 GAACGTGAGACCAAAATGCGCAACCTCTTGGAGAGCAATTAATCAACATTTACTCTTTCA 960  
QY 966 CAATGTCCACCCACTGACATAGTGAATGAGTCCCAATATATGTAAATCGGAGAGTTGGT 1025

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DB 961 CAATGTCACCCACTGACAAATAGTAGTCCCAATATGTAATCGAGAGTTGGT 1020
QY 1026 CTTAGCAACAGAGCTAGAGATNTGCCAGATTGAATCAAGAGATGTTGGGCAAT 1085
DB 1021 CTTAGCAACAGAGCTAGAGATNTGCCAGATTGAATCAAGAGATGTTGGGCAAT 1080
QY 1086 ACCTGCTTTTATAGAGAGATGGCAGGAATGTTGACGGTGTATGATACATCA 1145
DB 1081 ACCTGCTTTTATAGAGAGATGGCAGGAATGTTGATGTTGATGATACATCA 1140
QY 1146 CAGCAATGACACAGGATCAAGGATATCAGACACAAGAAATCCACTCAAAAGGCATTGA 1205
DB 1141 CAGCAATGACACAGGATCAAGGATATCAGACACAAGAAATCCACTCAAAAGGCATTGA 1200
QY 1206 TGGAAATCACCACAAAGTAAATCTGATGTTGAAAGATTAACACCATTGAACCTGT 1265
DB 1201 TGGAAATCACCACAAAGTAAATCTGATGTTGAAAGATTAACACCATTGAACCTGT 1260
QY 1266 TGGGAAAGAAATTCGGTAATCTAGAGAAAGACTGAGAACTTGAACAAAAGATGAGAGA 1325
DB 1261 TGGGAAAGAAATTCGGTAATCTAGAGAAAGACTGAGAACTTGAACAAAAGATGAGAGA 1320
QY 1326 CCGGTTTCTAGATGTGTGACATACATGCTGACCTTTTATGTTCTGATGAGAAATGAGAG 1385
DB 1321 CCGGTTTCTAGATGTGTGACATACATGCTGACCTTTTATGTTCTGATGAGAAATGAGAG 1380
QY 1386 GACACTTGACTTCAATGATTTCAATGTCAGAAATCTGTATAGTAAAGTCAGATGAGCT 1445
DB 1381 GACACTTGACTTCAATGATTTCAATGTCAGAAATCTGTATAGTAAAGTCAGATGAGCT 1440
QY 1446 GAGAGACAACGTCACAAAGAACTAGAGAAATGATGTTTGAATTTATCACAATGTGATGA 1505
DB 1441 GAGAGACAACGTCACAAAGAACTAGAGAAATGATGTTTGAATTTATCACAATGTGATGA 1500
QY 1506 TGAATGCATGATAGTGTAAGAAAGGACATATGTTATCCCAATATGAGAAAGATC 1565
DB 1501 TGAATGCATGATAGTGTAAGAAAGGACATATGTTATCCCAATATGAGAAAGATC 1560
QY 1566 TAAATTAATAGAAATGAAATCAAGGGGTAAATATGAGACAGCATGGGGTTTATCAAT 1625
DB 1561 TAAATTAATAGAAATGAAATCAAGGGGTAAATATGAGACAGCATGGGGTTTATCAAT 1620
QY 1626 CTTTCCCATTTATGCTACAGTAGACAGTCTATGTCACATGCGAATCATGATGCGGAT 1685
DB 1621 CTTTCCCATTTATGCTACAGTAGACAGTCTCTGTCACATGCGAATCATGATGCGGAT 1680
QY 1686 CTTTTCGGGTCCTCCACAGGGTCTGTCAGAGTCAGATCTGATATGATTAAGT 1745
DB 1681 CTTTTCGGGTCCTCCACAGGGTCTGTCAGAGTCAGATCTGATATGATTAAGT 1740
QY 1746 CATTTTATTAATTAATAAACACCTTGTCTGCT 1778
DB 1741 CATTTTATTAATTAATAAACACCTTGTCTGCT 1773

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RESULT 3  
AA064452  
ID AA064452 standard; cDNA to mRNA; 1728 BP.

AC AA064452;  
XX 11-JAN-1995 (first entry)  
DE A/Tizumi/5/65 human influenza A type virus plasmid fragment.  
XX  
KW Antigens: main region; hemagglutinin; H1N1; H2N2; subtype: human;  
KW Influenza A type virus; H3N2; anti-human influenza virus antibody;  
KW diagnosis; prevention; treatment; vaccine; ss.  
OS Synthetic.  
XX JP06100594-A.

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XX 12-APR-1994.
PD 17-SEP-1992: 92JP-0272538.
PF 17-SEP-1992: 92JP-0272538.
PR 17-SEP-1992: 92JP-0272538.
XX (TAKI ) TAKARA SHUZO CO LTD.
XX WPI; 1994-156655/19.
DR
XX Anti human influenza virus antibody - for diagnosis and treatment
PT of influenza type A virus
XX
PS Disclosure; Page 14; 18pp; Japanese.
CC The sequences given in AA064451-65 represent fragments of plasmids which
CC encode antigenic peptides from the H1N1, H2N2 or H3N2 subtypes of human
CC influenza A type virus. These sequences were derived by PCR using the
CC primer sequences given in AA062141-50 and AA064439-50. The amplified
CC sequence encode at least one antigen which is derived from the main
CC region of hemagglutinin of the H1N1, H2N2, or H3N2 subtype of human
CC influenza A type virus. The anti-human influenza virus antibody of the
CC invention, is reactive against antigens derived from the H1N1 and H2N2
CC subtypes but not against H3N2 subtype derived peptides. This antibody
CC is useful for diagnosis, prevention and treatment of human influenza A
CC type virus. The antigenic peptides are important in vaccine production.
XX
SQ Sequence 1728 BP; 599 A; 318 C; 407 G; 404 T; 0 other:

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Query Match 90.1%; Score 1606.4; DB 15; Length 1728;  
Best Local Similarity 95.6%; Pred. No. 0;  
Matches 1652; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

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QY 27 ATAGAAACCAACCAACCAACCAATGCGCATATTTATCTCTTCTGTTACAGACAT 86
DB 1 ATAGAAACCAACCAACCAACCAATGCGCATATTTATCTCTTCTGTTACAGACAT 60
QY 87 GAGAGGGGACGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 146
DB 61 GAGAGGGGACGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 147 AATCTAGACGGAACGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 206
DB 121 AATCTAGACGGAACGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 180
QY 207 CGGAAGATTATGCAACACTTAACGGAATCCCTCCACTTGAATAGGGACATGACATTCG 266
DB 181 CGGAAGATTATGCAACACTTAACGGAATCCCTCCACTTGAATAGGGACATGACATTCG 240
QY 267 CGGATGGCTCCTTGGAAATCCCAAAATGATGATGATGATGATGATGATGATGATGATGAT 326
DB 241 CGGATGGCTCCTTGGAAATCCCAAAATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 327 TATATTTGAGAAAGAAACCCGAGAGAGCGTTTGTGTTATCCAGGACGCTTCAATGATTA 386
DB 301 TATATTTGAGAAAGAAACCCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 387 TGAAGAAATTTGAACATCTCTTCACAGCAGGTGAACATTTTGAAGAAATGATGATGATGAT 446
DB 361 TGAAGAAATTTGAACATCTCTTCACAGCAGGTGAACATTTTGAAGAAATGATGATGATGATGAT 420
QY 447 CAAGATAGATGACACAGCATATACAACTGAGAGGTTTCAAGGCGCTGCGGCGGTGCTGG 506
DB 421 CAAGATAGATGACACAGCATATACAACTGAGAGGTTTCAAGGCGCTGCGGCGGTGCTGG 480
QY 507 TAATTCATCATTTTTCAGAAACATGTCGCTGACAAAGAGATGATGATGATGATGATGATGAT 566
DB 481 TAATTCATCATTTTTCAGAAACATGTCGCTGACAAAGAGATGATGATGATGATGATGATGAT 540
QY 567 TGCCTAAGAGATCGTACAAACATATACAGCGGAGAAACAATGCTATATTTGGGGGATGCA 626
DB 541 TGCCTAAGAGATCGTACAAACATATACAGCGGAGAAACAATGCTATATTTGGGGGATGCA 600

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Oy	07	ATGCGAAGAAATGGTTTGACGGTGGTATGCATTCCACTCACACCATAATGCACAGGA
Dd	1081	ATGGCAAGAAGATGGTTGGATGGTGTGATGCATCCATCTCACAACCAATGCACAGGA
Oy	1167	GTA TGACAGACAGACAAGAAATCATCTCTCAAAGGCAATTGATGGAATCACCAACAG
Dd	1141	GTA TGACAGACAGACAAGAAATCATCTCTCAAAGGCAATTGATGGAATCACCAACAG
Oy	1227	TTC TGTGATTTGAAAAGATAAACACCCAATTTGAAGCTGTGGGAAAGAAATTCGTT
Dd	1201	TTC TGTGATTTGAAAAGATGAACACCCAATTTGAAGCTGTGGGAAAGAAATTCAT,
Oy	1287	AGAGAAAAAGCTGGAGAACTTGAAACAAAAAGATGGAAGAACGCGTTTTCTAGATGTG
Dd	1261	AGAGAAAAAGCTGGAGAACTTGAAACAAAAAGATGGAAGAACGCGTTTTCTAGATGTG
Oy	1347	ATACAAATCTGAGCTTTTAGTTCTGATGGAATAAGAGAGACACTTGACTTTCATAT
Dd	1321	ATACAAATCTGAGCTTTTAGTTCTGATGGAATAAGAGAGACACTTGACTTTCATAT
Oy	1407	TAA TCACAAGAAATCTGATAGTAAAGTCAGAAATGCAGCTGAGAGACAAGCTCAAA
Dd	1381	TAA TCACAAGAACTGATGATATAAGTCAGAAATGCAGCTGAGAGACAAGCTCAAA
Oy	1467	AGGAATGAGATGTTTGAATTTATATACAAATGTGATGATGAATGCAATGTAATGTT
Dd	1441	AGGAATGAGATGTTTGAATTTATACAAATGTGATGATGAATGCAATGTAATGTT
Oy	1527	AAAGCGGACATATGATTTATCCCAGTAGTAACAAGAGCTTAACTAAATAGAAATGT
Dd	1501	AAAGCGGACATATGATTTATCCCAGTAGTAACAAGAGAGAAATCTAAATAGAAATGT
Oy	1587	CAAGGGGTAAATTTGAGCAGCATGGGGGTTTATCAATGCCCTGCAATTTATGCTA
Dd	1561	CAAGGGGTAAATTTGAGCAGCATGGGGGTTTATCAATGCCCTGCAATTTATGCTA
Oy	1647	AGCAGGTTCTATGTCACTGGCAATCATGATGGCTGGGATCTCTTTCGGGTGCTT
Dd	1621	TGCAGGTTCTCTCTCACTGGCAATCATGATGGCTGGGATCTCTTTCGGGTGCTT
Oy	1707	CGGCTCTCTGACATGCGAGGATCGCATATGATTAATGATCATTTATTA 1754
Dd	1681	CGGCTCTCTGACATGCGAAATCTGCATATGATTAATTTATTTATTA 1728
<hr/>		
RESULT 5		
AAQ72806		
ID	AAQ72806	standard; cDNA; 1135 BP.
XX	XX	
AC	AAQ72806;	
XX	XX	
DT	25-MAR-2003	(updated)
DT	22-JUN-1995	(first entry)
DE	XX	
XX	XX	DNA encoding stem region of A/Oxudu/57 influenza virus.
KM	KM	Conserved peptide: stem region; hemagglutinin; HA; H1N1; H2N2;
KW	KW	subtype; human; Influenza A virus; immunogenic artificial peptide;
XX	XX	antigen; vaccine; infection; ss.
OS	XX	
XX	XX	Human influenza A virus.
FT	Key	
FT	CDS	Location/Qualifiers
FT	CDS	46..1092
XX	XX	/tag= a
EP	EP621339-A2.	
PD	26-OCT-1994.	
XX	XX	
FE	20-APR-1994;	94EP-0302819.
PR	20-APR-1993;	93JP-0115216.

PR 16-MAR-1994; 94JP-00701194.  
 XX (TAKI ) TAKARA SHUZO CO LTD.  
 PA  
 XX Isegawa Y, Okuno Y, Sabsao F, Ueda S;  
 PI WPI: 1994-325949/41.  
 XX P-PSDB: AAR63589.  
 DR  
 XX Human influenza A virus haemagglutinin polypeptide(s) - useful in  
 PT influenza A vaccine composition  
 PS Claim 17: Page 50; 68pp: English.  
 XX  
 CC This sequence encodes the stem region of the haemagglutinin (HA) molecule  
 CC of the A/Osaka/57 strain of human influenza A virus. This antigenic  
 CC molecule contains the conserved peptides derived from the stem region  
 CC of the H1N1 and H2N2 subtypes of human influenza A virus. Immunogenic  
 CC polypeptides such as this are antigenically equivalent to the stem region  
 CC of the HA molecule of influenza A virus. This artificial peptide may be  
 CC used as a vaccine for prophylaxis of influenza A virus infection.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX

SO Sequence 1135 BP; 395 A; 197 C; 265 G; 278 T; 0 other;

Query Match 51.8%; Score 908.8; DB 15; Length 1135;  
 Best Local Similarity 98.7%; Pred. No. 2.8e-232;  
 Matches 916; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 853 AAAATATCGAAGAAAGTACTTCAGGATCATGAAAACAGAGAGACCTTGAGAACTGT 912  
 DB 208 AAGTTAAGCAACTTAAACGGATCCGGGATCATGAAAACAGAGAGACCTTGAGAACTGT 267  
 QY 913 GAGACCAAAATGCCAACTCCTTTGGGCAATTAATCAACATTACTCTTTCACAAATGC 972  
 DB 268 GAGACCAAAATGCCAACTCCTTTGGGCAATTAATCAACATTACTCTTTCACAAATGC 327  
 QY 973 CACCCACTGCAATATCTGAGTGGCCCAATATGTAATAATCGGAGATTGGCTTAGCA 1032  
 DB 328 CACCCACTGCAATATCTGAGTGGCCCAATATGTAATAATCGGAGATTGGCTTAGCA 387  
 QY 1033 ACAGAGCTAAGGAATTTTCCCGAGATTGAATCAAGAGATTGTTGGGCAATAGCTGT 1092  
 DB 388 ACAGAGCTAAGGAATTTTCCCGAGATTGAATCAAGAGATTGTTGGGCAATAGCTGT 447  
 QY 1093 TTTATAGAAGGAGAAAGGCAAGAAATGTCAGCTGGTATGATGCATCCACAGCAAT 1152  
 DB 448 TTTATAGAAGGAGAAAGGCAAGAAATGTCAGCTGGTATGATGCATCCACAGCAAT 507  
 QY 1153 GACCAAGGATCAGGATATGAGAGACAAAGAAATCCACTCAAAAGCATTGTGATGAAATC 1212  
 DB 508 GACCAAGGATCAGGATATGAGAGACAAAGAAATCCACTCAAAAGCATTGTGATGAAATC 567  
 QY 1213 ACCAACAAGTAAATCTGTGATTTGAAAAGATTAACCCCAATTTGAAGCTTTGGGAAA 1272  
 DB 568 ACCAACAAGTAAATCTGTGATTTGAAAAGATTAACCCCAATTTGAAGCTTTGGGAAA 627  
 QY 1273 GAATTCGGTAACTTAAGAAAAGACTGAGAACTTGAACAAAAGATGGAAGCGGGTTT 1332  
 DB 628 GAATTCGGTAACTTAAGAAAAGACTGAGAACTTGAACAAAAGATGGAAGCGGGTTT 687  
 QY 1333 CTAGATGTGTGACAAACAAATGCTGAGCTTTTGAATCTGATGAAAATGAGAGACACTT 1392  
 DB 688 CTAGATGTGTGACAAACAAATGCTGAGCTTTTGAATCTGATGAAAATGAGAGACACTT 747  
 QY 1393 GACTTTCAATGATTTCAATGCAAGAAATCTGTATAGTAAGTCAAGTCAAGTCAAGTCAAG 1452  
 DB 748 GACTTTCAATGATTTCAATGCAAGAAATCTGTATAGTAAGTCAAGTCAAGTCAAGTCAAG 807  
 QY 1453 AACGTCAAAAGAACTAGAAATGATGTTTGAATTTATACAAATGATGATGATGATGATGATG 1512  
 DB 808 AACGTCAAAAGAACTAGAAATGATGTTTGAATTTATACAAATGATGATGATGATGATGATG 867

QY 1513 ATGAATAGTGTGAAAAACGGACATATGATTATCCCAAGTATGSAAGAAGCTCTAAACTA 1572  
 DB 868 ATGAATAGTGTGAAAAACGGACATATGATTATCCCAAGTATGSAAGAAGCTCTAAACTA 927  
 QY 1573 AATGAAATGAAATCAAAAGGGGTAAATATGAGCAGCATGGGGTTTATCAAAATCCTTGCC 1632  
 DB 928 AATGAAATGAAATCAAAAGGGGTAAATATGAGCAGCATGGGGTTTATCAAAATCCTTGCC 987  
 QY 1633 ATTATGCTACAGTAGAGAGTTCTATATGCTACCTGGCATCATGATGCTGGGATCTTTTC 1692  
 DB 988 ATTATGCTACAGTAGAGAGTTCTATATGCTACCTGGCATCATGATGCTGGGATCTTTTC 1047  
 QY 1693 TGGGTGTGCTCCAAAGGGGTCTCTGACAGATGCAATGATGATGATGATGATGATGATGAT 1752  
 DB 1048 TGGGTGTGCTCCAAAGGGGTCTCTGACAGATGCAATGATGATGATGATGATGATGATGAT 1107  
 QY 1753 TAATTAATAACACCTTTGTTCTGCTAG 1780  
 DB 1108 TAATTAATAACACCTTTGTTCTGCTAG 1135

## RESULT 6

AAC64297  
 ID AAC64297 standard; cDNA; 1770 BP.

AC AAC64297;

DT 23-FEB-2001 (first entry)

DE Influenza virus haemagglutinin (HA) gene.

KW Influenza virus: haemagglutinin; HA; Sendai virus vector;

OS recombinant protein expression; influenza vaccine; immunogen;

SS immunoassay; ss.

OS Influenza virus.

PN JP2000253876-A.

PD 19-SEP-2000.

PF 08-MAR-1999; 99JP-0060918.

PR 08-MAR-1999; 99JP-0060918.

PA (DINA-) DINABEKU KENKYUSHO KK.

DR WPI: 2000-624368/60.

DR P-PSDB: AAR29746.

PT A vaccine and a vaccine protein using Sendai virus vector

PS Example 2: Page 17-19; 28pp: Japanese.

XX The invention relates to a Sendai virus vector expressing an influenza  
 XX virus protein or a fragment thereof. The invention also relates to  
 XX an influenza vaccine comprising the Sendai virus vector of the  
 XX invention or a purified influenza virus protein obtained from the Sendai  
 XX virus vector; and a method for vaccination against influenza in which  
 XX the vaccine is administered to an intermediate non-human animal host of  
 XX influenza virus. The invention additionally encompasses a Sendai virus  
 XX vector comprising a gene from a pathogenic organism in an expressible  
 XX form, the preparation of the expressed protein from the Sendai virus  
 XX vector, and the use of the expressed protein as an immunogen or in  
 XX immunoassays. The present sequence represents an influenza virus  
 XX haemagglutinin (HA) cDNA used in an exemplification of the invention.  
 XX

Query Match 47.3%; Score 843; DB 21; Length 1770;  
 Best Local Similarity 69.3%; Pred. No. 1.2e-214;  
 Matches 1181; Conservative 0; Mismatches 515; Indels 9; Gaps 2;



















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Db 1231 AATCTGTAATCGAAAAATGACACTCATTTACAGCTGTGGCAAAAGATTCAACAAA 1290
Qy 1285 TTAGAGAAAAGACCTGGAGAACTTGAACAAAAAGATGACAGCGGTTCTAGATGTGG 1344
Db 1291 TTGGAAAAGAAAGATGAAATCTTAATAAAAAGTATGATGATTTCTGGACATTTGG 1350
Qy 1345 ACATACATGCTGCTTTAGTCTGTGATGAGAAATGAGAGACCTGACCTTCATCAT 1404
Db 1351 ACATATATGACAGATTTGCTGCTACTGAGAAATGAGAGACCTTGGATTTTCATGAC 1410
Qy 1405 TCTAATGTCAGAAATCTGTATAGTAAGTCAAGATGACAGTACAGACAGCTCAAGAA 1464
Db 1411 TCAAAATGTGAAGATCTGTATGAGAAAGTAAAGCCAAATGGAAGAAATGCAAAAGAA 1470
Qy 1465 CTGGAATGATGTTTGAATTTATACAAATGTATGATGATGATGATGATGATGATG 1524
Db 1471 ATAGGGAACGGGTGTTTGAATTTATCACAAGTCAATCAATGATGATGATGATGATG 1530
Qy 1525 AAAACGGGACATATGATATCCCAATGATGAGAGAGATGATGATGATGATGATGATG 1584
Db 1531 AAAAATGGAACCTATGATCTCCAAATATTCGAAAGATCAAAAGTTAAACAGGGGAAA 1590
Qy 1585 ATCAAAAGGCTAAATGATGACAGCAGATGGGGGTTTATCAAAATCCTTGCCATTTATGCTACA 1644
Db 1591 ATTGATGAGATGAAATGGAATGGAATGAGAGTCTATCAGATTTGGGATCTACTCAACT 1650
Qy 1645 GTAGCAGGTTCTATGTCACAGGCAATGATGATGATGATGATGATGATGATGATGATG 1704
Db 1651 GTCCGCAAGTTACTGCTGCTTTGGTCTCCCTGGGGCAATCAGCTTCTGATGCTTCT 1710
Qy 1705 AACGGGCTCTGCAAGTCAAGATGATGATGATGATGATGATGATGATGATGATGATG 1737
Db 1711 AATGGGCTTTTGCAGTCAAGAAATATGATGATGATGATGATGATGATGATGATGATG 1743

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## RESULT 13

AAD09587 standard; DNA; 1766 BP.

AAD09587;

10-SEP-2001 (first entry)

Influenza virus A/Texas/36/91 recombinant haemagglutinin (rHA) DNA.

Multivalent influenza vaccine; recombinant haemagglutinin; rHA;

61k protein; ds.

Chimeric - Autographa californica nuclear polyhedrosis virus.

Chimeric - Influenza virus type A.

Key promoter

Location/Qualifiers

CDS

/tag= a

/note= "Autographa californica Nuclear Polyhedrosis Virus

sig\_peptide

/product= "AcNPV 61k protein signal peptide-

misc\_signal

/note= "Universal translation termination signal"

US6245532-B1.

12-JUN-2001.

09-OCT-1998; 98US-0169027.

30-MAY-1995; 95US-0453848.

13-SEP-1993; 93US-0120607.

(PROT-) PROTEIN SCI CORP.

Smith GE, Volovitz F, Wilkinson BE, Voznesensky AI, Hackett CS; WPI: 2001-407272/43.

P-PSDB: AAE04952.

Expressing a protein e.g. recombinant influenza virus hemagglutinin comprising using a vector encoding a polypeptide comprising a baculovirus signal peptide and a baculovirus expression system is useful as a multivalent Influenza vaccine.

Claim 5; Column 41-44; 51pp; English.

The present invention relates to a method for expressing an exogenous protein in a baculovirus expression system which comprises using a vector encoding a polypeptide comprising a baculovirus signal peptide operably linked to a heterologous amino acid sequence. The method is especially useful for preparing a protein which may be used to make a multivalent influenza vaccine based on a mixture of recombinant haemagglutinin (HA) antigens cloned from influenza viruses having epidemic potential. The recombinant haemagglutinin proteins are full length, uncleaved (HA0) glycoproteins including both the HA1 and HA2 subunits (HA0) purified under non-denaturing conditions. The use of recombinant DNA (rDNA) technology to produce influenza vaccine offers several advantages, e.g., a recombinant DNA influenza vaccine can be produced under safer and more stringently controlled conditions; propagation with infectious influenza in eggs is not required; recombinant haemagglutinin (rHA) protein can be more highly purified; purification procedures for rHA do not have to include virus inactivation or organic extraction of viral membrane components; production of HA via rDNA technology provides an opportunity to avoid the genetic heterogeneity which occurs during the adaptation and passage through eggs, which should make it possible to better match vaccine strains with influenza epidemic strains, resulting in improved efficacy. The present sequence is recombinant haemagglutinin (rHA) DNA comprising Autographa californica Nuclear Polyhedrosis Virus (AcNPV) 61k gene partial polyhedrin promoter and signal sequence linked to Influenza virus A/Texas/36/91 mature HA coding region.

Sequence 1766 BP; 604 A; 331 C; 403 G; 428 T; 0 other;

Query Match 39.6%; Score 706.2; DB 22; Length 1766;

Best Local Similarity 64.7%; Pred. No. 46-178;

Matches 1069; Conservative 0; Mismatches 578; Indels 6; Gaps 1;

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Qy 91 GGGGACCAATATGCTTTGATACATGCAATTAATCCACAGAGAGGTGACACAAT 150
Db 91 GGGGACCAATATGATAGTACGATGCAAGCACTGCAAGCACTGTTGACACACTA 150
Qy 151 CTAGAGCGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 210
Db 151 CTGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 210
Qy 211 AAGTTATGCAAACTAAGGAAATCCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 270
Db 211 AAGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 270
Qy 271 TGGCTCTTGGAAATCCAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 330
Db 271 TGGCTCTTGGAAATCCAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 330
Qy 331 TTGAGAAAAGAAACCCGAGAGAGGTTTGGTATTCAGGACGCTCATGATTAAGAA 390
Db 331 GCAGAAACACCAACCCGAGAGAGGTTTGGTATTCAGGACGCTCATGATTAAGAG 390

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QY 391 GAATTTGAACATCTCTCAGACGGGTGAACATTTGAGAAAGTAAGATTCTCCCAA 450  
 Db 391 GAACTGAGGGGAGCAATTTGAGTTAGTATCATTCATTCAGAGATTGCAAAATTTCCCAA 450  
 QY 451 GATGAT-----GACACAGCATACAAACTGGAGTTACGGGCTCGGGGTCT 504  
 Db 451 GAAAGCTCAGTGGCCCAACCCACCGCTAACCAAGAGTAACGAGATCATGCTCCCATAT 510  
 QY 505 GGTAATCATCATTTTTCAGGAACATGTTGGGTGCAAGAGAGAGATGATATCCG 564  
 Db 511 GGGAAAAGCAGTTTTCAGAAATTTCTATGCTGACGGAGAGAAATGCGTTTACCA 570  
 QY 565 GTTCCCAAGAGTCTGACAAATACAGGAGGAGAAATGCTAATATTTGGGGGTG 624  
 Db 571 AATCTGAGCAAGTCCATGTAACACAAAGAGAAAGAGTCTGTAATGSGGCTT 630  
 QY 625 CACCATCCCATGATGAGACAGAAAGAAACATTTGACAGAAATGGGAACTATGTT 684  
 Db 631 CATCACCCGCTTAACATAAGGGACCAAGGCCATCTATCATACAGAAATGCTTATGTC 690  
 QY 685 TCCGTAGGACATCAACATTTGAACAAAGGTCAACCCAGAAATAGCAACAGGCCATAA 744  
 Db 691 TCTTAATGTCTTCAATTATAGCAGAAATTCACCCAGAAATAGCAAAAGACCCAAA 750  
 QY 745 GTGATGAGACAGAGATGAGAAATGCAATTCCTTGGACCCCTTGATATGGGACACC 804  
 Db 751 GTAGAGATCAAGAAATGAGAAATTAATCTACTACTGCGCTGCGGAAACCCGGGACACA 810  
 QY 805 ATAAATTTGAGAGTCTGATATCTAATTCACACAGATGATGATTCAAATATTCGAAA 864  
 Db 811 ATATATTTAGAGCAATGGAATCTAATAGCCGCAATGATGCTTCCGACTGATAGA 870  
 QY 865 AGAGGTGTTGAGGCTCATGAGAAACAGAGGAACACTGTAGAACTGTGACCAATATGC 924  
 Db 871 GCGTTTGGTCAGATTCATCAGAGGTTGTTGGAGCCATTTGCGGCAATGTC 930  
 QY 925 CAAATCTCTTTGGGCAATTAATATACAACTATCTTTCACATTCACCCACTGACA 984  
 Db 931 CAAACACCCAGGAGCTATAAACAGTAGTCTTCTTCCAGATATGACCCAGTACACA 990  
 QY 985 ATAGGTAGTGGCCCAATATGTAAATTCGAGAGATTTGCTTACGACAGAGACTAAG 1044  
 Db 991 ATAGGAGAGTGTCCAAAGTATGTACAGAGTACAAATTAAGATGTTACAGAGACTAAG 1050  
 QY 1045 AATGTTCCCAATGATGATCAAGAGATTTGTTGGGCAATAGCTGTTTATGAGAGA 1104  
 Db 1051 AATCTCCATTCATTCATCCAGAGGTTGTTGGAGCCATTTGCGGTTTCATTGAAGG 1110  
 QY 1105 GGATGGCAAGAAATGCTTGAAGGTTGATGATACATCAGACATGACCAAGATCA 1164  
 Db 1111 GGGGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1170  
 QY 1165 GGGATGACAGACAAAGATCCACTCAAAAGGCAATTTATGATATCACCACAGGTA 1224  
 Db 1171 GGGATGCTGCTCGAACCAAAAGCACAAATGCTTAAACGGATTTAAACCAAGTG 1230  
 QY 1225 AATTCGTGATGAAAGATTAACACCAATTTGAACTGTGTTGGGAAAGAAATTCGGTAA 1284  
 Db 1231 AATTCGTATTCAGAAATTAACACCAATTTGAACTGTGTTGGGAAAGAAATTCGGTAA 1290  
 QY 1285 TTGAGAAAGAACTGGTGAACCTTGAACAAAGATGAGAGCGGTTTCAATGATG 1344  
 Db 1291 TTGAGAAAGAACTGGTGAACCTTGAACAAAGATGAGAGCGGTTTCAATGATG 1350  
 QY 1345 ACATACATCTGAGACCTTTAGTTCGATGAGAAATGAGAGACACTTGCATTCATGAT 1404  
 Db 1351 ACATACATCTGAGACCTTTAGTTCGATGAGAAATGAGAGACACTTGCATTCATGAT 1410  
 QY 1405 TCTAATGTCAAGATCTGTATAGAAAGTCAAGATGAGAGAGACAGTCAAGAA 1464  
 Db 1411 TCAATGTCAAGATCTGTATAGAAAGTCAAGATGAGAGAGACAGTCAAGAA 1470

QY 1465 CTAGAAATGAGTGTGTAATTTATCACAATGTGATGATGATGATGATGATG 1524  
 Db 1471 ATAGGAAAGCGGCTGTTTGAATTCATCACAAGTGTAACTGATGATGATGATGATG 1530  
 QY 1525 AAAACGGGACATATGATTTATCCAAAGTATCAAGAGTAACTAATAGAAATGAA 1584  
 Db 1531 AAAATGAACTTATGACTATCCAAAATATTCAGAGATCAAGATTAACAGGGGAAA 1590  
 QY 1585 ATCAAGGGCTAAATGAGACATGAGGAGGTTATCAAACTTCGATTTATGATCA 1644  
 Db 1591 ATGATGAGATGAAATGGAATCAATGAGGACTATCAGATTCGAGATCTACTCACT 1650  
 QY 1645 GTACAGGTTCTATCTACTGCAATCATGATGAGGCTGGATCTCTTCTGGTGTGCTC 1704  
 Db 1651 GTGCCAGTTTACAGGAGCTTTTGGTCTCCCTGGGGAATCAGCTCTGATGTCTT 1710  
 QY 1705 AACGGTCTCTGCAAGTGCAGGATTCGATATGA 1737  
 Db 1711 AATGGTCTTTGCACTGAGTCAAGATATGAAATCGA 1743  
 RESULT 14  
 AAAT6188  
 ID AAAT6188 standard; DNA; 1724 BP.  
 AC AAAT6188;  
 XX 15-DEC-2000 (first entry)  
 DT  
 XX Swine influenza virus haemagglutinin gene SIV-HA.  
 DE Swine; haemagglutinin; nucleoprotein; SIV; HA; NP; vaccine;  
 KW immunisation; ss.  
 KW  
 OS Swine influenza virus.  
 XX  
 PN CA2290197-A1.  
 XX  
 PD 23-MAY-2000.  
 XX  
 XX 23-NOV-1999; 99CA-2290197.  
 FE  
 XX 23-NOV-1998; 98US-0197679.  
 PR  
 XX (FOLE/) FOLEY P. L.  
 PA  
 XX FOLEY PL.  
 PI  
 XX  
 DR WPI: 2000-524822/48.  
 XX  
 XX Novel recombinant vaccinia virus for immunizing swine against  
 PT Influenza, contains inserts of hemagglutinin and nucleoprotein genes  
 PT from swine influenza virus  
 XX  
 XX Disclosure: Page 12; 27pp; English.  
 XX  
 CC The present sequence is swine influenza virus (SIV) haemagglutinin (HA)  
 CC gene. This sequence was used to produce a recombinant vaccinia virus  
 CC containing as inserts the present sequence and the swine influenza virus  
 CC nucleoprotein (NP) gene (see AAAT6189). The present sequence was  
 CC amplified by RT-PCR and cloned, and then subsequently subcloned into a  
 CC transfection vector that allowed insertion of the SIV-HA sequence into  
 CC the genome of the modified vaccinia virus Ankara (MVA) strain of vaccinia  
 CC virus. The recombinant vaccinia virus is useful as a vaccine for  
 CC immunizing a swine against influenza. In addition, by protecting pigs  
 CC from influenza infection, the human population would be protected from  
 CC transfer of infection from swine to the human population.  
 XX  
 SO Sequence 1724 BP; 607 A; 316 C; 377 G; 424 T; 0 other;  
 Query Match 39.18; Score 696.4; DB 21; Length 1724;  
 Best Local Similarly 64.38; Pred. No. 1.7e-175;  
 Matches 1078; Conservative 0; Mismatches 591; Indels 7; Gaps 2;



XX The sequences given in A064451-65 represent fragments of plasmids which  
 CC encode antigenic peptides from the H1N1, H2N2 or H3N2 subtypes of human  
 CC influenza A type virus. These sequences were derived by PCR using the  
 CC primer sequences given in A062141-50 and A064439-50. The amplified  
 CC sequence encode at least one antigen which is derived from the main  
 CC region of hemagglutinin of the H1N1, H2N2, or H3N2 subtype of human  
 CC influenza A type virus. The anti-human influenza virus antibody of the  
 CC invention, is reactive against antigens derived from the H1N1 and H2N2  
 CC subtypes but not against H3N2 subtype derived peptides. This antibody  
 CC is useful for diagnosis, prevention and treatment of human influenza A  
 CC type virus. The antigenic peptides are important in vaccine production.

XX Sequence 1754 BP; 615 A; 327 C; 394 G; 418 T; 0 other;

Query Match 39.8%; Score 695.6; DB 15; Length 1754;

Best Local Similarity 64.8%; Pred. No. 2.7e-175;

Matches 1068; Conservative 0; Mismatches 594; Indels 6; Gaps 1;

QY	76	TTCCAGCAGTGAAGGAGGACAGATATGATGGATACATGGCAATTAATTCACAGAC	135
DB	54	TTTACAGCTACAGATTCAGACACATATGTATAGCTACCATCGGACCACTCAACCGAC	113
QY	136	AAGTTCACACATTTAGAGCGGAGCTACTGTACTATGCCAAGGACATCTTGAG	195
DB	114	ACTGTTGACACAGTATTTGAGAAAGACGTGACAGTACACCTGTCAACCTTGTAG	173
QY	196	AAGACCATTAACGAAAGTATGCAAACTTAACGATCCCTCCTTGAACCTGAGGAGAC	255
DB	174	GACAGTACACAGGAAACTATGTCTGACTTAAGAGATAGCCCTACATCAATTTGGTAT	233
QY	256	TGTAGCTTGCCTGAGTCCCTTGAATTCCTGATAGCTTCTTCAAGTGTGCA	315
DB	234	TGCAGCTTGCCTGAGTCCCTTGAATTCCTGATAGCTTCTTCAAGTGTGCA	293
QY	316	GAAAGCTCTATATATGAGAGAAAGAAACCCGAGAGAGCTTTGTGTATCCAGGAC	375
DB	294	TCAATGCTCTATATATGAGAGAAAGAAACCCGAGAGAGCTTTGTGTATCCAGGAC	353
QY	376	TTCAATGCTCTATATATGAGAGAAAGAAACCCGAGAGAGCTTTGTGTATCCAGGAC	435
DB	354	TTCCCTGCTCTATATATGAGAGAAAGAAACCCGAGAGAGCTTTGTGTATCCAGGAC	413
QY	436	AAGATTCCTGCTCTATATGAGAGAAAGAAACCCGAGAGAGCTTTGTGTATCCAGGAC	489
DB	414	GAAATTCCTGCTCTATATGAGAGAAAGAAACCCGAGAGAGCTTTGTGTATCCAGGAC	473
QY	490	GCTTGCCTGCTCTATATGAGAGAAAGAAACCCGAGAGAGCTTTGTGTATCCAGGAC	549
DB	474	TCATGCTCTATATATGAGAGAAAGAAACCCGAGAGAGCTTTGTGTATCCAGGAC	533
QY	550	GATCAGATTCCTGCTCTATATGAGAGAAAGAAACCCGAGAGAGCTTTGTGTATCCAGGAC	609
DB	534	AATGCTCTATATATGAGAGAAAGAAACCCGAGAGAGCTTTGTGTATCCAGGAC	593
QY	610	ATATTCCTGCTCTATATGAGAGAAAGAAACCCGAGAGAGCTTTGTGTATCCAGGAC	669
DB	594	GTAATTCCTGCTCTATATGAGAGAAAGAAACCCGAGAGAGCTTTGTGTATCCAGGAC	653
QY	670	GTTGAGATTCCTGCTCTATATGAGAGAAAGAAACCCGAGAGAGCTTTGTGTATCCAGGAC	729
DB	654	GAAATTCCTGCTCTATATGAGAGAAAGAAACCCGAGAGAGCTTTGTGTATCCAGGAC	713
QY	730	GCAACAGGCTTAAGATGAGAGAGAGATGAGATTAATTCCTGAGCCCTCTG	789
DB	714	GCAAAAGAGCTTAAGATGAGAGAGAGATGAGATTAATTCCTGAGCCCTCTG	773
QY	790	GATATGAGAGAGAGATTAATTCCTGAGCCCTCTGAGATTAATTCCTGAGCCCTCTG	849
DB	774	GAAACCGGAGAGAGATTAATTCCTGAGCCCTCTGAGATTAATTCCTGAGCCCTCTG	833
QY	850	TTCAAAATTCAGAAAATGAGTATGAGGATGATGAAAACAGAGAGACATTTGAGAC	909

DB	834	TTCCACTGAGTAGAGCTTTGGTCAAGAAATCATCACTCAACCAAGCATGATGAA	893
QY	910	TGTGAGCCCAATGCAAACTCTTTGGACATTAATTAACATTAATTCATCAT	969
DB	894	TGTGAGCCCAATGCAAACTCTTTGGACATTAATTAACATTAATTCATCAT	953
QY	970	GTTCCACCTGAGATGAGTGTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1029
DB	954	GTTACACCTGAGATGAGTGTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1013
QY	1030	GCAACAGAGCTTAAGATGTTCCCAAGATTAATCAATCAAGAGATTTGAGGACAT	1089
DB	1014	GTTACAGAGCTTAAGATGTTCCCAAGATTAATCAATCAAGAGATTTGAGGACAT	1073
QY	1090	GTTTATGAGAGAGATGAGTGTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1149
DB	1074	GTTTATGAGAGAGATGAGTGTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1133
QY	1150	AATGACAGGAGATGAGTGTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1209
DB	1134	AATGACAGGAGATGAGTGTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1193
QY	1210	ATCAACCAAGATTAATTCCTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1269
DB	1194	ATCAACCAAGATTAATTCCTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1253
QY	1270	AAAGATTCCTGCTGCTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1329
DB	1254	AAAGATTCCTGCTGCTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1313
QY	1330	TTTCTAGATGCTGCTGCTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1389
DB	1314	TTTCTAGATGCTGCTGCTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1373
QY	1390	CTTACCTTCTGCTGCTGCTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1449
DB	1374	CTTACCTTCTGCTGCTGCTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1433
QY	1450	GACACGCTCAAGAGATGAGTGTGCTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1509
DB	1434	AATATGCTCAAGAGATGAGTGTGCTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1493
QY	1510	TGATGATGCTGCTGCTGCTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1569
DB	1494	TGATGATGCTGCTGCTGCTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1553
QY	1570	CTAATGATGCTGCTGCTGCTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1629
DB	1554	CTAATGATGCTGCTGCTGCTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1613
QY	1630	GCCATTTATGCTGCTGCTGCTGCTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1689
DB	1614	GCCATTTATGCTGCTGCTGCTGCTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1673
QY	1690	TTCTGCTGCTGCTGCTGCTGCTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1737
DB	1674	TTCTGCTGCTGCTGCTGCTGCTGCTGCTCAAAATATGAAATGAGAGAGTGTGCTTA	1721

Search completed: August 10, 2003, 02:11:14  
 Job time : 347.17 secs

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penCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 18:20:24 ; Search time 217.814 Seconds  
(without alignments)  
14066.412 Million cell updates/sec

Title: US-09-918-568-49

Perfect score: 1135  
Sequence: 1 CTAGCAAAAGCGGGCTAT.....AACACCCCTGTTCTGCTAG 1135

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Sapept 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfied by chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq\_19Jun03:\*

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6: /SIDSI/gc/pdata/geneseq/geneseqn-emb1/NA1985.DAT:\*  
7: /SIDSI/gc/pdata/geneseq/geneseqn-emb1/NA1986.DAT:\*  
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21: /SIDSI/gc/pdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
22: /SIDSI/gc/pdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDSI/gc/pdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1135	100.0	1135	15	AA072806
2	908.8	80.1	1783	15	AA072849
3	884.4	77.9	1773	24	AA073057
4	838	73.8	1728	15	AA064452
5	834.8	73.6	1728	15	AA072831
6	494	43.5	1773	24	AA039863
7	491.2	43.3	1770	21	AA064297
8	466.8	41.1	1777	11	AA068442

9	461.2	40.6	1721	19	AAV26247	Genomic DNA SEQ 10
10	451	39.7	1766	18	AAV59213	Influenza A/Texas/
11	451	39.7	1766	20	AAV00774	Influenza virus A/
12	451	39.7	1766	22	AA009587	Influenza virus A/
13	448.6	39.5	1724	21	AA076188	Swine influenza vi
14	447.8	39.5	1754	15	AA064451	A/Suila/1/89 human
15	447.8	39.5	1754	15	AA072830	HA gene of A/Suila
16	443	39.0	1701	19	AAV49294	Siv strain H1N1 ha
17	400	35.2	400	15	AA064457	A/Okuda/57 human
18	400	35.2	400	15	AA072836	HA gene fragment o
19	397	35.0	409	15	AA064458	A/Adachi/2/57 huma
20	397	35.0	409	15	AA072837	HA gene fragment o
21	382.4	33.7	410	15	AA064459	A/Kumamoto/1/65 hu
22	382.4	33.7	410	15	AA072838	HA gene fragment o
23	379.6	33.4	394	15	AA064460	A/Kaizuka/2/65 hum
24	379.6	33.4	394	15	AA072839	HA gene fragment o
25	373	32.9	924	11	AA004072	Coding region for
26	373	32.9	924	14	AA047364	Sequence encoding
27	373	32.9	924	15	AA070195	Sequence encoding
28	372.6	32.8	810	14	AA047366	Sequence encoding
29	372.6	32.8	810	15	AA070198	Sequence encoding
30	368.2	32.4	670	14	AA047360	Sequence encoding
31	368.2	32.4	670	15	AA070206	Influenza haemaggl
32	361.4	31.8	912	15	AA070202	Sequence encoding
33	356.6	31.4	912	14	AA047370	Sequence encoding
34	293.6	25.9	1697	24	AA037088	Influenza A virus
35	293.6	25.9	1753	24	AA037087	Influenza A virus
36	293.6	25.9	1753	24	AA037089	Influenza A virus
37	280.2	24.7	1757	24	AA037090	Influenza A virus
38	263.8	23.2	729	11	AA004073	Coding region for
39	263.8	23.2	729	14	AA047365	Sequence encoding
40	263.8	23.2	729	15	AA070197	Sequence encoding
41	263	23.2	1777	15	AA072855	Full length H3N2.1
42	259.2	22.8	630	15	AA070199	Sequence encoding
43	257.6	22.7	630	14	AA047367	Sequence encoding
44	256.4	22.6	474	15	AA070203	Sequence encoding
45	254.8	22.4	474	14	AA047371	Sequence encoding

#### ALIGNMENTS

RESULT 1	AA072806	standard; cDNA; 1135 BP.
ID	AA072806	
AC	AA072806;	
XX		
DT	25-MAR-2003 (updated)	
DT	22-JUN-1995 (first entry)	
XX		
DE	DNA encoding stem region of A/Okuda/57 influenza virus.	
XX		
KW	Conserved peptide; stem region; hemagglutinin; HA; H1N1; H2N2;	
KW	subtype; human; influenza A virus; immunogenic artificial peptide;	
KW	antigen; vaccine; infection; ss.	
XX		
OS	Human influenza A virus.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	46..1092
FT		/*tag= a
XX		
PN	EP621339-A2.	
XX		
PD	26-OCT-1994.	
XX		
PF	20-APR-1994;	94EP-0302819.
XX		
PR	20-APR-1993;	93JP-0115216.
PR	16-MAR-1994;	94JP-0070194.
XX		
PA	(TAKI ) TAKARA SHUZO CO LTD.	

XX Isegawa Y, Okuno Y, Sasao F, Ueda S;  
 XX WPI; 1994-325949/41.  
 DR P-PSDB; AAR63589.  
 XX  
 XX Human influenza-A virus haemagglutinin polypeptide(s) - useful in  
 PT influenza-A vaccine composition  
 PS  
 XX Claim 17; Page 50; 68pp; English.  
 CC This sequence encodes the stem region of the hemagglutinin (HA) molecule  
 CC of the A/Okuda/57 strain of human influenza A virus. This antigenic  
 CC molecule contains the conserved peptides derived from the stem region  
 CC of the H1N1 and H2N2 subtypes of human influenza A virus. Immunogenic  
 CC polypeptides such as this are antigenically equivalent to the stem region  
 CC of the HA molecule of influenza A virus. This artificial peptide may be  
 CC used as a vaccine for prophylaxis of influenza A virus infection.  
 CC (updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SO Sequence 1135 BP; 395 A; 197 C; 265 G; 278 T; 0 other;  
 Query Match 100.0%; Score 1135; DB 15; Length 1135;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-290;  
 Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGCAAAAGCAGGGGTTATCCATAGAAAACCAAAACCAACATGCGCCATCATTTAT 60  
 DB 1 CTAGCAAAAGCAGGGGTTATCCATAGAAAACCAAAACCAACATGCGCCATCATTTAT 60  
 QY 61 CTCATCTCCTCTTCCACAGCAGTGAAGGGGACAGATGATGATGATGATGATGATGAT 120  
 DB 61 CTCATCTCCTCTTCCACAGCAGTGAAGGGGACAGATGATGATGATGATGATGATGAT 120  
 QY 121 AATTCACAGAGAGAGGTCGACACATTTAGAGCGGAGACGTCATGCTCATGCGCAAG 180  
 DB 121 AATTCACAGAGAGAGGTCGACACATTTAGAGCGGAGACGTCATGCTCATGCGCAAG 180  
 QY 181 GACATCCTTGAGAGAGCCCATAGCGGAAGTTATGCAACTTAAACGATCCGGATATG 240  
 DB 181 GACATCCTTGAGAGAGCCCATAGCGGAAGTTATGCAACTTAAACGATCCGGATATG 240  
 QY 241 AAAACAGAGAGAGACCTTGAGAACTGTGAGACCAACCAATGCCAACTCTTTGGGAGCATA 300  
 DB 241 AAAACAGAGAGAGACCTTGAGAACTGTGAGACCAACCAATGCCAACTCTTTGGGAGCATA 300  
 QY 301 AATACACATTTACCTTTTACAAATGTCCACCACTGACCAATAGTGAGTCCCAATAT 360  
 DB 301 AATACACATTTACCTTTTACAAATGTCCACCACTGACCAATAGTGAGTCCCAATAT 360  
 QY 361 GTAATAATCGGAGAGAGTGTGTTAGCAACAGGCTAAGGAATGTTCCCGCAGATTGAATCA 420  
 DB 361 GTAATAATCGGAGAGAGTGTGTTAGCAACAGGCTAAGGAATGTTCCCGCAGATTGAATCA 420  
 QY 421 AGAGATTGTTGGGCAATAGCTGTTTATAGAGAGAGGATGGCAAGGAATGTTGAC 480  
 DB 421 AGAGATTGTTGGGCAATAGCTGTTTATAGAGAGAGGATGGCAAGGAATGTTGAC 480  
 QY 481 GGTGGTATGATACCATCAGACAAATGACAGAGGATCAGGATATCAGACAGCAAGAA 540  
 DB 481 GGTGGTATGATACCATCAGACAAATGACAGAGGATCAGGATATCAGACAGCAAGAA 540  
 QY 541 TCCACTCAAAAGGCAATTTGATGGAATCACCACAGGTAATTTCTGATGAAAAGATA 600  
 DB 541 TCCACTCAAAAGGCAATTTGATGGAATCACCACAGGTAATTTCTGATGAAAAGATA 600  
 QY 601 AACACCAATTTGAGAGCTGTTGGGAAAGAAATTCGTAACCTTGAGAGAAAGACTGGAGAAC 660  
 DB 601 AACACCAATTTGAGAGCTGTTGGGAAAGAAATTCGTAACCTTGAGAGAAAGACTGGAGAAC 660  
 QY 661 TTGAACAAAAGATGGAAGACGGGTTTCTAGATGTGTGACATACATCTGAGCTTTTA 720  
 DB 661 TTGAACAAAAGATGGAAGACGGGTTTCTAGATGTGTGACATACATCTGAGCTTTTA 720

QY 721 GTTCGATGAAATGAGAGACACTTACTTTCATGATTCATATGTCAGAAATCTGTAT 780  
 DB 721 GTTCGATGAAATGAGAGACACTTACTTTCATGATTCATATGTCAGAAATCTGTAT 780  
 QY 781 AGTAAAGTCAGATGACGCTGAGACACAGCTCAAGAACTAGGAAATGATTTTGA 840  
 DB 781 AGTAAAGTCAGATGACGCTGAGACACAGCTCAAGAACTAGGAAATGATTTTGA 840  
 QY 841 TTTATCACAATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
 DB 841 TTTATCACAATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
 QY 901 CCCAAGATGAAAGAGTCTAAACCTAATAGAAATCAAGGGGTAATAATTTAGAC 960  
 DB 901 CCCAAGATGAAAGAGTCTAAACCTAATAGAAATCAAGGGGTAATAATTTAGAC 960  
 QY 961 AGCATGGGGGTTTATCAAACTCTGCAATTTATGCTACAGTACCAGGTTCTATGCTAG 1020  
 DB 961 AGCATGGGGGTTTATCAAACTCTGCAATTTATGCTACAGTACCAGGTTCTATGCTAG 1020  
 QY 1021 GCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080  
 DB 1021 GCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080  
 QY 1081 ATCTGATATGATTAATAGTCAATTTTAAATTAATAAACAACCCCTTTCTGCTAG 1135  
 DB 1081 ATCTGATATGATTAATAGTCAATTTTAAATTAATAAATAAACAACCCCTTTCTGCTAG 1135

RESULT 2  
 AAQ72849 standard; cDNA; 1783 BP.  
 ID AAQ72849;  
 XX  
 AC AAQ72849;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 23-JUN-1995 (first entry)  
 XX  
 DE Full length HA gene of A/Okuda/57 H2N2 Influenza A virus.  
 XX  
 KW Conserved peptide; stem region; hemagglutinin; HA; H1N1; H2N2; PCR;  
 KW subtype; human; Influenza A virus; Immunogenic artificial peptide;  
 KW antigen; vaccine; infection; polymerase chain reaction; primer;  
 KW amplification; C179; region A; region B; ds.  
 XX  
 OS Influenza A virus.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 49..1137  
 FT /\*tag= a  
 FT /product= Full length HA  
 FT 49..93  
 FT sig\_peptide  
 FT /\*tag= b  
 FT 94..231  
 FT /\*tag= c  
 FT /product= Stem region of N-terminal domain  
 FT 232..873  
 FT /\*tag= d  
 FT /product= Globular head region  
 FT 874..11734  
 FT /\*tag= e  
 FT /product= Stem region of C-terminal domain  
 EP621339-A2.  
 PD 26-OCT-1994.  
 XX  
 PF 20-APR-1994; 94EP-0302819.  
 XX  
 PR 20-APR-1993; 93JP-0115216.  
 PR 16-MAR-1994; 94JP-0070194.  
 XX



CC for the manufacture of whole-virus vaccine, preferably attenuated live  
CC vaccine. It is useful for prophylactic or therapeutic administration  
CC against viral infection, preferably influenza virus infections. The  
CC present sequence is influenza A virus/singapore/1/57/ca (cold adapted)  
CC HA mutant cDNA. This sequence is used in the exemplification of the  
CC invention.

50 Sequence 1773 BP; 611 A; 321 C; 417 G; 424 T; 0 other;

Query Match	77.9%	Score 884.4	DB 24	Length 1773
Best Local Similarity	97.2%	Pred. No. 4.2e-224		
Matches 900; Conservative	0	Mismatches 26	Indels 0	Gaps 0

QY	208	AAAGTATCAACATTAAGCGATCCGGGATTCATGAAACAGAAAGAACACTTGAGAACCTG	267
Db	848	AAAATATCGAAAAGAGGTAAATTCAGGGATCATGAATAAGAGGAACCTTGAGAACCTG	907
QY	268	GAGACCAAAATCCCAAACTCTTTGGGACCAATAAATACAACTTACCTTTTCCAAATGTC	327
Db	908	GAGACCAAAATCCCAAACTCTTTGGGACCAATAAATACAACTTACCTTTTCCAAATGTC	967
QY	328	CACCACATGCAATAAGGTGAGTGGCCCCAAATATGTAAATGTGGGAAATGTGTGTAGCA	387
Db	968	CACCACATGCAATAAGGTGAGTGGCCCCAAATATGTAAATGTGGGAAATGTGTGTAGCA	1027
QY	388	ACAGACTTAAGGAATGTTCCCCAGATTTGAATCAAGAGACTTGTGGGGCAATAGCTGT	447
Db	1028	ACAGAGCAAGAATGTTCCCCAGATTTGAATCAAGAGACTTGTGGGGCAATAGCTGT	1087
QY	448	TTTATAGAGAGAGATGGCAAGGAATGTTACGCGTTGTATGCAATCCATCACAGCAAT	507
Db	1088	TTTATAGAGAGAGATGGCAAGGAATGTTACGCGTTGTATGCAATCCATCACAGCAAT	1147
QY	508	GACCAGGATCAGGGATATGACGACACAAATCCACTCAAAAGGCATTTGATGGATC	567
Db	1148	GACCAGGATCAGGGATATGACGACACAAATCCACTCAAAAGGCATTTGATGGATC	1207
QY	568	ACCAACAAGGTAAATTTCTGTGATTTGAAAAGATTAACACCCAAATTTGAAGCTTTGGGAAA	627
Db	1208	ACCAACAAGGTAAATTTCTGTGATTTGAAAAGATTAACACCCAAATTTGAAGCTTTGGGAAA	1267
QY	628	GAATTCGCTAACTTAGAGAAAAGACTGAGAACTGTGAACAAAAGATGGAAAGACGGGTTT	687
Db	1268	GAATTCGCTAACTTAGAGAAAAGACTGAGAACTGTGAACAAAAGATGGAAAGACGGGTTT	1327
QY	688	CTGATGTCGTGACATCAAAATGCTGAGCTTTTACTTCTGATGAGTGAATAAGAGACACTT	747
Db	1328	CTGATGTCGTGACATCAAAATGCTGAGCTTTTACTTCTGATGAGTGAATAAGAGACACTT	1387
QY	748	GACTTATGATATCTATGTCAGAAATCTGTATGTAAATCGAAATGACAGCTGAGAGAC	807
Db	1388	GACTTATGATATCTATGTCAGAAATCTGTATGTAAATCGAAATGACAGCTGAGAGAC	1447
QY	808	AACGTCAAAAGACTAGGAAATGATGTTTGAATTTTATCACAATTTGATGATGATGTC	867
Db	1448	AACGTCAAAAGACTAGGAAATGATGTTTGAATTTTATCACAATTTGATGATGATGTC	1507
QY	868	ATGAATAGTGTGAAAAACGGGACATATGATTTTCCCAAGTATGAGAAGAGTCTAAACTA	927
Db	1508	ATGAATAGTGTGAAAAACGGGACATATGATTTTCCCAAGTATGAGAAGAGTCTAAACTA	1567
QY	928	AATAGAAATGAATTCAAAGGGGTAAAAATTGAGCAGCATGGGGGTTTATCAAATCTTGGC	987
Db	1568	AATAGAAATGAATTCAAAGGGGTAAAAATTGAGCAGCATGGGGGTTTATCAAATCTTGGC	1627
QY	988	ATTATATGCTACAGTAGCAGGTTCTATATGTCAGTGGCAATCATGATGCGTGGGATCTTTTC	1047
Db	1628	ATTATATGCTACAGTAGCAGGTTCTCTCTCTCACTGGCAATCATGATGCGTGGGATCTTTTC	1687
QY	1048	TGGGTGTGCTCAACGGGTCCTGCACTGCGAGATCGCATATGATTTATTAAGCATTTTA	1107
Db	1688	TGGATGTGCTCAACGGGTCCTGCACTGCGAGATCTGCATATGATTTATTAAGCATTTTA	1747

Qy	1108 TAAATTAAAAACACCCTTGTTCGCT	1133 
Db	1748 TAAATTAAAAACACCCTTGTTCTACT	1773 

RESULT 4  
AAQ64452  
ID AAQ64452 standard; cDNA to mRNA; 1728 BP.

AC	AAQ64452;
XX	
DT	11-JAN-1995 (first entry)
XX	

DE A/Izumi/5/65 human influenza A type virus plasmid fragment.  
XY

KW Antigens; main region; hemagglutinin; H1N1; H2N2; subtype; human;  
 KW Influenza A type virus; H3N2; anti-human influenza virus antibody;  
 KW diagnosis; prevention; treatment; vaccine; ss.

Synthetic.

PN JP06100594-A.

PD 12-APR-1994.

PF 17-SEP-1992; 92JJP-0272538.

PR 17-SEP-1992; 92JP-0272538.

PA (TAKI ) TAKARA SHUZO CO LTD.

DR WPI; 1994-156655/19.

PT Anti human influenza virus antibody - for diagnosis and treatment  
PT of influenza type A virus

PS Disclosure; Page 14; 18pp; Japanese

CC The sequences given in AAO64451-65 represent fragments of plasmids which  
CC encode antigenic peptides from the H1N1, H2N2 or H3N2 subtypes of human  
CC Influenza A type virus. These sequences were derived by PCR using the  
CC primer sequences given in AAO62141-50 and AAO64439-50. The amplified  
CC sequence encode at least one antigen which is derived from the main  
CC region of haemagglutinin of the H1N1, H2N2, or H3N2 subtype of human  
CC Influenza A type virus. The anti-human Influenza virus antibody of the  
CC invention, is reactive against antigens derived from the H1N1 and H2N2  
CC subtypes but not against H3N2 subtype derived peptides. This antibody  
CC is useful for diagnosis, prevention and treatment of human influenza A  
CC type virus. The antigenic peptides are important in vaccine production.

50 Sequence 1728 BP; 599 A; 318 C; 407 G; 404 T; 0 other;

Query Match	73.8%;	Score 838;	DB 15;	Length 1728;
Best Local Similarity	95.6%;	Pred. No. 8.2e-212;		
Matches 862; Conservative	0;	Mismatches 40;	Indels 0;	Gaps 0;

QY	208	AAAGTATGCAAACTTAACGATCCGGGATCATGAAAACGAGAGAACACTTTGAGAACTG	267
Db	827	AAATATATGAAAAGGAGGTAGTTACGAGGATATAGAGCAGAAAGCAACTCTTGGGAACTGT	886
QY	268	GAGACCAATATGCAAACTCCTTTGGAGCAATATAATACAACATTTACCTTTTGCATATGTC	327
Db	887	GAGACCAATATGCAAACTCCTTTGGAGCAATATAATACAACACTACTCTTTTGCATATGTC	946
QY	328	CACCACTGACAAATAGTGAATGCCCCCAATATGTATAAATCGAGAAAGTTGGTCTTTAGCA	387
Db	947	CACCACTGACAAATAGTGAATGCCCCCAATATGTATAAATCGAGAAAGTTGGTCTTTAGCA	1006
QY	388	ACAGCACTAAGGATGTTCCCGAGATTTGAATCAAGAGGATTTGTTGGGGCAATACCTGCT	447
Db	1007	ACAGCACTAAGGATGTTCCCGAGATTTGAATCAAGAGGATTTGTTGGGGCAATACCTGCT	1066
QY	448	TTTATAGAGAGGATGCGAAGAGATGTTGACAGGTGGTATAGATACCATCACAGCAAT	507







```

Db      1067 TTTATGAGAGAGATGGCCAGGAATGTTGATGTTGATGATACATCACACCAAT 1126
QY      508 GACCGAGGATCAGGGATATCCACAGCAGCAAGAAATCCACCTCAAAAGGACATTTGATGAATC 567
Db      1127 GACCGAGGATCAGGGATATCCACAGCAGCAAGAAATCCACCTCAAAAGGACATTTGATGAATC 1186
QY      568 ACCCAAGAGTAAATCTGTGATGTTGAAAGATAAACACCAATTTGAACTGTGGGAA 627
Db      1187 ACCCAAGAGTAAATCTGTGATGTTGAAAGATGAAACCAATTTGAACTGTGGGAA 1246
QY      628 GAATTCGGTAACTTAAAGAAAGACTGAGAACTTGAAACAAAAGATGAGAACGGGTT 687
Db      1247 GAATTCAAATTAATTTAAGAAAGACTGAGAACTTGAAACAAAAGATGAGAACGGGTT 1306
QY      688 CTAGATGTTGAGACAACAATGCTGAGCTTTTATGTTCTATGGAATATAGAGACACT 747
Db      1307 CTAGATGTTGAGACAACAATGCTGAGCTTTTATGTTCTATGGAATATAGAGACACT 1366
QY      748 GACTTTCATGATCTTATGTCAGAAATCTGTATAGTAAAGTCAAGATGAGCTGAGAGAC 807
Db      1367 GACTTTCATGATCTTATGTCAGAAATCTGTATAGTAAAGTCAAGATGAGCTGAGAGAC 1426
QY      808 AACGTCAAAGAACTAAAGAAATGATTTTGAATTTTATCACAATATGATGATGAATC 867
Db      1427 AACGTCAAAGAACTAAAGAAATGATTTTGAATTTTATCACAATATGATGATGAATC 1486
QY      868 ATGATAGTGTGAATACGGGACATATGATTTCCCACTATGAGAGACAGTCTAACTA 927
Db      1487 ATGATAGTGTGAATACGGGACATATGATTTCCCACTATGAGAGACAGTCTAACTA 1546
QY      928 AATGAAATGAATATCAAGGGGTAATAGACAGATGGGGGTTTATCAATATCCTTGGC 987
Db      1547 AATGAAATGAATATCAAGGGGTAATAGACAGATGGGGGTTTATCAATATCCTTGGC 1606
QY      988 AATTATGCTACAGTACAGTTCTATGTCACATGCGCAATGATGAGCTGCTCTTTC 1047
Db      1607 AATTATGCTACAGTACAGTTCTATGTCACATGCGCAATGATGAGCTGCTCTTTC 1666
QY      1048 TGGGCTGTGCTCAACCGCTCTCTGACATGACAGATCTGATATGATTAATGATTTTA 1107
Db      1667 TGGGCTGTGCTCAACCGCTCTCTGACATGACAGATCTGATATGATTAATGATTTTA 1726
QY      1108 TA 1109
Db      1727 TA 1728

RESULT 5
AA072831
ID      AA072831 standard: cDNA: 1728 BP.
XX
AC      AA072831:
XX
DT      25-MAR-2003 (updated)
DT      23-JUN-1995 (first entry)
XX
DE      HA gene of A/Izumi/5/65 strain H2N2 subtype influenza A virus DNA.
XX
KW      Conserved peptide: stem region; hemagglutinin; HA; H1N1; H2N2; PCR;
KW      subtype; human; influenza A virus; immunogenic artificial peptide;
KW      antigen; vaccine; infection; polymerase chain reaction; primer;
KW      amplify; C179; region A; region B; ds.
XX
OS      Influenza A virus.
XX
FH      Key Location/Qualifiers
FH      Misc_feature 1007..1011
FT      /tag=
FT      /note="encodes A region of HA stem - TGLRN"
FT      Misc_feature 1181..1246
FT      /tag=
FT      /note="encodes B region of HA stem - GITNKVSVIER"

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XX      XX
PN      EP621339-A2.
XX      26-OCT-1994.
PD      20-APR-1994; 94EP-0302819.
PF      20-APR-1994; 94EP-0302819.
XX      20-APR-1994; 94EP-0302819.
PR      16-MAR-1994; 94JP-0070194.
XX      (TAKI) TAKARA SHUZO CO LTD.
PA      Isegawa Y, Okuno Y, Sasao F, Ueda S;
PI      WPI; 1994-325949/41.
DR      Human influenza-A virus haemagglutinin polypeptide(s) - useful in
PT      Influenza-A vaccine composition
PS      Example A; Page 35-36; 68pp; English.
XX      XX
CC      This sequence represents the hemagglutinin (HA) molecule of the H2N2
CC      subtype of human influenza A virus, strain A/Izumi/5/65. This molecule
CC      was amplified using the primers given in AA072808-17. The molecules
CC      given in AA072836-39, represent the HA genes from various strains of
CC      H2N2 subtype influenza A virus. The proteins encoded by these cDNAs
CC      contain two conserved regions, the A region, TGLRN and the B region,
CC      GITNKVSVIER. These regions are close to each other in the stem of the
CC      HA molecule and they represent epitopes which are recognised by the
CC      antibody C179. C179 binds to the stem region of the HA molecule and
CC      thus inhibits the membrane fusion action of the HA molecule and
CC      neutralises the virus. Polypeptide molecules which contain the
CC      conserved peptide regions, A and B, are antigenically equivalent to
CC      the stem region of the HA molecule of influenza A virus. These
CC      artificial peptides may be used as vaccines for prophylaxis of
CC      influenza A virus infection.
CC      (updated on 25-MAR-2003 to correct PN field.)
XX      XX
SO      Sequence 1728 BP; 599 A; 319 C; 406 G; 404 T; 0 other;

Query Match      73.6%; Score 834.8; DB 15; Length 1728;
Best Local Similarity 95.3%; Pred. No. 5,8e-211;
Matches 860; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY      208 AAGTTATGCAAACTAAGGATCCGGGATCATGAAACAGAGGAGACCTTGGAGACTG 267
Db      827 AAATATGCAAAAGAGGTAGTTCAGGATCATGAAACAGAGGAGACCTTGGAGACTG 886
QY      268 GAGACCAATGCGCAAACTCCTTGGAGCAATTAATCAACATTTACCTTTTCAGATGTC 327
Db      887 GAGACCAATGCGCAAACTCCTTGGAGCAATTAATCAACATTTACCTTTTCAGATGTC 946
QY      328 CACCCACTGACAAATAGGTAGTCCCAAAATATGTAAATCGGAGAGTTGGCTTATGCA 387
Db      947 CACCCACTGACAAATAGGTAGTCCCAAAATATGTAAATCGGAGAGTTGGCTTATGCA 1006
QY      388 ACAGGACTAAGAAATGTTCCCAAGATTAATCAAGAGGATTTGGGGCAATAGCTGCT 447
Db      1007 ACAGGACTAAGAAATGTTCCCAAGATTAATCAAGAGGATTTGGGGCAATAGCTGCT 1066
QY      448 TTTATGAGAGGAGATGGCAGAAATGTTGACGTTGATGATGATACCATCAGCAAT 507
Db      1067 TTTATGAGAGGAGATGGCAGAAATGTTGATGATGATGATGATACCATCAGCAAT 1126
QY      508 GACCGAGGATCAGGGATATCCACAGCAGCAAGAAATCCACCTCAAAAGGACATTTGATGAATC 567
Db      1127 GACCGAGGATCAGGGATATCCACAGCAGCAAGAAATCCACCTCAAAAGGACATTTGATGAATC 1186
QY      568 ACCCAAGAGTAAATCTGTGATGTTGAAAGATAAACACCAATTTGAACTGTGGGAA 627
Db      1187 ACCCAAGAGTAAATCTGTGATGTTGAAAGATGAAACCAATTTGAACTGTGGGAA 1246
QY      628 GAATTCGGTAACTTAAAGAAAGACTGAGAACTTGAAACAAAAGATGAGAACGGGTT 687

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Db 1247 GAATTCATATATTTAGAGAAAGACTGGAGACTTGACAAAAAGATGAGACGGGTTT 1306
OY 668 CTAGATGCTGACATACATCTCTGAGCTTTAGTTCTGATGGAATATGAGAGACATT 747
Db 1307 CTAGATGCTGACATACATCTCTGAGCTTTAGTTCTGATGGAATATGAGAGACATT 1366
OY 748 GACTTTCATGATTTATATGTAAGAATCTGTATAGTAAGTCAGATGACAGTGAAGAC 807
Db 1367 GACTTTCATGATTTATATGTAAGAATCTGTATAGTAAGTCAGATGACAGTGAAGAC 1426
OY 808 AACGTCAAGAACTAGGAATGAGATGTTTGAATTTTACAAATGATGATGATGAC 867
Db 1427 AACGTCAAGAACTAGGAATGAGATGTTTGAATTTTACAAATGATGATGATGAC 1486
OY 868 ATGATAGTGTGAAAAACGGGACATGATGATTTATCCCAATGTAAGAAAGTCAACTA 927
Db 1487 ATGATAGTGTGAAAAACGGGACATGATGATTTATCCCAATGTAAGAAAGTCAACTA 1546
OY 928 AATAGAAATGAATCAAAAGGGGTAAATTAATGAGCAGCATGGGGTTTATCAATCTTGC 987
Db 1547 AATAGAAATGAATCAAAAGGGGTAAATTAATGAGCAGCATGGGGTTTATCAATCTTGC 1606
OY 988 ATTATGCTACAGTACAGGCTCTATGCTACGTCGCAATGATGCTGGATCTCTTC 1047
Db 1607 ATTATGCTACAGTACAGGCTCTCTGCTACGTCGCAATGATGCTGGATCTCTTC 1666
OY 1048 TGGGCTGCTCCACAGGGCTCTGCTGAGTCGAGATGTCATATGATTAAGCTTTA 1107
Db 1667 TGGATGCTCTCCACAGGGCTCTGCTGAGTCGAGATGTCATATGATTAAGCTTTA 1726
OY 1108 TA 1109
Db 1727 TA 1728

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## RESULT 6

AA139863 ID AA139863 standard; DNA; 1773 BP.

AA139863;

13-SEP-2002 (first entry)

DNA of HA hologene.

Transgenic crop: fowl virus; avian influenza; Newcastle disease; chicken;

infective cloacal bursa disease; hologene; plant; feed; HA; ds.

Unidentified.

CN133370-A.

30-JAN-2002.

16-AUG-2001; 2001CN-0125352.

16-AUG-2001; 2001CN-0125352.

(SHEN-) SHENZHEN SANFANGYUAN INFORMATION TECHNOL.

Zhong A, Qin Z;

WPI; 2002-292920/34.

Crops capable of resisting virus diseases of poultry and production

method thereof -

Claim 1; Page 1-2 (Claims); 22pp; Chinese.

The invention relates to a transgenic crop capable of simultaneously  
resisting up to three kinds of fowl viruses of avian influenza, Newcastle  
disease and infective cloacal bursa disease. The invention also relates

to the production method of the crop. The method of the invention  
includes the following processes: insertion of HA, F and VP2 hologene  
into a plasmid vector, expression of the recombinant plasmid transferred  
into the plant, pairwise hybridisation of the plants which respectively  
possess the action of resisting the above-mentioned three viruses or  
simultaneous hybridisation of three plants. The transgenic seeds can be  
planted into soil to obtain crops for use as a raw material of feed for  
cows with the feed containing a recombinant active protein. This  
polynucleotide sequence represents the 1773 nucleotide DNA of the HA  
hologene relating to the invention.

Sequence 1773 BP; 605 A; 336 C; 403 G; 429 T; 0 other;

Query Match 43.5%; Score 494; DB 24; Length 1773;

Best local Similarity 73.5%; Pred. No. 1,1e-120;

Matches 664; Conservative 0; Mismatches 225; Indels 15; Gaps 2;

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OY 235 ATCATGAAAAACGAAGAACACTTGAGAACTGTGAGACCAATGCCAATCTCTTGGGA 294
Db 854 ATTATGAAAAAGTGAATGGAATATGTAATGTAATGTAATGTAATGTAATGTAATG 913
OY 295 GCAATTAATACACATTAATCTTTTACCAATGTCACACCAATGACATTAATGAGTCC 354
Db 914 GCAATTAATACACATTAATCTTTTACCAATGTCACACCAATGACATTAATGAGTCC 973
OY 355 AATATGTAATTAATCGAGAGAGTGTGCTTACCAACAGCACTAAGCAATGTTCCCAATT 414
Db 974 AATATGTAATTAATCGAGAGAGTGTGCTTACCAACAGCACTAAGCAATGTTCCCAATT 1033
OY 415 G-----AATCAAGAGGATGTTGGGGCAATAGCTGTTTATGANGAGAGA 462
Db 1034 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1093
OY 463 TGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 522
Db 1094 TGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1153
OY 523 TATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 582
Db 1154 TATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1213
OY 583 TCTGATGATGAAAGATTAACACCAATTTGAGCTGTTGGGAAAGATTTGGTAATCTTA 642
Db 1214 TCTGATGATGAAAGATTAACACCAATTTGAGCTGTTGGGAAAGATTTGGTAATCTTA 1273
OY 643 GAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 702
Db 1274 GAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1333
OY 703 TACAAATGCTGAGCTTTAGTCTGATGGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 762
Db 1334 TACAAATGCTGAGCTTTAGTCTGATGGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1393
OY 763 AATGCAAGATCTGTATAGTAAGTCAAGATGCAAGCTGAGAGAGAGAGAGAGAGAGAGAG 822
Db 1394 AATGCAAGATCTGTATAGTAAGTCAAGATGCAAGCTGAGAGAGAGAGAGAGAGAGAGAG 882
OY 823 GGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 882
Db 1454 GGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1513
OY 883 AACGAGAGATGATTAATGCAAGATGCAAGATGCAAGATGCAAGATGCAAGATGCAAGATG 942
Db 1514 AACGAGAGATGATTAATGCAAGATGCAAGATGCAAGATGCAAGATGCAAGATGCAAGATG 1573
OY 943 AAAGGGTAAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1002
Db 1574 AAAGGGTAAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1633
OY 1003 GAGAGTCTATGCTCCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1062
Db 1634 GAGAGTCTATGCTCCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1693

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CC Autographa californica nuclear polyhedrosis virus (AcNPV) 61k protein  
 CC gene signal sequence. The vaccine is used for vaccinating animals  
 CC (including humans) or birds against influenza.

XX Sequence 1766 BP; 604 A; 331 C; 403 G; 428 T; 0 other;

Query Match 39.7%; Score 451; DB 20; Length 1766;  
 Best Local Similarity 70.8%; Pred. No. 2.8e-109;  
 Matches 607; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

226 GGATCCGGGATCATGTAAGAAAGAGAAACCTTGAGAACTGTGAGAACCAATGCCAAACT 285  
 877 GGGTCAGAGATCATCTCCCTCAAGCATCATGATGATGATGATGATGATGATGATGATGAT 936  
 286 CCTTGGGAGCAT 345  
 937 CCCCAGGAGGAGCTATTAACAGTACTCTCTTCCCAAGATGATACACCCAGTCAAGATGAG 996  
 346 GAGTGGCCCCAAT 405  
 997 GATGTCCCAAGAT 1056  
 406 CCCCAGATGATATCAAGAGATGTTGGGCAATAGCTGTTTATAGAAAGAGATG 465  
 1057 CCATCCATCAATCCAGAGGTTGTTGGAGCATTCGCGTTTCATTTGAAGGGGGTGG 1116  
 466 CAAGAAATGGTGGAGTGGTGTATGATNCCATCAGACATACAGATACAGAGATAGGAT 525  
 1117 ACTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1176  
 526 GCAGCAGACAAAGATATCACTCAAAAGCATTTGATGATGATGATGATGATGATGATGAT 585  
 1177 GCTGGGAGCAAAAGAGACACAAATGCCATTAACGGGATTCAGAAAGAGATGCT 1236  
 586 GTATATGAAAAGATTAACACCCCAATTTGAAGCTGTTGGAGAAATTCGGTAACTAGAG 645  
 1237 GTATATGAGAAATGAACTCAATTCAGAGCTGAGGCAAAATTAATCAAAATTAAGAA 1296  
 646 AAAAGACTGGAGAACTTGAACAAAGATGAGAGAGAGAGGTTGTATGATGATGATGATGAT 705  
 1297 AGAGAGATGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1356  
 706 AATGCTGAGACTTTTGTCTGATGAGAAATGAGAGAGACATTTGATGATGATGATGATGAT 765  
 1357 AATGCAAGATTTGTTGTCTACTGAGAAATGAGAGACATTTGATGATGATGATGATGAT 1416  
 766 GTCAACAATCTGTATAGTAAGTCAGATGACGCTGAGAGACAGCTCAAGAGACTAGGA 825  
 1417 GTGAAAGATCTGTATAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 1476  
 826 AATGATGTTTGAATTTTATATCAAAATGATGATGATGATGATGATGATGATGATGATGAT 885  
 1477 AACGGGTGTTTGAATTTTATATCAAAATGATGATGATGATGATGATGATGATGATGATGAT 1536  
 886 GGGACATATGATTAATCCCAAGTATGAGAGAGAGTCTAAATTAATTAATTAATTAATTAAT 945  
 1537 GGAATCTATGACATGCAAAATATTCGGAAGATCAAAAGTAAACAGGGGAAAAATTCAT 1596  
 946 GGGGTAAATTTGAGACATGGGGGTTTATCAAAATCTTCCATTTATGCTACAGTAGGA 1005  
 1597 GGGGTAAATTTGAGATTTGAGAGAGTCTATCAAGATCTGCGCATCTACATCACTGCGCC 1656  
 1006 GGTTCATGTCACACTGCATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1065  
 1657 AGTTCAGTGTGCTTTGGTCTCCCTGGGGGCAATAGCTTCTGAGTGTGTTCTAAVGGG 1716  
 1066 TCTCTGACAGTGCAGATTCATGATATAGA 1092  
 1717 TCTTTCAGTGCAGATATATGATATCTGA 1743

RESULT 12  
 AAD09587

ID AAD09587 standard; DNA: 1766 BP.  
 XX AAD09587;  
 AC 10-SEP-2001 (first entry)  
 DT Influenza virus A/Texas/36/91 recombinant haemagglutinin (rHA) DNA.  
 XX  
 DE Multivalent influenza vaccine; recombinant haemagglutinin; rHA;  
 KW baculovirus expression system; virucide; fusion protein;  
 KM 61k protein; ds.  
 OS Chimeric - Autographa californica nuclear polyhedrosis virus.  
 OS Chimeric - Influenza virus type A.  
 FH Key Location/Qualifiers  
 FH promoter 1..18  
 FT /\*tag- a  
 FT /note- "Autographa californica Nuclear Polyhedrosis Virus  
 FT (AcNPV) polyhedrin promoter"  
 FT /partial  
 FT CDS 19..1737  
 FT /\*tag- b  
 FT /product- "AcNPV 61k protein signal peptide-  
 FT Influenza virus A/Texas/36/91 mature HA fusion protein"  
 FT sig-peptide 19..72  
 FT /\*tag- c  
 FT /note- "AcNPV 61k signal sequence"  
 FT mat-peptide 73..1734  
 FT /\*tag- d  
 FT /product- "Influenza virus A/Texas/36/91 mature  
 FT HA protein"  
 FT misc\_signal 1756..1766  
 FT /\*tag- e  
 FT /note- "universal translation termination signal"  
 PN US6245532-B1.  
 XX 12-JUN-2001.  
 PD 09-OCT-1998; 98US-0169027.  
 PF 30-MAY-1995; 95US-0453848.  
 PR 13-SEP-1993; 93US-0120607.  
 XX (PROT-) PROTEIN SCT CORP.  
 PA Smith GE, Volovitz F, Wilkinson BE, Voznesensky AI, Hackett CS;  
 PI WPI: 2001-407272/43.  
 DR P-PSDB; AAE04952.  
 DR  
 XX  
 PT Expressing a protein e.g. recombinant influenza virus haemagglutinin  
 PT comprising using a vector encoding a polypeptide comprising a  
 PT baculovirus signal peptide and a baculovirus expression system is  
 PT useful as a multivalent influenza vaccine -  
 XX  
 XX Claim 5: Column 41-44; 51pp: English.  
 XX  
 XX The present invention relates to a method for expressing an exogenous  
 XX protein in a baculovirus expression system which comprises using a vector  
 XX encoding a polypeptide comprising a baculovirus signal peptide operably  
 XX linked to a heterologous amino acid sequence. The method is especially  
 XX useful for preparing a protein which may be used to make a multivalent  
 XX influenza vaccine based on a mixture of recombinant haemagglutinin  
 XX (HA) antigens cloned from influenza viruses having epidemic potential.  
 XX The recombinant haemagglutinin proteins are full length,  
 XX uncleaved (HA0) glycoproteins including both the HA1 and HA2 subunits  
 XX (HA0) purified under non-denaturing conditions. The use of recombinant  
 XX DNA (rDNA) technology to produce influenza vaccine offers several  
 XX advantages, e.g., a recombinant DNA influenza vaccine can be produced  
 XX under safer and more stringently controlled conditions; propagation with  
 XX infectious influenza in eggs is not required; recombinant haemagglutinin

CC (rHA) protein can be more highly purified, purification procedures for  
 CC rHA do not have to include virus inactivation or organic extraction of  
 CC viral membrane components, production of HA via rDNA technology provides  
 CC an opportunity to avoid the genetic heterogeneity which occurs during  
 CC the adaptation and passage through eggs, which should make it possible to  
 CC better match vaccine strains with influenza epidemic strains, resulting in  
 CC improved efficacy. The present sequence is recombinant haemagglutinin  
 CC (rHA) DNA comprising Autographa californica Nuclear Polyhedrosis Virus  
 CC (AcNPV) 61k gene partial polyhedrin promoter and signal sequence linked  
 CC to Influenza virus A/Texas/36/91 mature HA coding region.  
 CC  
 XX

Sequence 1766 BP; 604 A; 331 C; 403 G; 428 T; 0 other;

Query Match 39.7%; Score 451; DB 22; Length 1766;

Best Local Similarity 70.0%; Pred. No. 2.8e-109;

Matches 607; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

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OY 226 GGATCCGGATCATGAAAAACAGAGAACACTTGAGACTGTGACGCCAATGCCAACT 285
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 877 GGGTCAGGATCATCACTCAACCGCATATGATGATGATGATGATGATGATGATGAT 936
OY 286 CCTTGGGAGACATAATACACATACCTTTTCCATATGTCACCCAGTACCAATAGCT 345
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 937 CCCCAAGGAGCTATTAACAGTACTCTCTTCCAGATGTACACCCAGTACCAATAGGA 996
OY 346 GAGTCCCCCAATATGTAATCGAGAAAGTGGCTTACACAGAGACTAAGGAATGTT 405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 997 GAGTGCACCAAGATGTGAGAGTACCAAAATTAAGATGGTTACAGACTAAGCAATC 1056
OY 406 CCCCAGATTGAATCAAGAGATGTTGGGGCAATAGCTGTTTATAGAGAGAGATGG 465
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1057 CCATCCATTCAATCCAGAGGTTGTTTGGAGGCCATTGCGTTTCAATTGAGGGGGTGG 1116
OY 466 CAAGGAATGTTGACGGTGTATGATGATCATCAGCAATGACCAAGGATGAGGTTAT 525
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1117 ACTGAAATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1176
OY 526 GCAGAGACAAAGAAATCCACTCAAAAGGATTTGATGATGATGATGATGATGATGAT 585
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1177 GCTGCGGACCAAAAAAGCACCAAAATGCCATTAAAGGATTTACAAACAGTGATTC 1236
OY 586 GTGATGAAAAAATTAACCCCAATTTGAAGCTGTGGGAAAGATTCGTAATCTTAGAG 645
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1237 GTAATCGAAAAATGACACTCAATTCACAGCTGTGGGCAAGAAATTAACCAATTTGAA 1296
OY 646 AAAAGACTGAGAACTTGAACAAAAAGATGAGAGAGCGGTTCTAGATGTCGATCATC 705
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1297 AGAAGATGCAAACTTAATAAAAAAGTTGATGATGATGATGATGATGATGATGATGAT 1356
OY 706 AATGCTGAGCTTTAGTTCTGATGGAAGATGAGAGACACTTGACTTTGATGATTCAT 765
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1357 AATGCAAGATTGTTGTTCTACTGTAAGAAATGGAAGACTTTGATTTCTATGACTCA 1416
OY 766 GTCAAGAACTGATAGTAAGTCAAGAACTGAGAGAGACAACTCAAAAGACTAGAGA 825
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1417 GGAAGAAATCTGATAGAAATAAAAGCCCAATGGAAGAAATTAATGCGGAAAGATGG 1476
OY 826 AATGATGTTTGAATTTTATCACAAAATGTGATGATGATGATGATGATGATGATGATG 885
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1477 AACGGGTGTTTGAATTTTATCACAAGTATACATGATGATGATGATGATGATGATGAT 1536
OY 886 GGGACATATGATTTATCCCAAGTATGAGAGAGCTAAACTAATAGAAATGAATCAAA 945
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1537 GGAATTTATGACTATCCAAATATTCGGAAGATCAAAAGTTAAACAGGGGAAAAATGAT 1596
OY 946 GGGGTAATTTGAGAGACATGGGGTTTAAATCCTTGCAATTTATCTCAAGTAGAGA 1005
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1597 GGAGTGAATTTGGAATCAATGGAGCTATACAGATTTGGCGATCTACTCAACTGTCGCC 1656
OY 1006 GGTTCATGCTACTGCAATCATGATGGCTGGGATCTCTTCTGGGTGTCTCAACGGG 1065
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1657 AGTTCACGAGGCTTTTGGTCTCCCTGGGGGCAATCAGCTTCTGATGTGTTCTAATGGG 1716

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OY 1066 TCTCTGACAGTCAGAGATCTGCATATGA 1092  
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 DB 1717 TCTTTCAGTGCAGATATGAAATCTGGA 1743

# RESULT 13

ID AAA76188 standard; DNA: 1724 BP.

AAA76188:

15-DEC-2000 (first entry)

Swine Influenza virus haemagglutinin gene SIV-HA.

Swine: haemagglutinin; nucleoprotein; SIV; HA; NP; vaccine;  
 immunisation; ss.

Swine Influenza virus.

CA2290197-AI.

23-MAY-2000.

23-NOV-1999; 99CA-2290197.

23-NOV-1998; 98US-0197679.

(FOLE/) FOLEY P. L.

Foley PL;

WPI; 2000-524822/48.

Novel recombinant vaccinia virus for immunizing swine against  
 influenza, contains inserts of haemagglutinin and nucleoprotein genes  
 from swine influenza virus

Disclosure; Page 12; 27pp; English.

The present sequence is swine influenza virus (SIV) haemagglutinin (HA)  
 gene. This sequence was used to produce a recombinant vaccinia virus  
 containing as inserts the present sequence and the swine influenza virus  
 nucleoprotein (NP) gene (see AAA76188). The present sequence was  
 amplified by RT-PCR and cloned, and then subsequently subcloned into a  
 transfection vector that allowed insertion of the SIV-HA sequence into  
 the genome of the modified vaccinia virus Ankara (MVA) strain of vaccinia  
 virus. The recombinant vaccinia virus is useful as a vaccine for  
 immunising a swine against influenza. In addition, by protecting pigs  
 from influenza infection, the human population would be protected from  
 transfer of infection from swine to the human population.

Sequence 1724 BP; 607 A; 316 C; 377 G; 424 T; 0 other;

Query Match 39.5%; Score 448.6; DB 21; Length 1724;  
 Best Local Similarity 70.3%; Pred. No. 1.2e-108;  
 Matches 615; Conservative 0; Mismatches 259; Indels 1; Gaps 1;

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OY 226 GGATCCGGATCATGAAAAACAGAGAACACTTGAGAACTGTGACCAATGCCAACT 285
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 835 GGAATCGGATTAATATATTTTCAATACACAGTCCAGATGATTAATAGACCTGTCAACA 894
OY 286 CCTTGGGAGCAATTAATCAACATTTTTCATATGTCACCACTGACATGAATAGT 345
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 895 CCCAAGAGGTCTATAACACAGCGCTCCATTTTCAGATATATACATCCAGTACATTTGA 954
OY 346 GAGTCCCCCAATATATGTAATCGAGAAAGTGGCTTTAGCAACAGACTAAGGAATGTT 405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 955 GAATCTCCAAATATGTCACAAAGTAACAAATTTGAGAAATGCTACAGGATTAAGGAATATC 1014
OY 406 CCCCAGATTGAATCAAGAGATGTTGGGCAATAGCTGTTTATAGAAAGAGATGG 465
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1015 CCGTCTATTCATCTAAGGGGCTGTTTGGAGCCATTCCTGCTGCTTATTTAGAGGGGGTGG 1074

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QY	466	CAAGGAATGTTGAC	GTGGTATGATGATACCATCACAGCATGACAGGATCAGCGTAT	525
Db	1075	ACAGGAATGATAGAT	GGATGGTACGGTATATCACATCAAAATGAGCGGGATCAGATAT	11334
QY	526	GCAGCAGCAAGAAN	CCACTCAAAAGGCATTGTGATGGAATCCACCAACAGTAATCT	585
Db	1135	GCAGCGCAGCAAAAG	GCACACAGATGCCATTGCGGGATCCTAAACAAAGTAATCT	1194
QY	586	GTGATTGAAAGATAT	ACACCCATTTTAACTGTGTGGGAAAGATTTGGTACTTAAAG	645
Db	1195	GTATTATGAAAGATAT	ACACACAAATTCACACAGAGGGGTAAGATTTAAACCACTTGAA	1254
QY	646	AAAAGACTGAGAACT	TGACAAAAAGATGAGAGAGCGGGTCTTAGATGTGTGCACATAC	705
Db	1255	AAAAGAAATAGAGAT	TTTAATTAAGATGGTATGATGGTTTTCTTGATGTTTGGACTTAC	1314
QY	706	AATGTGAGCTTTTAT	GTTCGTGAGAAAATGAGAGACCTTGACTTTCATGATTTAT	765
Db	1315	AATGCCGAATTTGTTG	TTCTATTGGAAAAATGAAAGAACTTTGGATTACCATGACTCAAT	1374
QY	766	GTCAGAACTCTGTAT	ATATTAATGATGAGAGAGAGAGCAACGTCAAGAACTAGAGA	825
Db	1375	GTGAAGAACTATATG	AGAAAGTAGAAGCCAGCTAAAAAACAATGCCAAGAAATTGGA	14334
QY	826	AATGATGTTTGAAT	TTTATCACAAATGTGATGATGATGATCATGATTAATGATGAAAAAC	885
Db	1435	AATGGCTCTTTGAAT	TTTACCACAAATGTGATGATGATGATGATGATGATGATGATGAT	1494
QY	886	GGGACATATGTTTAC	CAAGTATGAGAAAGAGCTAACTTAATTAATAGAAATGAATCAA	945
Db	1495	GGGACTTATGATTTAC	CCAAATTAATGAGAAATCAAACTTAACAGAGAGAGATAGAT	1554
QY	946	GGGGTAAATTTGAGCA	TCATGGGGTTTATCAAAATCCTTGCCATTATGTATACATAGCA	10059
Db	1555	GGAGTAAAGCTGGAAT	TAAACAAGATTTACAGATTTGGGAGATATTAACAAGTGTGCC	16144
QY	1006	GGTCTATATGTAC	TGCATCATGATGATGGGATCTCTTTCTGGTGTGCTCCACAGG	1064
Db	1615	AGTTCATTGGTACTTG	TAGTCTCCCTGGGAGCAATGATTTCTGGATGTCTCCAAATGG	1674
QY	1065	GTCCTCGCAGTGACAG	TCTGCATATGATTTAAG	1099
Db	1675	GTCCTTACGTGCAGAT	TATATTTAAATTAGG	1709
RESULT 14				
AA064451				
ID	AA064451	standard:	cDNA tc mRNA; 1754 BP.	
XX	AA064451:			
AC				
XX				
DT	11-JAN-1995	(first entry)		
XX				
DE	A/Suila/1/89	human influenza A type virus plasmid fragment.		
XX				
KW	Antigens: main region; hemagglutinin; HN1; HN2; subtype: human;			
KW	influenza A type virus; H3N2; anti-human influenza virus antibody;			
KW	diagnosis; prevention; trethment; vaccine; ss.			
XX	Synthetic.			
OS				
PN	Jp06100594-A.			
XX				
PD	12-APR-1994.			
XX				
PE	17-SEP-1992;	92JP-0272531.		
XX				
PR	17-SEP-1992;	92JP-0272531.		
XX				
EA	(TAKI ) TAKARA SHUZO CO LTD.			
XX				
DR	WPI; 1994-156655/19.			

XX	Anti human influenza virus antibody - for diagnosis and treatment
PT	of influenza type A virus
PS	Disclosure: page 13-14; 18pp; Japanese.
XX	The sequences given in AA064451-65 represent fragments of plasmids which
CC	encode antigenic peptides from the H1N1, H2N2 or H3N2 subtypes of human
CC	influenza A type virus. These sequences were derived by PCR using the
CC	primer sequences given in AA062141-50 and AA064439-50. The amplified
CC	sequence encode at least one antigen which is derived from the main
CC	region of hemagglutinin of the H1N1, H2N2, or H3N2 subtype of human
CC	influenza A type virus. The anti-human influenza virus antibody of the
CC	invention, is reactive against antigens derived from the H1N1 and H2N2
CC	subtypes but not against H3N2 subtype derived peptides. This antibody
CC	is useful for diagnosis, prevention and treatment of human influenza A
CC	type virus. The antigenic peptides are important in vaccine production.
XX	
XX	Sequence 1754 BP; 615 A; 327 C; 394 G; 418 T; 0 other:
XX	
XX	Query Match 39.5%; Score 447.8; DB 15; Length 1754;
XX	Best Local Similarity .69.8%; Pred. No. 2e-108;
XX	Matches 605; Conservative 0; Mismatches 265; Indels 0; Gaps 0;
QY	226 GGATCCGGGATCATGAAACAAAGAGAACACTTGAGAACTGTGAGACCAATGCCAACT 285
DB	855 GGGTCAGAAATCATCTACCTCAACAGCATCAATGATGATGAGCGGAAGTCTCAACA 914
QY	286 CCTTTGGAGCAATTAATCAACAATTAACCTTTTCAATATGTCACCACTGACATTAAGT 345
DB	915 CCCCAGGAGGATTAATACAGTAAGTCTCTTCCAGAAATGTACACCAGTCAATTAAGA 974
QY	346 GAGTGCCTCCCAATATGTAAATTCGAGAGAGTGTGCTTCAGAACACAGACTAAGAAATTT 405
DB	975 GAGTGTCCAAAGTATGTGAGAGATTCACAAATTAAGATGTTATACAGAGCTAAGAAACATC 1033
QY	406 CCCCAGATTGAATCAAGAGATTTGTTGGGCATAGCTGGTTTATAGAAAGAGATGG 465
DB	1035 CCATTCATTCATCCAGAGAGTTGTTGGACCAATGCGGGTTTCATTGAAGGGGGGTGG 1094
QY	466 CAAAGATGGTGTGAGCGTTGGTATGGAATACCATCAACAGTACAGAGATTCAGGGAT 525
DB	1095 ACTGGAATGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1154
QY	526 GCAGCAGCAAAAGATCCATCAAAAGGCAATTTGATGGAATCACCACAGGTAATTTCT 585
DB	1155 GCTCGCGATCAAAAAGACACACAAATCCATTAAGCAATTAACAAAGTGAATCT 1214
QY	586 GTGATTTGAAAGATTAACACCAATTTGAACCTGTGGGAAAGATTTGGTAACTTAGAG 645
DB	1215 GTATTCGAGAAATGAACATCAATTCACACTGTGGGCAAAAGAAATTAACAAATTAAGA 1274
QY	646 AAAAGACTGAGAACTTGACAAAAGAGTGAAGACGCGTTTCTAGATGTGTGCATATC 705
DB	1275 AGAAGGATGGAATCTTAATTAATAAAGATGATGATGATGATGATGATGATGATGAT 1334
QY	706 AATGCTGAGCTTTAGTTAGTTCTGATGAGAAATGAGAGACACTTGACTTTCATGATTTCAAT 765
DB	1335 AATCGAGAAATGTTGGTTCTACTGGAATTAAGAGGACTTTGGATTTTTCATGACTCAAT 1394
QY	766 GTCAAGAAATCTGTATAGTAAGTCAAGATGAGGTGAGAGACAGCTCAAAAGACTAGGA 825
DB	1395 GTGAAGAAATCTGTATGAGAAAGTAAAGGCAATTAAGAAATTAATGCCAAAGAAATAGGA 1454
QY	826 AATGAGATTTTGAATTTTATACAAATGTGATGATGATGATGATGATGATGATGATGAT 885
DB	1455 TACGGGTGTTTGAATTTCTACCAAGGTAAATGATGATGATGATGATGATGATGATGAT 1514
QY	886 GGAACATATGATTTATCCCAAGTATGAGAGAGAGTCTAACTTAATAGAAATGAATCAAA 945
DB	1515 GGAACATATGATTTTCAAAATATTTCCGAGAAATCAAAAGTTAAACAGGAAATAAATTCAT 1574
QY	946 GGGGTAAATTTGACAGAGATGGGGTTTATCAAAATCCTGGCATTTATGTATCAAGTACGA 1005

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DB      1575 GGAGTGAATTCATGCAATGGAGTCTATCAGATTCTGGCGATCTACTCACTGCGCC 1634
OY      1006 GGTTCATGTCACATGTCATCATGATGGGATGCTCTTCGGGTCGTCACACGGG 1065
DB      1635 ATTTCATGTCGCTTTTGGTCTCCCTGGGGCATACGCTTCTGATGTCTTAATGGG 1694
OY      1066 TCTCTGACATGACAGATCTGCATATGA 1092
DB      1695 TCTTTCAGCTGTAGATATGACATCTGA 1721

RESULT 15
AA072830
ID      AA072830 standard; cDNA; 1754 BP.
XX
AC      AA072830;
XX
DT      25-MAR-2003 (updated)
DT      23-JUN-1995 (first entry)
XX
DE      HA gene of A/SuIta/1/89 strain H1N1 subtype Influenza A virus DNA.
XX
KM      Conserved peptide: stem region: hemagglutinin; HA; H1N1; H2N2; PCR;
KM      subtype: human; Influenza A virus; immunogenic artificial peptide;
KM      antigen; vaccine; infection; polymerase chain reaction; primer;
KM      amplify; C179; region A; region B; ds.
XX
OS      Influenza A virus.
XX
XX      Key      Location/Qualifiers
XX      FT      Misc_feature      1017..1031
XX      FT      /tag= a
XX      FT      /note= "Encodes A region of HA stem - TGLRN"
XX      FT      Misc_feature      1191..1226
XX      FT      /tag= b
XX      FT      /note= "Encodes B region of HA stem - GITNKNVSVIEK"
XX
XX      EP621339-A2.
XX      PN      26-OCT-1994.
XX      PD      20-APR-1994; 94EP-0302819.
XX      PF      20-APR-1993; 93JP-0115216.
XX      PR      16-MAR-1994; 94JP-0070194.
XX      PA      (TAKI ) TAKARA SHUZO CO LTD.
XX
XX      Isegawa Y, Okuno Y, Sasao F, Ueda S;
XX      WPI; 1994-325949/41.
XX
XX      Human influenza-A virus haemagglutinin polypeptide(s) - useful in
XX      Influenza-A vaccine composition
XX
XX      Example A: Page 33-34; 68pp; English.
XX
XX      This sequence represents the hemagglutinin (HA) molecule of the H1N1
XX      subtype of human influenza A virus, strain A/SuIta/1/89. This molecule
XX      was amplified using the primers given in AA072808-17. The molecules
XX      given in AA072830-36, represent the HA genes from various strains of
XX      H1N1 subtype Influenza A virus. The proteins encoded by these cDNAs
XX      contain two conserved regions, the A region, TGLRN and the B region,
XX      GITNKNVSVIEK. These regions are close to each other in the stem of the
XX      HA molecule and they represent epitopes which are recognised by the
XX      antibody C179. C179 binds to the stem region of the HA molecule and
XX      thus inhibits the membrane fusion action of the HA molecule and
XX      neutralises the virus. Polypeptide molecules which contain the
XX      conserved peptide regions, A and B, are antigenically equivalent to
XX      the stem region of the HA molecule of influenza A virus. These
XX      artificial peptides may be used as vaccines for prophylaxis of
XX      Influenza A virus infection.

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CC      (Updated on 25-MAR-2003 to correct PN field.)
XX      SO      Sequence 1754 BP; 615 A; 327 C; 394 G; 418 T; 0 other;
XX
XX      Query Match      39.5%; Score 447.8; DB 15; Length 1754;
XX      Best Local Similarity 69.8%; Pred. No. 26-108;
XX      Matches 605; Conservative 0; Mismatches 262; Indels 0; Gaps 0;
XX
OY      226 GGATCCGGGATCATGAAAACAGAGAAACACTTGTAGAGTGAACCAATGCCAACT 285
DB      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB      855 GGATCGAGATCATCTACCTCAACCATCATCATGATGATGACCGCAAGTGTCAACA 914
OY      286 CCTTTGGAGCAATAAATCAACATTACCTTTTCAATGTCACCACTGACATATAGT 345
DB      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB      915 CCCAGAGAGAGCTAIAAACAGTAGTCTCTTCCAGAAATGTAACCCAGTCATATAGGA 974
OY      346 GAGTCCCCCAATATGTAAATCGAGAACTTGTCTTACCAACAGGACTAAGAAATGTT 405
DB      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB      975 GAGTGTCCAAAGATGTCTCAGAGACTCAAAATTAAGATGTTCACGAGCTAAGCAATC 1034
OY      406 CCCAGATTGAATCAAGAGATGTTTGGGGCAATAGCTGGTTTATGAGAGAGATGG 465
DB      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB      1035 CCATCCATTCAATCCAGAGAGTTGTGTGAGCCATTGCCGTTTCATTGAAGGGGGTGG 1094
OY      466 CAAGAAATGTTGACGGTTGTATGATATCATCATCAGACCAATGACCAAGGATCAGGAT 525
DB      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB      1095 ACTGGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1154
OY      526 GCAGCAGACAAGAAATCCACTCAAAAGCAATTTGATGCAATCCACAAAGTAAATCT 585
DB      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB      1155 GCTGCGGATCAAAAAGCACAAACCAATGCCATTAAAGCAATTAACAAACAGTAAATCT 1214
OY      586 GTGATTAAGAAAGTAACACCCCAATTTGAGCTGTGGGAAAGAAATGCTTAATCTAGAG 645
DB      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB      1215 GTATATGACAAATATGACCTAATTCACAGCTGTGGCCAAAGATTTACAAATTTGAA 1274
OY      646 AAAAGACTGAGAACTTGAACAAAAGATGGAAGAGGGTTTCTAGATGTGTGACATAC 705
DB      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB      1275 AGAAGATGAGAAATTAATTAATAAAGTTGATGATGATGATGATGATGATGATGAT 1334
OY      706 AATGCTGAGCTTTTACTTCTGATGGAATATGAGAGACACTTGATTCATGATTCAT 765
DB      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB      1335 AATGCAAAATTTGTGTTCTACTGGAATAAGAAAGACTTTGATTTCAAGACTCAAT 1394
OY      766 GTCAAGAAATCTGTATAGTAAGTCAAGATGACAGAGACAAAGTCAAGAACTGGA 825
DB      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB      1395 GTCAAGAAATCTGTATGAGAAATTAAGAAAGCAATTAAGAAATTAAGCAAGAAATGGA 1454
OY      826 AATGATGTTTGAATTTATCAAAATGTGATGATGATGATGATGATGATGATGATGAT 885
DB      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB      1455 TACGGGTGTTTGAATTTACCAAAAGTGAATGAATGATGATGATGATGATGATGAT 1514
OY      886 GGCACATATGATTAATCCCAAGTATGACAAAGTCTTAACATTAATGAAATGAAATCAA 945
DB      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB      1515 GGAACCTTAAGACTATCAAAATATTCGAGGAAATCAAAAGTTAAACAGGAAATTAATGAT 1574
OY      946 GGGTAAATATGAGACAGATGGGGTTTAATCAATCCCTTGCCATTATGCTACAGTGA 1005
DB      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB      1575 GGAGTGAATTTGGAATCAATGGAATGGAATCTATGATGATGATGATGATGATGATGAT 1634
OY      1006 GGTTCATGTCACATGTCATCATGATGGGATGCTCTTCGGGTCGTCACACGGG 1065
DB      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB      1635 ATTTCATGTCGCTTTTGGTCTCCCTGGGGCATACGCTTCTGATGTCTTAATGGG 1694
OY      1066 TCTCTGACATGACAGATCTGCATATGA 1092
DB      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB      1695 TCTTTCAGCTGTAGATATGACATCTGA 1721

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Search completed: August 10, 2003, 02:11:17  
 Job time : 220.814 secs

PenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 18:45:33 : Search time 4490.7 Seconds

(without alignments)  
16242.876 Million cell updates/sec

Title: US-09-918-568-46

Perfect score: 1783

Sequence: 1 CGCGTAGCAAAAGCAGCGGT.....ACCCCTGTCTCTGCTAGCCG 1783

Scoring table: IDENTITY\_NUC

Gapop 10.0, Expect 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: gb\_da:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
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32: em\_htg\_other:\*  
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35: em\_htg\_ro:\*  
36: em\_htg\_man:\*  
37: em\_htg\_vir:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	1783	100.0	1783	6	ARI81961	ARI81961 Sequence
2	1783	100.0	1783	6	I32526	I32526 Sequence 46
3	1783	100.0	1783	6	I43471	I43471 Sequence 46
4	1741	97.6	1773	14	FLAARJ3055	J02127 Influenza A
5	1741	97.6	1773	14	FLAARJ3055	J02127 Influenza A
6	1734.6	97.3	1773	14	FLAARJ3055	J02127 Influenza A
7	1734.6	97.3	1773	14	FLAARJ3055	J02127 Influenza A
8	1729.8	97.0	1773	14	FLAARJ3055	J02127 Influenza A
9	1728.2	96.9	1773	14	FLAARJ3055	J02127 Influenza A
10	1726.6	96.8	1773	14	FLAARJ3055	J02127 Influenza A
11	1726.6	96.8	1773	14	FLAARJ3055	J02127 Influenza A
12	1725	96.7	1773	6	AX399727	AX399727 Sequence
13	1720.2	96.5	1773	14	AB056699	AB056699 Influenza
14	1671.4	93.7	1773	14	FLAARJ3055	J02127 Influenza A
15	1659.4	93.1	1773	14	FLAARJ3055	J02127 Influenza A
16	1649.8	92.5	1773	14	FLAARJ3055	J02127 Influenza A
17	1648.2	92.4	1773	14	FLAARJ3055	J02127 Influenza A
18	1637	91.8	1773	14	FLAARJ3055	J02127 Influenza A
19	1606.4	90.1	1728	6	ARI81943	ARI81943 Sequence
20	1606.4	90.1	1728	6	E07248	E07248 Haemagglut
21	1606.4	90.1	1728	6	I32508	I32508 Sequence 28
22	1606.4	90.1	1728	6	I43453	I43453 Sequence 28
23	1565	87.8	1773	14	FLAARJ3055	J02127 Influenza A
24	1537.8	86.2	1773	14	FLAARJ3055	J02127 Influenza A
25	1525	85.5	1773	14	FLAARJ3055	J02127 Influenza A
26	1523.4	85.4	1773	14	FLAARJ3055	J02127 Influenza A
27	1515.4	85.0	1773	14	FLAARJ3055	J02127 Influenza A
28	1514.6	84.9	1772	14	FLAARJ3055	J02127 Influenza A
29	1511.4	84.8	1772	14	FLAARJ3055	J02127 Influenza A
30	1481.8	83.1	1773	14	FLAARJ3055	J02127 Influenza A
31	1462.4	82.0	1773	14	FLAARJ3055	J02127 Influenza A
32	1460.8	81.9	1773	14	FLAARJ3055	J02127 Influenza A
33	1460.8	81.9	1773	14	FLAARJ3055	J02127 Influenza A
34	1459.2	81.8	1773	14	FLAARJ3055	J02127 Influenza A
35	1365	76.6	1773	14	FLAARJ3055	J02127 Influenza A
36	1348.2	75.6	1772	14	FLAARJ3055	J02127 Influenza A
37	1325	74.3	1773	14	FLAARJ3055	J02127 Influenza A
38	1322.6	74.2	1772	14	FLAARJ3055	J02127 Influenza A
39	1321	74.1	1772	14	FLAARJ3055	J02127 Influenza A
40	1262.4	70.8	1773	14	FLAARJ3055	J02127 Influenza A
41	1066.4	59.8	1077	14	AF231354	AF231354 Influenza
42	1063.2	59.6	1077	14	AF231355	AF231355 Influenza
43	999.4	56.1	1017	14	AF270717	AF270717 Influenza
44	997.8	56.0	1017	14	AF270716	AF270716 Influenza
45	997.8	56.0	1017	14	AF270728	AF270728 Influenza

#### ALIGNMENTS

RESULT 1  
LOCUS ARI81961 1783 bp DNA  
DEFINITION Sequence 46 from patent US 6337070.  
ACCESSION ARI81961  
VERSION ARI81961.1 GI:20224877  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1783)  
TITLE Okuno,Y., Isegaawa,Y., Sasao,F. and Ueda,S.  
Polypeptides for use in generating anti-human influenza virus  
antibodies  
JOURNAL Patent: US 6337070-A 46 08-JAN-2002;

FEATURES		Location/Qualifiers	
source	1..1783	/organism="unknown"	
BASE COUNT	610 a 323 c 424 g 426 t		
ORIGIN			
Query Match	100.0%:	Score 1783;	DB 6; Length 1783;
Best Local Similarity	100.0%:	Pred. No. 0;	
Matches 1783;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	CGGCTAGCAAAAGCAGGGGTTATACCATGAAAACCAAAAGCAAAACATGGCCATCATT	60
Db	1	CGGCTAGCAAAAGCAGGGGTTATACCATGAAAACCAAAAGCAAAACATGGCCATCATT	60
QY	61	TATCTCATTTCTCCTGTTCCACAGCAGTGAGAGGGGACAGATATGCAATTGGATACCATGCC	120
Db	61	TATCTCATTTCTCCTGTTCCACAGCAGTGAGAGGGGACCAATATGCAATTGGATACCATGCC	120
QY	121	AATTAATTCACAGAGAGTGCACACAAATCTTAGAGCGGAGACGTGACTGTGACTCATGCC	180
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QY	181	AAGGACATCTCTTGAGAGAGCCCATTAACGGAAAGTTATGCAAACTAAACGGAAATCCCTCA	240
Db	181	AAGGACATCTCTTGAGAGAGCCCATTAACGGAAAGTTATGCAAACTAAACGGAAATCCCTCA	240
QY	241	CTTGAACATGAGGGGACTGTAGCATTTGCCGAGTGGCTCTTGGAAATCCAAATGTGATAGG	300
Db	241	CTTGAACATGAGGGGACTGTAGCATTTGCCGAGTGGCTCTTGGAAATCCAAATGTGATAGG	300
QY	301	CTTCTAAGTGTCCCAAGACGGTCTATATATTGAGAAAGAAAACCCGAGAGCGGTTTG	360
Db	301	CTTCTAAGTGTCCCAAGACGGTCTATATATTGAGAAAGAAAACCCGAGAGCGGTTTG	360
QY	361	TGTTATCCAGGACGCTTCATGATTATGAAAGATTGAACATCTCTCAGCAGCGCTGAAA	420
Db	361	TGTTATCCAGGACGCTTCATGATTATGAAAGATTGAACATCTCTCAGCAGCGCTGAAA	420
QY	421	CATTTGCGAAGAAAGTAAAGATTCTGCCCAAAAGATGATGACACAGATATACAACTGGA	480
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QY	481	GGTTCACGGGCTGCGCGGTGTCTGTATCCATCATTTTTCAGAAACATGGTGGCTG	540
Db	481	GGTTCACGGGCTGCGCGGTGTCTGTATCCATCATATTTTTCAGAAACATGGTGGCTG	540
QY	541	ACAAAGGAAGATCAGATTATCCGGTGGCAAAAGATGTACAACAATACACGGAGAA	600
Db	541	ACAAAGGAAGATCAGATTATCCGGTGGCAAAAGATGTACAACAATACACGGAGAA	600
QY	601	CAATGCTAATTAATTTGGGGGGTGACCATCCATGATGAGACGACAAACAAACATTTG	660
Db	601	CAATGCTAATTAATTTGGGGGGTGACCATCCATGATGAGACGACAAACAAACATTTG	660
QY	661	TACCAAGATGTGGGAACCTATGTTCCGTAGGCACATCAACATTTGAACAAAAGGTCAAC	720
Db	661	TACCAAGATGTGGGAACCTATGTTCCGTAGGCACATCAACATTTGAACAAAAGGTCAAC	720
QY	721	CCAGAAATAGCAACAGGCTTAAAGTGAATGACAAAGAGGTAGATTTCTTTGG	780
Db	721	CCAGAAATAGCAACAGGCTTAAAGTGAATGACAAAGAGGTAGATTTCTTTGG	780
QY	781	ACCCCTTGGATATGTGGGACACCAATTAATTTTGAGAGTACGTGTAATTTGACACA	840
Db	781	ACCCCTTGGATATGTGGGACACCAATTAATTTTGAGAGTACGTGTAATTTGACACA	840
QY	841	GAGTATGATTCACAAATATCGAAAAGAGTACTTGAAGGATGATGAAGACAGAGACA	900
Db	841	GAGTATGATTCACAAATATCGAAAAGAGTACTTGAAGGATGATGAAGACAGAGACA	900
QY	901	CTTGAAGACTGTGAGACCAAAATGCAAACTCTTTGGAGCAATTAATCAACATTTACT	960
Db	901	CTTGAAGACTGTGAGACCAAAATGCAAACTCTTTGGAGCAATTAATCAACATTTACT	960

QY	961	TTTCACATGTCCACCCACTGACAAATAGTGTGCCCCCAATATGTAAATCGAGAG	1020
DB	961	TTTCACATGTCCACCCACTGACAAATAGTGTGCCCCCAATATGTAAATCGAGAG	1020
QY	1021	TTGGCTTTACACACAGGACTTAAGGAATGTTCCCAATTTGAATCAAGAGATTTTGGG	1080
DB	1021	TTGGCTTTACACACAGGACTTAAGGAATGTTCCCAATTTGAATCAAGAGATTTTGGG	1080
QY	1081	GCAATACCTGGTTTTATAGAGAGATGGCAAGGAATGTTGACCGTTGATGTATG	1140
DB	1081	GCAATACCTGGTTTTATAGAGAGATGGCAAGGAATGTTGACCGTTGATGTATG	1140
QY	1141	CATCACAGCAATGACACAGGATCAGGTTATGACAGACAAAGAAATCCACTAAAAGCA	1200
DB	1141	CATCACAGCAATGACACAGGATCAGGTTATGACAGACAAAGAAATCCACTAAAAGCA	1200
QY	1201	TTTGATGATTCACACCAAGGTAATTTCTGTATTTGAAAAGATTAACCCCAATTTGAA	1260
DB	1201	TTTGATGATTCACACCAAGGTAATTTCTGTATTTGAAAAGATTAACCCCAATTTGAA	1260
QY	1261	GCTGTTGGAAAGAAATTCGGTAACTTGAAGAAAGACTGAGAACTTGAACAAAAGATG	1320
DB	1261	GCTGTTGGAAAGAAATTCGGTAACTTGAAGAAAGACTGAGAACTTGAACAAAAGATG	1320
QY	1321	GAAGACGGGTTTCTAGATGTGTGACATACATGCTGACCTTTTGAATTCGATGAAAT	1380
DB	1321	GAAGACGGGTTTCTAGATGTGTGACATACATGCTGACCTTTTGAATTCGATGAAAT	1380
QY	1381	GAGAGGACATCTGATCTTCAATGATTTCAATGTCAAACATCTGATAGTAAATCGAATG	1440
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QY	1561	GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1620
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QY	1681	GGATCTCTTTCTGGGTGTCTCCAAAGGCTCTGCAAGTGCAGATGATGATGATGATG	1740
DB	1681	GGATCTCTTTCTGGGTGTCTCCAAAGGCTCTGCAAGTGCAGATGATGATGATGATG	1740
QY	1741	TAAATGATTTTAAATTAATAAACACCCCTGTTTCTGAGAGCGG	1783
DB	1741	TAAATGATTTTAAATTAATAAACACCCCTGTTTCTGAGAGCGG	1783

RESULT 2  
13256 1783 bp DNA linear PAT 06-FEB-1997  
LOCUS 13256  
DEFINITION Sequence 46 from patent US 5589174.  
ACCESSION 13256  
VERSION 13256.1 GI:182317  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1783)  
AUTHORS Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.  
TITLE Anti-human influenza virus antibody  
JOURNAL Patent: US 5589174-A 46 31-DEC-1996;  
FEATURES Location/Qualifiers

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Best Local Similarity	100.0%;	Pred. No. 0;			
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QY	181	AAGACATCTCTTG	AAGAACCCCATACGGAAGTTAT	GCACAACTAAACGGATCCCTCCA	240
Db	181	AAGACATCTCTTG	AAGAACCCCATACGGAAGTTAT	GCACAACTAAACGGATCCCTCCA	240
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Db	241	CTTGAATAGGGG	ACTGTAGCATTCGCGATGGCTC	CTTGGAAATCCAAATGTGATAGG	300
QY	301	CTTCTAAGTGTGCC	BAAGCGTCTATATATTTGAGA	AAAGAAACCCGAGAGCGGTTTG	360
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QY	361	TGTTATCCAGG	AGCTTCATGATATGAAATTTGA	AAACATCTCCACAGCGGTAA	420
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Db	421	CATTTCGAGAAG	ATPAAGATTTCTGCCCAAGAT	TGATGACACAGCATACCAACTGCA	480
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Db	721	CCGAAATAGCA	CAAGGCTTAAAGTGAAGG	AGAGGTGAAGGATTTCTCTGG	780
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Db	1381	GAGAGAC	ACTTGCATGATTTCTAATG	TCAGAAATCTGTATGTAAGTCAGAAATG	1440
QY	1441	CAGCTGAG	ACACACGTCGCAAGAACT	AGAAATGTTGTAATTTATCACAAAATG	1500
Db	1441	CAGCTGAG	ACACACGTCGCAAGAACT	AGAAATGTTGTAATTTATCACAAAATG	1500
QY	1501	GATGATGA	ATGCATGAATAGTAGTG	TAAGAAAACGGGACATATGATTTCCAAATG	1560
Db	1501	GATGATGA	ATGCATGAATAGTAGTG	TAAGAAAACGGGACATATGATTTCCAAATG	1560
QY	1561	GAGCTTA	ACTTAATTAAGAAATGA	ATCAAGGGGTTAAATTTGACAGCATG	1620
Db	1561	GAGCTTA	ACTTAATTAAGAAATGA	ATCAAGGGGTTAAATTTGACAGCATG	1620
QY	1621	CAATTCCT	GTGCATTTATGCTACAGT	AGAGTCTATGTCACATGATATGATG	1680
Db	1621	CAATTCCT	GTGCATTTATGCTACAGT	AGAGTCTATGTCACATGATATGATG	1680
QY	1681	GGGATCT	CTTTCTGGGTGCTCCAA	CGGGTCTCTGCAAGTCTGCATATGATTA	1740
Db	1681	GGGATCT	CTTTCTGGGTGCTCCAA	CGGGTCTCTGCAAGTCTGCATATGATTA	1740
QY	1741	TAACTCAT	TTTTTAATTAATAAAC	ACCCTGTTCTGCTAGCCG	1783
Db	1741	TAACTCAT	TTTTTAATTAATAAAC	ACCCTGTTCTGCTAGCCG	1783

RESULT 3  
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LOCUS 143471  
DEFINITION Sequence 46 from patent US 5631350.  
ACCESSION 143471  
VERSION 143471.1 GI:2468715  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1783)  
AUTHORS Okuno, Y., Iseigawa, Y., Sasao, F. and Ueda, S.  
TITLE Anti-human influenza virus antibody  
JOURNAL Patent: US 5631350-A 46 20-MAY-1997;  
FEATURES location/Qualifiers  
source 1. 1783

BASE COUNT 610 a /organism="unknown" 424 g 426 t  
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Query Match 100.0%; Score 1783; DB 6; Length 1783;  
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 Matches 1783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4  
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 VERSION L20407.1  
 KEYWORDS haemagglutinin.  
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 ORGANISM Influenza A virus  
 Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza  
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 Connor, R.J., Kawakita, Y., Webster, R.G. and Paulson, J.C.  
 Receptor specificity in human, avian, and equine H2 and H3  
 influenza virus isolates  
 Virology 205 (1), 17-23 (1994)





QY 1686 CTCCTTCGTGGTGTCCACAGGGTCTCTGCAGTGCAGATCTGCATATGATTATAGT 1745  
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 ORGANISM Influenza A virus  
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 REFERENCE 1 (bases 1 to 1773)  
 AUTHORS McCauley, J., Bye, J., Elder, K., Gething, M.J., Skehel, J.J., Smith, A. and Waterfield, M.D.  
 JOURNAL Influenza virus haemagglutinin signal sequence  
 PUBLISHED FEB5 Lett. 108 (2), 422-426 (1979)  
 MEDLINE 80092143  
 PUBMED 520584  
 TITLE 2 (bases 1 to 1773)  
 AUTHORS Gething, M.J., Bye, J., Skehel, J. and Waterfield, M.  
 JOURNAL Cloning and DNA sequence of double-stranded copies of  
 PUBLISHED haemagglutinin genes from H2 and H3 strains elucidates antigenic  
 MEDLINE shift and drift in human influenza virus  
 PUBMED Nature 287 (5780), 301-306 (1980)  
 COMMENT 81030852  
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 [2] actually makes use of a laboratory recombinant strain, a/Japan/305/57:a/del/42:a/pr/8/34 (h2n1), containing the a/Japan/305/57 hemagglutinin gene. [2] compared to NBRF data, [1] to sunex tape.  
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 Matches 1753; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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QY	1386	GACACTGACTTCAATGATCTAATGTCAGAAATCTGTATAGTAAAGTCAGATGACGCT	1445
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QY	1686	CTCTTTCTGGGTGTGTTCCACAGGGTCTCTGCAAGTGCAGATGTCATATGATTAAGT	1745
Db	1681	CTCTTTCTGGGTGTGTTCCACAGGGTCTCTGCAAGTGCAGATGTCATATGATTAAGT	1740
QY	1746	CATTTATATTAATAAACAACCTTGTGTTGCT	1778
Db	1741	CATTTATATTAATAAACAACCTTGTGTTGCT	1773
RESULT 6	FLAHA3055J	1773 bp RNA linear VRL 27-MAR-1995	
LOCUS	FLAHA3055J	Influenza A/Japan/305+/57 (H2N2) haemagglutinin (seg 4) gene,	
DEFINITION	complete cds.		
ACCESSION	L20406.1	GI:305114	
VERSION	L20406.1	GI:305114	
KEYWORDS	haemagglutinin.		
SOURCE	Influenza A virus		
ORGANISM	Influenza A virus		
REFERENCE	A viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza		
AUTHORS	1 (bases 1 to 1773)		
TITLE	Connor,R.J., Kawabuka,Y., Webster,R.G. and Paulson,J.C.		
JOURNAL	Receptor specificity in human, avian, and equine H2 and H3		
MEDLINE	infect 205 (1), 17-23 (1994)		
PUBMED	95065649		
COMMENT	Original source text: Influenza virus type A (individual isolate		
FEATURES	A/Japan/305+/57) RNA.		
Source	Location,Qualifiers		
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LOCUS Influenza A virus (A/Krasnodar/101/59 (H2N2)) hemagglutinin (HA)
DEFINITION gene, complete cds.
ACCESSION L11134.1
VERSION L11134.1 GI:408524
KEYWORDS haemagglutinin.
SOURCE Influenza A virus (A/Krasnodar/101/59 (H2N2))
ORGANISM Influenza A virus (A/Krasnodar/101/59 (H2N2))
REFERENCE 1 (bases 1 to 1773)
AUTHORS Schaffer, J.R., Kawoka, Y., Bean, W.J., Suss, J., Senne, D. and Webster, R.G.
TITLE Origin of the pandemic 1957 H2 influenza A virus and the persistence of its possible progenitors in the avian reservoir
JOURNAL Virology 194 (2), 781-788 (1993)
MEDLINE 93276567
PUBMED 7684877
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RESULT 8  
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LOCUS  
DEFINITION  
INFLUENZA A/R1/5-/57 (H2N2) haemagglutinin (seg 4) gene, complete  
ACCESSION  
L20409.1 GI:305116  
VERSION  
L20409.1 GI:305116  
KEYWORDS  
haemagglutinin.  
SOURCE  
Influenza A virus  
ORGANISM  
Influenza A virus  
viruses: ssRNA negative-strand viruses: Orthomyxoviridae; Influenza A viruses; Influenzavirus A.  
REFERENCE  
1 (bases 1 to 1773)  
Connor,R.J., Kawacka,Y., Webster,R.G. and Paulson,J.C.  
Receptor specificity in human, avian, and equine H2 and H3  
TITLE  
Influenza virus isolates  
JOURNAL  
Virology 205 (1), 17-23 (1994)  
MEDLINE  
95065649  
PUBMED  
7975212  
COMMENT  
Original source text: Influenza virus type A (individual isolate A/R1/5-/57) RNA.  
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 DB 1501 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560  
 QY 1566 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1625  
 DB 1561 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620  
 QY 1626 CTTGTCATTTATGCTTACAGTACAGAGTTCATGATGATGATGATGATGATGATGATGAT 1685  
 DB 1621 CTTGTCATTTATGCTTACAGTACAGAGTTCATGATGATGATGATGATGATGATGATGAT 1680  
 QY 1686 CTCTTCTGGGTGTGCTCAACGGGTCTCTGACGTGAGATGATGATGATGATGATGATGAT 1745  
 DB 1681 CTCTTCTGGGTGTGCTCAACGGGTCTCTGACGTGAGATGATGATGATGATGATGATGAT 1740  
 QY 1746 CATTATTAATTAATAAACACCCCTGTTCTGCT 1778  
 DB 1741 CATTATTAATTAATAAACACCCCTGTTCTGCT 1773

RESULT 9  
 FLAHAS157A 1773 bp RNA linear VRL 27-MAR-1995  
 LOCUS FLAHAS157A  
 DEFINITION Influenza A/Singapore/1/57 (H2N2) haemagglutinin (seg 4) gene,  
 complete cds.  
 ACCESSION L20410  
 VERSION L20410.1 GI:305170  
 KEYWORDS haemagglutinin.  
 SOURCE Influenza A virus  
 ORGANISM Influenza A virus  
 A viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza  
 A viruses; Influenzavirus A.  
 REFERENCE 1 (bases 1 to 1773)  
 AUTHORS Connor,R.J., Kawakita,Y., Webster,R.G. and Paulson,J.C.  
 TITLE Receptor specificity in human, avian, and equine H2 and H3  
 Influenza virus isolates

JOURNAL MEDLINE PUBMED COMMENT	VIROLOGY 205 (1), 17-23 (1994) 7975212	Original source text: Influenza virus type A (individual isolate A/Singapore/1/57) RNA.
FEATURES	source	Location/Qualifiers
gene	1..1773	/organism="Influenza A virus" /mol_type="genomic RNA" /isolate="A/Singapore/1/57" /db_xref="taxon:11320"
CDS	44..1732	/gene="HA" 44..1732 /gene="HA" 44..1732 /codon_start=1 /product="hemagglutinin" /protein_id="AA064366.1" /db_xref="GI:305171"
BASE COUNT	612 a 319 c 417 g 425 t	
ORIGIN	Query Match 96.3%; Score 1728.2; DB 14; Length 1773; Best Local Similarity 98.3%; Pred. No. 0; Matches 1745; Conservative 0; Mismatches 28; Indels 0; Gaps 0.	
QY	6 AGCAAAAGCAGGGGTATACCATAGAAAACCAAAAGCAAAACATGCCATCATTTATCT	65
Db	1 AGCAAAACAGGGGTATATCCATAGACAAACCAAAAGCAAAACATGCCATCATTTATCT	60
QY	66 CATCTCTCTGTTCACAGCATGAGAGGGGACAGATATGCAATGGATACATGCCAATTA	125
Db	61 AATTCTCTGTTCACAGCATGAGAGGGGACCAATATGCAATGGATACATGCCAATTA	120
QY	126 TTCACAGAGAAGGTGACACAAATCTTGAGCGGAACCTCACTGACTATGCCAAGA	185
Db	121 TTCACAGAGAAGGTGACACAAATCTTGAGCGGAACCTCACTGACTATGCCAAGA	180
QY	186 CATCTTGAGAGAAGCATATAACGGAAGTATGCCAACTAAACGGAATCCTCCACTTGA	245
Db	181 CATCTTGAGAGAAGCATATAACGGAAGTATGCCAACTAAACGGAATCCTCCACTTGA	240
QY	246 ACTATGAGGACGTGTGATTTGCCGCGATGCTCTGGAAATCCAAATGATGATAGGCTCT	305
Db	241 ACTATGAGGACGTGTGATTTGCCGCGATGCTCTCTGGAAATCAGATGTGATGAGCTCT	300
QY	306 AAGTGTGCAGAACGCTCCATATATATGGAGAAAAGAAACCCGAGAGAGGTTTGTCTTA	365
Db	301 AAGTGTGCAGAAATGCTCCATATATATGGAGAAAAGAAACCCGAGAGAGGTTTGTCTTA	360
QY	366 TTCAGGACGCTTCAAGGATTTATGAAGATTAAGAACATCTCTCAGACAGCTGAACAATT	425
Db	361 TTCAGGACGCTTCAAGGATTTATGAAGATTAAGAACATCTCTCAGACAGCTGAACAATT	420
QY	426 CGAAGAAAGTAAGATTTCTGCCCAAAAGATAGATGAGACACAGATACAAACTGGAAGTTC	485
Db	421 CGAAGAAAGTAAGATTTCTGCCCAAAAGATAGATGAGACACAGATACAAACTGGAAGTTC	480
QY	486 ACGGAGCCTGCAGGCTGTCTGTATTCATCTATTTTCAGAAACATGCTGGCTGACAAA	545
Db	481 ACGGAGCCTGCAGGCTGTCTGTATTCATCTATTTTCAGAAACATGCTGGCTGACAAA	540
QY	546 GGAAGATCAGATTATTCGGTTTGCCAAAGATCGTACACAAATACAAAGCGAGAACAAAT	605

Db	541	GAAAGAAATCAAAATTTATCCGGTTGGCCAAAGAGATCGTACACATATCAAGCGGAGACAAAT	600
Qy	606	GCTAATTAATTTGGGGGTGCACCAATCCATTTGATGAGACAGAAACAAAGACATTTGACCA	665
Db	601	GCTATATATTTGGGGGTGCACCAATCCCAATGATGAGACAGACAAAGAACATTTGTACCA	660
Qy	666	GAATGTGGGAACCTATGTCTTCCGTAGGACATCAATGTAACAAAGAGTCCACCCAGA	725
Db	661	GAATGTGGGAACCTATGTCTCCGTAGGCATCAACATGTGAACAAAGAGTCCACCCAGA	720
Qy	726	AATACCAACAGGCTTAAGTGAATGGACAAAGAGTGAATGGAATTTCTTTGGACCCCT	785
Db	721	CATACCAACAAGGCTTAAGTGAATGGACAAAGAGTGAATGGAATTTCTTTGGACCCCT	780
Qy	786	CTTGATATGTGGGACACCATTAATTTTGAAGATACGTGTATCTTAATTTGGACAGAGTA	845
Db	781	ATTGATATGTGGGACACCATTAATTTTGAAGATACGTGTATCTTAATTTGCACAGAGTA	840
Qy	846	TGGATTTCAAAATATCGAAAAGAGGTAGTTCAGGATCATGAIAACAGAGAACATTTGA	905
Db	841	TGGATTTCAAAATATCGAAAAGAGGTAGTTCAGGATCATGAIAACAGAGAACATTTGA	900
Qy	906	GAACGTGTAGACCAATATCCCAACTCCTTTGGGAGCAATAATACAACTTACTTTTCA	965
Db	901	GAACGTGTAGACCAAAATATCCCAACTCCTTTGGGAGCAATAATATCAACATTTGCCCTTTTCA	960
Qy	966	CAATTCACCCACTGACAAATAGGTGAGTGGCCCCAAATATGTAAATTCGGAGAGTTGGT	1025
Db	961	CAATTCACCCACTGACAAATAGGTGAGTGGCCCCAAATATGTAAATTCGGAGAGTTGGT	1020
Qy	1026	CTTAGCAACAGGACTAAGGAATGTTCCCCAGATTTGAATCAAGAGATTTGTTTGGGGCAAT	1085
Db	1021	CTTAGCAACAGGACTAAGGAATGTTCCCCAGATTTGAATCAAGAGATTTGTTTGGGGCAAT	1080
Qy	1086	AGCTGTGTTTATAGAAGAGAGATGGCAAGCATGCTTGACGGTTGGTATGGATACATCA	1145
Db	1081	AGCTGTGTTTATAGAAGAGAGATGGCAAGCATGCTTGATGATGGATACCATCA	1140
Qy	1146	CAGCAATACCAAGGATCAGGTTATGCGACGACAAAGAAATCCACTCAAAAAGCATTTGA	1205
Db	1141	CAGCAATACCAAGGATCAGGTTATGCGACGACAAAGAAATCCACTCAAAAAGCATTTGA	1200
Qy	1206	TGGAATCCACAACAGGTAAATTTCTGTATTGAAGAAGATAAACACCCCAATTTGAAGCTGT	1265
Db	1201	TGGAATCCACAACAGGTAAATTTCTGTATTGAAGAAGATAAACACCCCAATTTGAAGCTGT	1260
Qy	1266	TGGCAAGCAATTCGGTAACTTAGAGAAAGACTGGAGACTTGAACAAAAAGATGAGAGA	1325
Db	1261	TGGCAAGCAATTCGGTAACTTAGAGAGAACTGGAGAACTTGAACAAAAAGATGAGAGA	1320
Qy	1326	CGGGTTTCTAATGTGTGGACATTCATGTCTGACCTTTTGTTGTTGTAAGAAATGAGAG	1385
Db	1321	CGGGTTTCTAATGTGTGGACATTCATGTCTGACCTTTTGTTGTTGTAAGAAATGAGAG	1380
Qy	1386	GACACTTGACTTTCATGATTTCTAATGTGCACAAATCTGTATAGTAAAGTTCGAATGCAGCT	1445
Db	1381	GACACTTGACTTTCATGATTTCTAATGTGCACAAATCTGTATAGTAAATTCGAATGCAGCT	1440
Qy	1446	GAGAGACAGCTCAAGACACTAGGAATGTGTTTGAATTTTATCACAATGTGATGA	1505
Db	1441	GAGAGACAGCTCAAGACACTAGGAATGTGTTTGAATTTTATCACAATGTGATGA	1500
Qy	1506	TGAATGCATGAATGTGTGA AAAACGGGACATATGATTAATCCCAAGTATCAAGAGAGTGC	1565
Db	1501	TGAATGCATGAATGTGTGA AAAACGGGACATATGATTAATCCCAAGTATCAAGAGAGTGC	1560
Qy	1566	TAAACTTAATTAATGAATGAATCAAAAGGGGTAAATTTAGCAGCATGTGGGGTTTATCAAT	1625
Db	1561	TAACTTAATTAATGAATGAATCAAAAGGGGTAAATTTAGCAGCATGTGGGGTTTATCAAT	1620
Qy	1626	CTTGCCATTTATCTACAGTAGGAGGTTCTATGTCACTGGCAATCATGATGCGTGGCAT	1685



Db 1621 CCTGGCATTTATGCTACAGTAGACAGTTCCTCTCTGCTACCTGGCATATCATGTCGGAT 1680  
QY 1686 CTCCTTGGGGTCTCCCAACGGGTCTCTGACGTGACAGATCTCATATGATTAATAGT 1745  
Db 1681 CTCCTTGGGGTCTCCCAACGGGTCTCTGACGTGACAGATCTCATATGATTAATAGT 1740  
QY 1746 CATTATTAATTAATAAACACCCCTTCTCTGCT 1778  
Db 1741 CATTATTAATTAATAAACACCCCTTCTCTGCT 1773

RESULT 10  
FLAHARIS57  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

FLAHARIS57 1773 bp RNA linear VRL 27-MAR-1995  
Influenza A/R1/5+/57 (H2N2) haemagglutinin (seg 4) gene, complete  
cds.  
L20408  
L20408.1 GI:305162  
haemagglutinin.  
Influenza A virus  
Influenza A virus  
viruses: ssRNA negative-strand viruses; Orthomyxoviridae; Influenza  
A viruses; Influenza virus A.  
1 (bases 1 to 1773)  
Conor, R.J., Kawoka, Y., Webster, R.G. and Paulson, J.C.  
Receptor specificity in human, avian, and equine H2 and H3  
Influenza virus isolates  
Virology 205 (1), 17-23 (1994)  
95065649  
7975212  
COMMENT  
Original source text: Influenza virus type A (individual isolate  
A/R1/5+/57) RNA.  
FEATURES  
source  
location/Qualifiers  
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NSVIERKMTQFPAVERKERSNLEKRLNKKMKEDGLDWVTYNAELLVLMENERTLDF  
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BASE COUNT 610 a 321 c 418 g 424 t

ORIGIN

Query Match 96.8%; Score 1726.6; DB 14; Length 1773;  
Best Local Similarity 98.4%; Pred. No. 0;  
Matches 1744; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 6 AGCAAAACGAGGGTTATACATAGAAAACCAAAACCAAAATGCGCATCTATTATCT 65  
Db 1 AGCAAAACGAGGGTTATACATAGAAAACCAAAACCAAAATGCGCATCTATTATCT 60  
QY 66 CATTCTCTGTTACAGCAGTAGAGGGGACAGATATGATTCATGATACATGCAATTA 125  
Db 61 CATCTCTCTGTTACAGCAGTAGAGGGGACAGATATGATTCATGATACATGCAATTA 120  
QY 126 TTCACAGAGAGAGTGAACACATTTCTAGAGGGAAGCTCACTGTGACTCATGCCAAGA 185

Db 121 TTCACAGAGAGAGTGAACACATTTCTAGAGCGGAAACCTCACTGTGACTCATGCCAAGA 180  
QY 186 CATCTTGAAGAGACCCATTAACGAAAGTTATGCAAACTAAGGAATCCCTCCACTTGA 245  
Db 181 CATTTCTTGAAGAGACCCATTAACGAAAGTTATGCAAACTAAGGAATCCCTCCACTTGA 240  
QY 246 ACTAGGGAGCTGTAGCAATGCGCGATGCGCTCTGGAATTCAAATATGTATAGGCTTCT 305  
Db 241 ACTAGGGAGCTGTAGCAATGCGCGATGCGCTCTGGAATTCAAATATGTATAGGCTTCT 300  
QY 306 AAGTGTGCAACAGCGTCTCTATATTTGGAGAAAACCCGAGAGCGTTTGTGTTA 365  
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Db 361 TCCAGGCGCTTCAACGATTTATGAAGATTAACATCTCTCGAGCGGCGTGAACATTT 420  
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QY 486 ACGGCGCTGCGGCTGTCTGTAATTCATCATTTTGGAGAACATGCTGCTGCAAA 545  
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QY 546 GGAAGATCAGATTATTCGGTTGCCAAGAGATGATACAAATACAAAGCGGAGACAAT 605  
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QY 606 GCTAATATTTGGGGGCTGCAACATCCATTTGATGAGACAGAAACCAACATTTGACCA 665  
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QY 1026 CTTAGCAACAGGACTAGAAATGTTCCAGATTAATACAGAGATGTTGGGCAAT 1085  
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QY 1206 TGGATTCACCAACAGGATTAATTTCTGATTTGAAAAGATGAACACCAATTTGAAGCTGT 1265  
Db 1201 TGGATTCACCAACAGGATTAATTTCTGATTTGAAAAGATGAACACCAATTTGAAGCTGT 1260



OY	1266	TGGGAAGAATTGCTTAACCTAGAGAAAAGACTGGAGACTTGAACAAAAGATGAGAGA	1325
Db	1261	TGAAGAAAGATTCACCTAATCTAGAGAGAGAGCTGGAGACTTGAACAAAAGATGAGAGA	1320
OY	1326	CGGGTTCTAGATGCTGTGGACATCAATGCTGAGCTTTTAACTTCTGATGGAATAAGAG	1385
Db	1321	CGGGTTCTAGATGCTGTGGACATCAATGCTGAGCTTCTAGTCTGATGGAATAAGAG	1380
OY	1386	GACCTGACCTTCACTATCTCTATGTCANAACTCTGTATGTAAGTCAGAAATGACAGCT	1445
Db	1381	GACCTGACCTTCACTATCTCTATGTCANAACTCTGTATGTAAGTCAGAAATGACAGCT	1440
OY	1446	GAGAGACAGCTCAAG	1505
Db	1441	GAGAGACAGCTCAAG	1500
OY	1506	TGAATGCATGATAGTGTGAAAAAGGAGACATATGATTTATCCAGATGAGAAAGATC	1565
Db	1501	TGAATGCATGATAGTGTGAAAAAGGAGACATATGATTTATCCAGATGAGAAAGATC	1560
OY	1566	TAACTAATATGAAATCAATCAAGGGGTAAATTTGACAGCATGGGGCTTTTCAAT	1625
Db	1561	TAACTAATATGAAATCAATCAAGGGGTAAATTTGACAGCATGGGGCTTTTCAAT	1620
OY	1626	CCTTGCCATTTATGCTACAGTACAGGCTTCTATGCTACCTGACATCATGATGCTGGAT	1685
Db	1621	CCTTGCCATTTATGCTACAGTACAGGCTTCTCTCTCTACTGCAATCATGATGCTGGAT	1680
OY	1686	CTCTTCTGGGTGTGCTTCCAAAGGGTCTCTGACATGACAGATCTCATATGATTAAGT	1745
Db	1681	CTCTTCTGGGTGTGCTTCCAAAGGGTCTCTGACATGACAGATCTCATATGATTAAGT	1740
OY	1746	CATTTATATTAATAAACACCCCTGTTCTGCT	1778
Db	1741	CATTTATATTAATAAACACCCCTGTTCTACT	1773
RESULT 11	FLASINS7HA	1773 bp ss-RNA linear VRL 13-OCT-2000	
LOCUS	FLASINS7HA	Influenza A virus (A/Singapore/1/57 (H2N2)) hemagglutinin (HA)	
DEFINITION	Influenza A virus	gene, complete cds.	
ACCESSION	L11142	L11142.1 GI:408676	
VERSION	L11142	hemagglutinin.	
KEYWORDS	Influenza A virus	(A/Singapore/1/57 (H2N2))	
SOURCE	Influenza A virus	(A/Singapore/1/57 (H2N2))	
ORGANISM	Influenza A virus	(A/Singapore/1/57 (H2N2))	
REFERENCE	Schaefer J.R., Kawakita, Y., Bean, W.J., Suss, J., Sene, D. and Webster, R.G.	Origin of the pandemic 1957 H2 influenza A virus and the persistence of its possible progenitors in the avian reservoir virology 194 (2), 781-788 (1993)	
TITLE	JOURNAL MEDLINE PUBMED	7684877	
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Db	1	AGCAAAAGCAGGGGTTATACCATAGAACCAAAAGCAAAACAAATGGCCATATTATCT	60
OY	66	CATTCTCTGTTTCACAGCAGTGAAGGGGACCAATATGATTTGGATACATGCCAATA	125
Db	61	CATTCTCTGTTTCACAGCAGTGAAGGGGACCAATATGATTTGGATACATGCCAATA	120
OY	126	TTCACAGAGAGAGTGCACACATTTCTAGACGGAGAGTCACTGATCATGTCACCAAGA	185
Db	121	TTCACAGAGAGAGTGCACACATTTCTAGACGGAGAGTCACTGATCATGTCACCAAGA	180
OY	186	CATCTTGAAGAGACCCATTAACGAAAGTATGCAAACTAAACGAAATCCCTCCACTGA	245
Db	181	CATCTTGAAGAGACCCATTAACGAAAGTATGCAAACTAAACGAAATCCCTCCACTGA	240
OY	246	ACTAGGGGACTGTAGCATTTGCCGATGCTCTTGGAAATTCGAAATGTATAGGCTTCT	305
Db	241	ACTAGGGGACTGTAGCATTTGCCGATGCTCTTGGAAATTCGAAATGTATAGGCTTCT	300
OY	306	AAGTGTGCAGAACGGTCTATATATTTGAGAAAGAAACCCGAGAGCGGTTGTGTTA	365
Db	301	AAGTGTGCAGAACGGTCTATATATTTGAGAAAGAAACCCGAGAGCGGTTGTGTTA	360
OY	366	TCCAGGAGAGTTCATGATTAAGAAATGAAACATCTCTGACAGCGGTGAACAATTT	425
Db	361	TCCAGGAGAGTTCATGATTAAGAAATGAAACATCTCTGACAGCGGTGAACAATTT	420
OY	426	CGAAGAAAGTAAGATTCTGCCAAGAGATAGTGAACAGCATACCAACTGAGGTTTC	485
Db	421	CGAAGAAAGTAAGATTCTGCCAAGAGATAGTGAACAGCATACCAACTGAGGTTTC	480
OY	486	ACGGGCTGCGCGGTGCTGTGATTCATCTTTTTCAGAAACATGGTCTGGTGAACAA	545
Db	481	ACGGGCTGCGCGGTGCTGTGATTCATCTTTTTCAGAAACATGGTCTGGTGAACAA	540
OY	546	GGAAGGATCAGATTATCCGTTGGCAAGAGTCTACACAAATCAAGCGGAGAAAT	605
Db	541	GGAAGGATCAGATTATCCGTTGGCAAGAGTCTACACAAATCAAGCGGAGAAAT	600
OY	606	GCTAATATTTTGGGGGTGACACATCTCCATTTGATGACAGACAGAAAGACATTGTACA	665
Db	601	GCTAATATTTTGGGGGTGACACATCTCCATTTGATGACAGACAGAAAGACATTGTACA	660
OY	666	GAATGTGGGAACCATGTTTCCGTAAGGACATCAACATTTGAACAAAGGTCACCCAGA	725
Db	661	GAATGTGGGAACCATGTTTCCGTAAGGACATCAACATTTGAACAAAGGTCACCCAGA	720
OY	726	AATAGCAACAGGCTTAAATGAAATGACAGAGAGTGAATGGAATTTCTTGACACCT	785
Db	721	AATAGCAACAGGCTTAAATGAAATGACAGAGAGTGAATGGAATTTCTTGACACCT	780
OY	786	CTTGATATGTGGGACACCAATTTTGGAGAGTACGTATATTTGACACAGATA	845
Db	781	ATTGGATATGTGGGACACCAATTTTGGAGAGTACGTATATTTGACACAGATA	840

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DB 841 TGGATTCAAAATTCGAAAAGAGTAGTACGGATCATGAAAACAGACACACTTGA 900  
QY 906 GAACGTGGAGACAAATGCCAACTCCTTTGGGAGCAATTAATCAACATTAACCTTTCA 965  
DB 901 GAACGTGGAGACAAATGCCAACTCCTTTGGGAGCAATTAATCAACATTAACCTTTCA 960  
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DB 961 CAATGTCCACCCACTGCAATAGTAGTGGTCCCAATATGTAAATCGGAGAATGTGT 1020  
QY 1026 CTTAGCAACAGGCTAAGAGATGTTCCCGCATTTGAATCAAGAGATGTTTGGGCAAT 1085  
DB 1021 CTTAGCAACAGGCTAAGAGATGTTCCCGCATTTGAATCAAGAGATGTTTGGGCAAT 1080  
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DB 1081 AGCTGTTTATATGAAGAGAGATGGCAAGAAATGGTGGAGGTTGATGATACATCA 1140  
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DB 1141 CAGCAATGACACAGGATCAGGGATGACAGACAAAGAAATCCACTCAAAAGCATTTGA 1200  
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QY 1386 GACACTGACTTTCATGATTTCTAATGCAAGAAATCTGTAAGTAAGTCAGATGACGT 1445  
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QY 1446 GAGAGCAACGTCMAAGAACTAGGAATGGATGTTTGAATTTATCACAAATGTGATGA 1505  
DB 1441 GAGAGCAACGTCMAAGAACTAGGAATGGATGTTTGAATTTATCACAAATGTGATGA 1500  
QY 1506 TGAATGATGATAGTGTGAAAAACGGACATATGATTTCCCAAGTATGAGAAGATC 1565  
DB 1501 TGAATGATGATAGTGTGAAAAACGGACATATGATTTCCCAAGTATGAGAAGATC 1560  
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DEFINITION Sequence 4 from Patent WO0224876.  
ACCESSION AX399727  
VERSION AX399727.1 GI:21335485  
KEYWORDS  
SOURCE Influenza A virus (STRAIN A/SINGAPORE/1/57)

ORGANISM Influenza A virus (STRAIN A/SINGAPORE/1/57)  
VIRUSES; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A; Influenza A virus; unidentified subtype.  
REFERENCE 1  
AUTHORS Perko,B., Borov,A., Romanova,J., Kalinge,D. and Kalinge,H.  
TITLE Live vaccine and method of manufacture  
JOURNAL Patent: WO 0224876-A 4 28-MAR-2002;  
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 REFERENCES  
 1. Schaefer J.R., Kawocka Y., Bean W.J., Suss J., Senne D. and Webster R.G.  
 TITLE Origin of the pandemic 1957 H2 influenza A virus and the  
 JOURNAL persistence of its possible progenitors in the avian reservoir  
 MEDLINE virology 194 (2), 781-788 (1993)  
 93276567

PUBMED 7684877		Location/Qualifiers	
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Query Match		93.1% Score 1659.4: DB 14: Length 1773:	
Best Local Similarity		96.0%: Pred. No. 0:	
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QY	66 CATTCCTCTTACAGCAGTGAAGGGGACACAGATATGATTGATACCATGCCAATAA	125	666 GAATGTGGGACCTATGTTTCCGTAGGACATCACAATTTGAACAAAAGSTCAACCCAGA
DB	61 CATACCTCTTACAGCAGTGAAGGGGACACAGATATGATTGATACCATGCCAATAA	120	661 GAAAGTGGGACCTATGTTTCCGAMACCATCAATTTGAACAAAAGSTCAACCCCTGA
QY	126 TTCCACAGAGAGGTGACACAAATTTAGAGCGGACGTCAGTGTGACTATGCCAAGA	185	726 AATAGCAACAGGCTCAAGTGTGATGACAGAGGTGATGATGATTTCTGTGGACCT
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Job time : 4495.7 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 19:11:43 ; Search time 2736.47 seconds  
(without alignments)  
15836.045 Million cell updates/sec

Title: US-09-918-568-46

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Sequence: 1 CGCGTAGCAGAACAGAGGGT.....ACCGTGTCTGCTAGCCG 1783

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000010000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hlc.\*  
9: gb\_estl.\*  
10: gb\_est2.\*  
11: gb\_hlc.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfln.\*  
16: em\_eston.\*  
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27: em\_gss\_vrt.\*  
28: gb\_gssl.\*  
29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 2	62.2	3.5	1101	29	CNS0039G AL063921 Drosophila
C 3	55	3.1	639	29	CNS0170D AL108367 Drosophila
C 4	54.2	3.0	994	13	BX414650 BX414650

5	52.8	3.0	1101	29	CNS0006J	AL062049 Drosophila
C 6	52.4	2.9	997	29	CNS005FE	AL060767 Drosophila
C 7	52.2	2.9	1167	13	BX463903	BX463903
C 8	51.8	2.9	847	29	CNS02JEX	AL200130 Tetradon.
C 9	50.2	2.8	1101	29	CNS0182P	AL108811 Drosophila
C 10	49.6	2.8	468	29	CNS06XGD	AL419699 17 end of
C 11	49.4	2.8	918	29	CNS006MW	AL065768 Drosophila
C 12	48.8	2.7	1201	13	BX406178	BX406178 BX406178
C 13	48.6	2.7	938	29	CNS006RT	AL065906 Drosophila
C 14	48.4	2.7	1201	13	BX461128	BX461128 BX461128
C 15	47.8	2.7	500	9	A0087765	A0087765 A0087765
C 16	47.6	2.7	1200	29	CNS016CO	AL106578 Drosophila
C 17	47.4	2.7	1101	29	CNS0106X	AL098595 Drosophila
C 18	47	2.6	1101	29	CNS000D1	AL065414 Drosophila
C 19	46.8	2.6	1200	13	BX414560	BX414560 BX414560
C 20	46.2	2.6	1106	13	BX438107	BX438107 BX438107
C 21	46	2.6	1001	13	BX329654	BX329654 BX329654
C 22	46	2.6	1101	29	CNS00EST	AL069797 Drosophila
C 23	46	2.6	1201	9	AL536104	AL536104 AL536104
C 24	46	2.6	1201	13	BX355654	BX355654 BX355654
C 25	45.8	2.6	1101	29	CNS016HF	AL106749 Drosophila
C 26	45.8	2.6	1101	29	CNS017KX	AL108171 Drosophila
C 27	45.6	2.6	516	28	A0879779	A0879779 HS_4821_A
C 28	45.2	2.5	781	29	AG171177	AG171177 Pan trogl
C 29	45.2	2.5	932	9	AL514901	AL514901 AL514901
C 30	45.2	2.5	941	28	A2682404	A2682404 ENT1016TF
C 31	45.2	2.5	1044	13	BX415231	BX415231 BX415231
C 32	44.8	2.5	673	12	BM485652	BM485652 pmt1c.pko
C 33	44.8	2.5	1201	13	BX345693	BX345693 BX345693
C 34	44.6	2.5	963	29	CNS006XI	AL066049 Drosophila
C 35	44.6	2.5	984	9	AL525973	AL525973 AL525973
C 36	44.6	2.5	1001	29	CNS01400	AL103554 Drosophila
C 37	44.4	2.5	930	29	CNS01644	AL106270 Drosophila
C 38	44.4	2.5	1100	29	CC206010	CC206010 CH261-159
C 39	44.2	2.5	1101	29	CNS0039W	AL0665937 Drosophila
C 40	44	2.5	630	14	CB271310	CB271310 ta21c05.
C 41	44	2.5	644	14	CD567533	CD567533 tab78g10.
C 42	44	2.5	917	28	BH166948	BH166948 EMT58TF
C 43	44	2.5	1201	13	BX461310	BX461310 BX461310
C 44	43.8	2.5	467	13	B0497794	B0497794 PESTab8
C 45	43.8	2.5	859	29	CNS00KLL	AL077728 Drosophila

## ALIGNMENTS

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LOCUS BX376097 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens  
DEFINITION CDNA Clone CS0DC022YM12 5-PRIME, mRNA sequence.

ACCESSION BX376097  
VERSION BX376097.1 GI:30434756  
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1201)  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Li, W.-B., Gruber, C., Jesse, J., and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 2866.f  
Contact: Feng Liang Email: fliang@life.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DC022B6060P1.  
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FEATURES  
source

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ORIGIN
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Db	752	GKMKGKMGTMHTMKMVMMHMMHMMHMKMKMKMKMKNNMAHMKMKMTHTMTGTMIM	693		
OY	1073	TGTTTTGGGCAATAGCTGTTTTATAGAAGAGAGTGGCAAGAAATGTTTGACCGTGTGT	1137		
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Db	632	KNNKKNNNNNNHKKNNMKKMGKNNMGAKANNMKM--KNNNNKMMHNNMKKKKKNNNM	575		
OY	1193	AAAAGCATTTGATGGAATCAACCAAGGTAAATTTCTGTGATTTGAAAAGATAAACCCC	1255		
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OY	1313	AAAAGATGGAAGACGGGTTCTTAGATGTGTGGACATACATCTGAGCTTTAGTTCTGA	1372		
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Db	394	KKTRAKKNNNNNNMMHMRANKNAKRAKCCNCNNNNKKNNAAKAARANANNAANAANNAAC	335		
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OY	1553	ATGAAGAGAGTCTAAACTAAATGAAATGAAATCAAAAGGGGTAAA	1599		
Db	214	CCACAAAACCAKTAAGAATAGTGCACAACCAAAAATATCAACAAGAGA	168		

RESULT 2	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
CNS00396/c												
CNS00396	1101 bp	DNA	linear	GSS	02-JUN-1999							
<p>Drosophila melanogaster genome survey sequence JET3 end of BAC # BACR08K10 of RFL1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.</p> <p>AL063921</p> <p>AL063921.1 GI:4941778</p> <p>GSS.</p> <p>Drosophila melanogaster (fruit fly)</p> <p>Drosophila melanogaster</p> <p>Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Phlebotomidae; Drosophilidae; Drosophila.</p> <p>1 (bases 1 to 1101)</p> <p>Genoscope.</p> <p>Direct Submission</p> <p>Submitted (02-JUN-1999) Genoscope - Centre National de Sequençage. : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)</p> <p>Determination of this BAC-end sequence was carried out as part of a</p>												

The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP *Drosophila melanogaster* BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamooser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES	Location/Qualifiers
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BRIN
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[illegible]

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OY		1425 TAGTAAGTCAGAATTGCACTGGACAGCACGTCAAAGACTAGGAATGGATGTTTGAA	1484
Dd		742 DRAGTAGGRKRTRWTMRFRMKRRRDTWRMDADDADDTAADDRRRRGDGADGAKCKTKRKRRR	683
OY		1445 ATTATAACAANA TGATGATGGAATGCATGAATCGTGTGAAAAACGCCACATATNGATTA	1544
Dd		662 RDRATWDPTDMVADNAAMVTITDVTDTDMDKRDRRRKKARRRRRTTARAAMDWTWKXMD	623
OY		1545 TCCCAAGTATGAAGAN GAGCTAAC TAAC TAAT GAAT GAAT CAAC AAG CGGT AAAT TGAG	1604
Dd		622 WAKMOWKTARBDNRWDNADDTMTDARKARDMAKAAMARBRDRRAAABADRRTWKXTT	563
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Dd		562 TATWTTWAARAAMA WMAMAT	542
<b>RESULT 3 CNS0170D</b>			
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DEFINITION		Drosophila melanogaster genome survey sequence SP6 end of BAC	
LOCUS		BACN37M13 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.	
ACCESSION		AL108367	
VERSION		ALI08367.1 GI:5628671	
KEYWORDS	SOURCE	GSS.  Drosophila melanogaster (fruit fly)  Drosophila melanogaster	
ORGANISM		Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 639)	
REFERENCE	AUTHORS	Genoscope. Direct Submission	
TITLE	JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr	
COMMENT		- Web : www.genoscope.cns.fr ) Determination of this BAC-end sequence was carried out as part of a collaboration with The European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This drosophila melanogaster BAC library (DrosBAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelOBac11.	
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Dd		106 AAAAAAAAAATATATCYCC GGATATAAKGTTTAAAAARA AAAAATTCGAA RAARAA CAAMAYAAAAAH	165
OY		1298 TGAAGAACTTGACA AAAAGATGAAGAGCGG GTTC TAGATGTGTG ACATCAATG CTG	1357
Dd		166 WRAAWMATWAAAG AAAAAAAAAA RAARAAGTAGAGAGCTATTAA MWTAAMWAARAA	225
OY		1358 AGCTTTAGTCTGAN TGSAAAATGAGAGCACTT GACTTCATCATGATTCATATGTCAGA	1417

Dd		226	AMAAANAMNATATCAACWAAAAAAAMRTAAWTAAAARAAAMWWMTAGAGTAATAAAAAAWTITA	285
Qy		1418	ATCTGTATTGTTAAACTGCAGAATTCAGTGAGACAACGTCGAAGAACCTAGCAAATCGAT :   :   :   :   :   :   :   :   :   :   :   :   :   : :::	1477
Dd		286	AMRTTTTTAAGAAAAAAAAAAWMWGOWMWARBARABARAAMCAMVAMAAMAAATGAABAARRNA	345
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Qy		1538	ATGATTTCCCAAGCATTGATCAAGACAGCTGTAACATTAATAGAAATGTAATCAACGGGGA	1596
Dd		406	AAWA-AAWWRRAWGMTATTTAAAAAANAANAANAANAANAANAANAANAANAANAACAAAGACGA	463
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LOCUS		BX414650 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP001YN02		
DEFINITION		3-PRIME, mRNA sequence.		
ACCSSION		BX414650		
VERSION		BX414650.1 GI:30763455		
KEYWORDS		EST.		
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 994) Li W.B., Gruber C.; Jesse J. and Polayes D. Full-length cDNA libraries and normalization Unpublished		
TITLE		Contact: Genoscope		
JOURNAL		Genoscope - Centre National de Sequencage, BP 191 91006 Evry cedex - France Email: seque@genoscope.cns.fr Web : www.genoscope.cns.fr		
AUTHORS		Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to Sequence Cluster 6015.f Contact : Feng liang Email : f.liang@litech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSOCPA001DGI0NP1.		
FEATURES		Location/Qualifiers  1..994 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSOCAP001YN02" /tissue.type="THYMUSt"    /clone.lib="Homo sapiens THYMUS" /note="Vector: pCMWSPORT_6: 1st strand cDNA was primed with a NotI-oiligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSORT 6 vector. Library was not normalized."		
BASE COUNT		185 a                  121 c         25 g         324 t         339 others		
ORIGIN				
Query Match		3.0%; Score 54.2; DB 13; Length 994;		
Best Local Similarity		21.1%; Pred. No.0.18;		
Matches		94; Conservative 171; Mismatches 178; Indels 2; Gaps 1;		
Qy		1254 ATTTCAGCTGTGGGAAAGTAATTCGGTAGTAGAGAAAGACTGGAGAACTTGAAACAA	1313	
Dd		: :::::   :   :   :   :   :   :   :   :   :   :   :   : :::::	:	
Qy		993 WTWKMMDDDDRKKDMAWMAADRMWAAADRBAARFRADMADDWAARWRMDRWTAW	934	
Dd		1314 AAAGTGAACAACGGGTTCAGANTGCTGACATACAACTCGTAGCTTTAGTTCAT	1373	
Qy		:   :::   :   :   :   :   :   :   :   :   :   :   :   :   :::	:	
Dd		933 WAARKKWDADTTTKTRKKPADADAEDDMDPATAMWMAAADWMAARPAATAATWTDW	874	
Qy		1374 GGAAATAGAGACACTTCAATTCATGATTCATAGTCCAAGAATCTGTATAGTAAGT	1433	
Dd		: : : : :   : : : :   :   :   :   :   :   :   :   :   :   : :::	:	
Qy		873 DTAMWTRDKKTAKDAADDDAKRTITTTTTTWKKAFTDMAIGWPKAKKWADATWADADAADW	814	
Dd		1434 CAGAATCGAGCTGAGAGACAACGTCAAAGAACTAGAAATGATGTTTGAATTTAVCA	1493	

D <sub>b</sub>	813	AARAAWAAAAAAMWAADDDMMWMMDMAADAAMW--AAADTCDKRAWRDPAWR	756
O <sub>y</sub>	1494	CAATGCGATGATGAATCATGAATAGTGTA AAAAGGGACATATGTATTCCAACTA	1553
D <sub>b</sub>	755	AAAAAAAAAWNDRCGRBADAAGDKKRAA MWDDAAGGRDKRDMRAARRDDDAARRAAAAA	696
O <sub>y</sub>	1554	TGAAGAAGAGTCCTAACTAAATAGAAATCAAAGGGSTAAAATTTGACACAGATGGG	1613
D <sub>b</sub>	695	ATAWAAWMMKKKDDMAAAAAMDPAKRGRRDDARDDMAWMTTTTTTTTTTAAAAAADKAW	636
O <sub>y</sub>	1614	GTTTTATCAAAATCCCTGCCATTTPATGCAACAGTAGCAGGTCATATGCACATGCAATCAT	1673
D <sub>b</sub>	635	KKMKTATTTTTTTTTTTTTTTTTTKTKKTATAKMTDMADMADWTTTTTTTTTTTTTTMAAATY	576
O <sub>y</sub>	1674	GATGGCGGAGATCTCTTCCTGGGGG	1698
D <sub>b</sub>	575	KTKTKTKTWTKTKKTTTTTRDTWD	551

RESULT 5			
CNS0006J			
LOCUS			
DEFINITION			
Accession			
CNS0006J	1101 bp	DNA	linear
Drosophila melanogaster	genome survey sequence TEF3 end of BAC #		
BACR01M22 of RPc1-98 library from Drosophila melanogaster (fruit			
fly), genomic survey sequence.			

ACCESSION	AL062049	
VERSION	AL062049.1	GI:4938511

ORGANISM

REFERENCE 1 (bases 1 to 1101)

JOURNAL

**COMMENT**

Submitted 22-JUN-1999) Genoscope - Centre National de Séquençage  
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr))  
determination of this BAC-end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs. For further information  
please see <http://www.fruitfly.org/TheBDGP/Drosophila>  
melanogaster BAC library was prepared by Kazuhiro Oosagawa and  
Aaron Mamoser in Pieter de Jong's laboratory in the Department of  
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
NY. The library is named RPc1-98 and was constructed by partial  
EcoRI digestion of Drosophila DNA provided by the BDGP from the  
isogenic strain y?; cn bw sp, the same strain used for the BDGP's  
p1 and EST libraries. A more detailed description of the library  
and how to order individual BAC clones, the entire library, or  
vectors for hybridization from the BACpac Resource Center can be  
found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
source

BASE COUNT	333 a	162 c	148 g	177 t	281 others
ORIGIN					

Query Match	3.0%;	Score 52.8;	DB 29;	Length 1101;
Best Local Similarity	25.7%;	Pred. No. 0.39;		
Matches 151;	Conservative 165;	Mismatches 268;	Indels 4;	Gaps 2

1098 ACAAGAGGAGCATGGCCAGAAGTAATGTTGATGCGCTTGGTATGCATTACCATCACAGCAATGACCA 1157  
 496 RRAATGAATATKWRARACGTTAAWTTGAAAAAAAAAAAWTTTAAAGAAAAAAAAAAAAAAAAWATA 555

OY	1158	GGGATTCAGCGATGATGAGCAGCAAGAGATCCACTCAAAAGCATTTTGATGAAATCACCA	1217
Db	556	TKAAATTTTTTTRRRRRRGGATTITTRDTRAKAAAAAAAATAATTATAGAAAAAGAAAAAA	615
OY	1218	CAAGGTAAATTCGTGATTGAAAGATGAACCCCAATTTGAGCTGTTGGGAAAGAAATT	1277
Db	616	AARAAAGCTTTTGAAGAAAAAAAATAATAAKAMAAAAAGGAAAAAAATATNAA	675
OY	1278	CGGTAACTTAGAGAAAAAGCTGGAGACTTGACAAAAAAGTGTGAAGCGGCTTTCTAGA	1337
Db	676	AAKAAWRTGKTATATAAAAAAAMAAABAGGAAAGGKRRGARRRGGGRRMRAAAA	735
OY	1338	TGTGTGCACATACATGCTGAGCTTTTAGTTCTGATGGAAAAATGAGAGACACTTGACTT	1397
Db	736	KTKRRKKTKTKRRRAAGRRARRAAAGAAAAAADAATKTGTYNKAAMRTAAWKKD	795
OY	1398	TCAATGATTCATATGCAAGAACTCGGTATGTAAGTGAAGATGACAGCTGACAGCAACGT	1457
Db	796	WKATDAAAKAAARTRDWTTAKADDKTKWGAATAAGAGAAARRRRGKGGKQTRRR	855
OY	1458	CAAGAACATAGGAATGGATGTTTGAATTTTATCACAAATGTGATGTAATGCATGAA	1517
Db	856	ARGAGDGDAAKAAAMAAWAAATATARMDTATAADDRRAKAWDKRRAAAADKRD - KGRRA	914
OY	1518	TAGTGTGAAAAACGGGACATATGATTAATCCCAAGTATGAAAGAAGCTTAACCTAATAG	1577
Db	915	GWGIGWRRRAARTRRKAKARRRGARAGAKAKRRRAKGDWKKGMKKMDKADAMAARAKKGT	974
OY	1578	AAATGAATCAAAAGGGTAAATATGAGCAGCATGGGGTGTATTATCAAAATCCTTGGCCATTTA	1637
Db	975	GDMMKRRARK - - AKTGMKARADKRRWRAAADDTWRFTKAMWWTDMRWNTATATKDKDTDKA	1031
OY	1638	TGCTACAGTAGCAGTCTCTATGCTACGCGCAATCATATATGGCTGGGAAAT	1685
Db	1032	KKGAAKMTTTRTDRAAKAKAKADDPATATATATAMCDADDKAARAPAKAK	1079

CNS005TE/C	CNS005TE	997 bp	DNA	linear	GSS 03-JUN-1999
LOCUS					
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR1K22 of RPL1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL060767				
VERSION	AL060767.1	GI:4943573			
KEYWORDS	GSS.				
SOURCE	Drosophila melanogaster	(fruit fly)			
ORGANISM	Drosophila melanogaster				

REFERENCE 1 (bases 1 to 997)

JOURNAL

COMMENT

Submitted 22/09/1999) Genoscope - Centre National de Séquençage  
BP 191 91006 Evry cedex - FRANCE (E-mail : segr@genoscope.cns.fr  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr))

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see <http://www.fulfly.org> The BDGP *Drosophila melanogaster* BAC library was prepared by Kazutoyo Osogawa and Aaron Mamoser in Pister de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RP11-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y?; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACpac Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES	source	Location	Qualifiers
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			/mol_type="genomic DNA"
			/db_xref="taxon:7227"
			/clone="BACR12K22"
			/clone_lib="RPCI-98"
			/note="end : TET3"
BASE COUNT	89 a	99 c	13 g 258 t 538 others
ORIGIN			
Query Match.	2.9%;	Score 52.4;	DB 29; Length 997;
Best Local Similarity	17.1%;	Pred. No. 0.46;	
Matches	68; Conservative	139; Mismatches	190; Indels 0; Gaps 0;
OY	1032 AACAGGACTAAGGAATGTTCCCGCAGATTGATCTCAAGAGATTGTTGGGCGCAATAGCTGG	1091	
Db	827 RARARRRRGAGARRAR	768	
OY	1092 TTTTATAGAGAGAGGATGTCGCAAGAATGTTGACGGTGGTATGATACCATCAGCAGCA	1151	
Db	767 GRRRAARARARARAR	708	
OY	1152 TGACCAGGATCAGGATATGACGACAGACAAAGAAATCCACTCAAAAGCATTGTGTAAT	1211	
Db	707 RRARAGAGGAARRRR	648	
OY	1212 CACCAACAGGTAAATCTGTGATTGAAAGATGAATACCCCAATTTGAAGCTGTTGGCA	1271	
Db	647 RGAGARRRRAGARR		

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source
1. 1167
   /organism="Homo sapiens"
   /mol_type="mRNA"
   /db_xref="taxon:9606"
   /clone="CS0DF015YA21"
   /tissue_type="FETAL BRAIN"
   /dev_stage="fetal"
   /clone_11b="Homo sapiens FETAL BRAIN"
   /note="Organ: Brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

BASE COUNT      190 a      163 c      114 g      356 t      344 others

ORIGIN

Query Match      2.9%; Score 52.2; DB 13; Length 1167;
Best Local Similarity 26.5%; Pred. No. 0.53; Mismatches 237; Indels 0; Gaps 0;
Matches 127; Conservative 115;

QY 1112 AAGCAATGGTTGACGGTTGGTATGATACCATCAGCAATGACCAGGATCAAGGTATG 1171
    || || || || || || || || || || || || || || || || || || || || ||
DB 1097 AAAAAARKKHKVHKBKTKTHMDMAGMAAAAKMAAGAAARGAARKKTTDAGAAAMCG 1038
                                           /tissue_type="FETAL BRAIN"
QY 1172 CAGCAGACAAAGAAATCCATCAATCAAGCAATTTGATGGAATCCACACAGTAATCTG 1231
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1037 TATMMHGGSCCGMMNGMAGCMGKMWVGSGKTTTTTTTTTTTTTAMKTMGGAMKAAATGK 978
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1232 TGATTGAAAGATATAACGCCCAATTTGTAAGCTGTGGGAAAGAAATTCGGTAACTTAGA 1291
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 977 TAAKKAADKTKTTTKKTTTNTKGGKGGTMMGKNTKKKGAAMAMKTKMTTGTGGAAA 918
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1292 AAAGACTGGAGACCTTGACAAAGATGAGAGAGCGGTTTCTGATGTGTGACATACA 1351
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 917 AAAAMAKKGAARAGAGCGKKAAMAMT KKKMGKTGMMKMKKAAAKKMDKAAAKATAT 858
    | : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1352 ATGCTGACCTTTTGCTGTGATGGAATGAGAGACACTTGACTTCATGATTTCTATG 1411
    | : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 857 AATTTKAAAANKATGKGCNCNTAAKKAARATATASKTTTWTTKTTTTTAATTKTT 798
    | : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1412 TCAGAATCTGTATAGTAAGTCAAGATGCAAGTGCAGAGACACGTCAAAGACTAGAA 1471
    | : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 797 WTTTMMHCAAAAAAMKAAAAAAATATATVKAATTKTRTAGAAMTTAAAKTKKWAAMAK 738
    | : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1472 ATGATGATTTTGAATTTTATCACAATGTGATGATGATCATGATGATGTGAAAAACG 1531
    | : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 737 WKKMTATATWTTTAAAKKTAAAMAAAAMKAAAMAAAMWTHKTKMTKTAATAAKATTATWTMARG 678
    | : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1532 GGACATATGATTAATCCCAAGTATGACAGAGAGTCTAAACTTAATAGATGAATCAAA 1590
    | : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 677 KAAAAAANKKAKAKGTAMKRRKATTAAMWMTKKAHTTKTAAAAAAAMAKAAAMKAA 619
    | : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
CNS02JEX/c
LOCUS      847 bp      DNA      linear      GSS 01-SEP-2000
DEFINITION Tetradon nigroviridis genome survey sequence PUC-Ort end of clone
14310 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION AL200130
VERSION   AL200130.1 GI:7858475
KEYWORDS  GSS: genome survey sequence.
SOURCE    Tetradon nigroviridis
ORGANISM  Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE 1
AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Pizanes,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissendach,J.
Estimate of human gene number provided by genome-wide analysis

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ORGANISM	Pichia farinosa
REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.
AUTHORS	Souci�t,J.L., Aigle,M., Artiguenave,F., Blandin,G., Boitlin-pukhara,M., Bon,E., Brotier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuisse,C., Ozler,Kalogreopoulos,O., Potier,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Weslowski-Douvel,M., Wincker,P. and Weissbach,J. Genomic exploration of the hemiascomycetous yeasts : 1. A set of yeast species for molecular evolution studies FEMS Lett. 487 (1), 3-12 (2000)
TITLE	FEMS Lett. 487 (1), 3-12 (2000)
JOURNAL MEDLINE	20584711
PUBMED	11152876
REFERENCE AUTHORS	2 (bases 1 to 468) de Montigny,J., Spohner,C., Souci�t,J., Tekala,F., Dujon,B., Wincker,P., Artiguenave,F. and Potier,S. Genomic exploration of the hemiascomycetous yeasts : 15. Pichia sorbitophila
TITLE	FEMS Lett. 487 (1), 87-90 (2000)
JOURNAL MEDLINE	20584725
PUBMED	11152890
REFERENCE AUTHORS	3 (bases 1 to 468) Genoscope. Submitted Submission Direct Submission Submitted (08-SEF-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr) This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert. Location/Qualifiers
COMMENT	1..468 /organism="Pichia farinosa" /mol_type="genomic DNA" /strain="CBS 7064" /db_xref="taxon:4920" /clone="XAXOAA002F07" /clone_1kb="XAXOXA" /note="end : 17" <13..>159 /note="similar to Saccharomyces cerevisiae ORF YLR127c [APC2 : component of the anaphase promoting complex ]" /evidence-not_experimental
FEATURES source	
BASE COUNT	124 a 59 c 55 g 212 t 18 others.
ORIGIN	
Query Match Best Local Similarity 50.%;	2.%; Score 49.6; DB 29; Length 468;
Matches 104; Conservative	Pred. No. 1.6; Mismatches 96; Indels 0; Gaps 0;
Db	
YQ	1380 TGAGAGACACTGCAATTTCATGTCTTCAATGTCGAAGATCTGTAAGTAAAGTCAGCAT 14399
Db	257 TAATAAACAAGTTAAACCTGTATATTTAGGATTTAAACAACCTACTAGAAAACBCYCVMTT 198
YQ	1440 GCAGCGTAGAGACACGTCGAAGAAGACATGAGAAATGGATTTGCATTTTATTCACAATG 14999
Db	197 AGAAGTTAAACAATATGTTTTAAATAAACCATATGATGATCTGATGTTAAAGAATAA 138
YQ	1500 TGATAGTGAATGCATTAATAGTGTAAGAAACGGACATATGATGATATCCCAAGTATGAGA 15599
Db	137 TGATACCTAATATCARAAAAACCTGGMAATATCAACACATTAGRTATGCCAGTATTAATG 78
YQ	1560 AGAGCTTAAACTAAATGGAATGAAA 1585

Db	77	ATACATAGTNCAGAGATATCAAA	52
RESULT 11			
CNS006MW	918 bp	DNA	linear
CNS006MW			GSS 03-JUN-1999
LOCUS			
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC #		
	BACR14FF09 of RPl-98 library from Drosophila melanogaster (fruit		
	fly), genomic survey sequence.		
ACCESSION	AL065768		
VERSION	AL065768.1		
KEYWORDS	GI:4944648		
SOURCE	GSS.		
ORGANISM	Drosophila melanogaster (fruit fly)		
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
	Ephydroidea; Drosophilidae; Drosophila.		
REFERENCE	1 (bases 1 to 918)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)		
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <a href="http://www.fruitfly.org">http://www.fruitfly.org</a> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPl-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2: cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at <a href="http://bdgpc.med.buffalo.edu/drosophila_bac.htm">http://bdgpc.med.buffalo.edu/drosophila_bac.htm</a> .		
FEATURES			
SOURCE	Location/Qualifiers		
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	/organism="Drosophila melanogaster"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:7227"		
	/clone="BACR14FF09"		
	/clone_lib="RPl-98"		
	/note="end : 77"		
BASE COUNT	251 a 169 c 125 g 130 t 243 others		
ORIGIN			
	Query Match 2.8%; Score 49.4; DB 29; Length 918;		
	Best Local Similarity 21.3%; Pred. No. 2.1;		
	Matches 60; Conservative 114; Mismatches 108; Indels 0; Gaps 0;		
QY	1335 AGATGTGTGCACATACATACGCTGACCTTTAGTTCTGATGGAATAAGAGACACCTGA	1394	
Db	637 AAAARKKRGGRMKWTATAKTKTDADDDGATRWKMKDDMTTAAANRTMTARMKATAGGA	696	
QY	1395 CTTTCATGATTTCTATGTCAAGATCTGTATAGTAAAGTGCAGATGCAGCTGAAGACAA	1454	
Db	697 DRTAAGAGAGGRTADKKRWGRAGTTRCKTATAGAGAAAGAAARAKADKKDATRKAATD	756	
QY	1455 CGTCAAGACACTAGGAATGATCTTTTGAATTTTATACCAAAATGATGATGAATGCAT	1514	
Db	757 AKKRWRTKRAAWKDKAKDKDKDKKKTDTTKAKKAKKAKKDKDKDKDKDKDKDKDKDK	816	
QY	1515 GAATATGTGTGAAAAACGGACATATGATATCCCAAGTATGAGAAGAGATCTTAACATAA	1574	
Db	817 TADRRDRDRDRDKTAKADAKDDAKAKAKADGARRPRAAGWGAGAKAGATGDRATKAW	876	
QY	1575 TAGAAATGAATCAAAAGGGTAANAATGAGACAGATGGGGT	1616	
Db	877 RDRGRAGAAAAAWKARRAKDKGRKKKAGKTDKDGWGGDKKK	918	

```

RESULT 12
BX406178/c 1201 bp mRNA linear EST 13-MAY-2003
LOCUS BX406178 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CS0DM010YN11 3-PRIME, mRNA sequence.
ACCESSION BX406178
VERSION BX406178.1 GI:30639385
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.-B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0AM010CG06NP1.
FEATURES
Source
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM010YN11"
/tissue_type="FETAL LIVER"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL LIVER"
/notes="Organ: liver; Vector: pCMVSPORT.6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
cloned, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT 239 a 246 c 241 g 220 t 255 others
ORIGIN
Query Match 2.7%; Score 48.8; DB 13; Length 1201;
Best Local Similarity 25.0%; Pred. No. 3.1; Mismatches 0; Gaps 0;
Matches 70; Conservative 100;
1282 AACCTAGAGAAAAGCTGAGAACTTGAACAAAAGATGAGAGCGTTCTAGATGTG 1341
1193 AAAAAAATAATATATATATATATATATATATATATATATATATATATATAT 1134
1342 TGCAATACATGCTGAGCTTTTGTGATGAGAAATGAGAGGACACTTGCATTGCAT 1401
1133 TTTTDRDDRRRFRDRTDNTADWADAARDAARAARAARATWDRRTTAMWMTTRDT 1074
1402 GATTCTAATGCAAGATCTGTATAGTAAGTCAGATGACGCTGAGACAAAGTCAAA 1461
1073 WDTWAKADTTTAAADATTRRDTTRDDTARATADWAKMTWADWRRATADATWTRARA 1014
1462 GAATAGAGAAATGATGTTTGTATATATCAAAATGATGATGATGATGATGATGATG 1521
1013 TWMAMARRATTRKADDTADRRTTRKTTTDDDRDTADRADTARDCRRTRRGDT 954
1522 GTGAAAAACGGACATATGATATATCCCAAGTATGAAGAAG 1561
953 AVDRTWDMMAATTTDTWBRKTDADADVDGDKTAADADAD 914

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ACCESSION AL065906
VERSION AL065906.1 GI:4944874
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 938)
AUTHORS Direct Submission
TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
COMMENT Genoscope
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org/The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPc1-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp. The same strain used for the BDGP's
PI and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
Source
1.938
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR14J11"
/clone_lib="RPc1-98"
/notes="end: T7"
BASE COUNT 86 a 98 c 85 g 334 t 335 others
ORIGIN
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Best Local Similarity 22.6%; Pred. No. 3.3; Mismatches 211; Indels 5; Gaps 1;
Matches 106; Conservative 148;
1007 TAAATCGAGAGATTGCTTTAGCAACAGCTAAGATGTTCCAGATTGAATCA 1066
925 DAKADAKADAKADAKADAKADAKADAKADAKADAKADAKADAKADAKADAKADAK 866
1067 GAGATGTTTGGGCAATAGCTGTTTATATGAAG----GAGATGCAAGAAAGT 1121
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1122 TGACGGTTGTTGATGATCATCATCAGCAAGTACCAAGGATGAGGTATGACGCA 1181
805 AKDKADADADADADADADADADADADADADADADADADADADADADADADAD 746
1182 AGATTCACCTCAAAAGCATTTGATGATGATGATGATGATGATGATGATGATG 1241
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1302 GAACCTGAACAAAAGATGAGAGAGGGTTCTACATGTGAGCATCATCATGAGCT 1361
625 RKDAGTAATKAAKAAKAAKAAKADDTTPTKTWDATATDKTKDGTATATATRAKT 566
1362 TTTAGTCTGATGAGAAATGAGAGAGCACTGATGATGATGATGATGATGATGATG 1421
565 GKATGKTWTTTATATATATATATATATATATATATATATATATATATATAT 506
1422 GTATAGTAAAGTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1471

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RESULT 13
CNS006TJ/c 938 bp DNA linear GSS 03-JUN-1999
LOCUS CNS006TJ Drosophila melanogaster genome survey sequence T7 end of BAC #
DEFINITION BACR14J11 of RPc1-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

```



Db 505 NANNNNNANNNNNNNNNNNNNNANNAANGANNANNAANNAANNAAAAA 456

RESULT 14  
BX461128 1201 bp mRNA linear EST 22-MAY-2003  
LOCUS BX461128 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
DEFINITION CSODF023YE09 5-PFIME, mRNA sequence.  
ACCESSION BX461128  
VERSION BX461128.1 GI:31035272  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1201)  
AUTHORS Li, W.-B., Gruber, C., Jesse, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 3830.f for  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CSODF023AC05Q1&cluster=3830.f. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CSODF023AC05Q1.  
Location/Qualifiers  
1. 1201  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSODF023YE09"  
/tissue\_type="FETAL BRAIN"  
/dev\_stage="fetal"  
/clone\_lib="Homo sapiens FETAL BRAIN"  
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA  
was primed with a NotI-Oligo(dT) primer. Five prime end  
enriched, double-strand cDNA was digested with Not I and  
cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
vector. Library was not normalized."

BASE COUNT 450 a 385 c 79 g 53 t 234 others  
ORIGIN

Query Match 2.7%; Score 48.4; DB 13; Length 1201;  
Best Local Similarity 28.5%; Pred. No. 3.8;  
Matches 94; Conservative 87; Mismatches 149; Indels 0; Gaps 0;

Db 1256 TTGAAGCTGTTGGCAAGAAATTCGTAACCTAGAGAAAGACTGGAGAACTGAACAAAA 1315  
872 TTTAAATATATGARAATAAAKADMAKAAADKADADAKAAAKAAKRAAAAAA 931  
1316 AGATGGAAGACGGGTCTCTGATGCTGACATACATGCTGAGCTTTTGAAGTCTGATGG 1375  
932 KKAATAADKAAADKAAKAKKDKKRAAAAADKRRKDKKKKDAADAAAMKKK 991  
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992 AAAAAAAKBTAAAKAATATKAKKKKKKKKMAAAAAAADAAGAARAAAKAAVAATKKA 1051  
1436 GAATGACGCTGAGAGACACAGCTCAAGAACTAGAGAAATGATGTTTGAATTTTATCACA 1495  
1052 AAAAAAAKKAAMKAAKAAAKKKKKKADKAAADKGAARAKKAKAKAGAAAGAAAAA 1111  
1496 AATGATGATGATGATATCATGATAGTGTGAAAAACGGACATATGATTAATCCCAAGATG 1555  
1112 ATKAAARAAAAAANA KADRAAAAAAARAAAAADAAAKRAAAKAKRAAABAAADKKKKKA 1171

Db 1556 AAGAGAGCTCTAAACTAATAGAAATGAAA 1595  
1172 AKKAAAAAKKKKRAAAAAAANAAAAA 1201

RESULT 15  
AU087765 500 bp mRNA linear EST 27-JAN-2001  
LOCUS AU087765  
DEFINITION AU087765 Sugano Malaria cDNA library Plasmodium falciparum 3D7 cDNA  
clone XFPn5652, mRNA sequence.  
ACCESSION AU087765  
VERSION AU087765.1 GI:12389906  
KEYWORDS EST.  
SOURCE Plasmodium falciparum 3D7  
ORGANISM Plasmodium falciparum 3D7  
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
REFERENCE 1 (bases 1 to 500)  
AUTHORS Watanabe, J., Sasaki, M., Suzuki, Y. and Sugano, S.  
TITLE Full-malaria: a database for a full-length enriched cDNA library  
JOURNAL from human malaria parasite, Plasmodium falciparum  
Nucleic Acids Res. 29 (1), 70-71 (2001)  
MEDLINE 20574754  
PUBMED 11125052  
COMMENT Contact: Junichi Watanabe  
Institute of Medical Science  
The University of Tokyo, Department of Parasitology  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Tel: 81-3-5449-5378  
Fax: 81-3-5449-5410  
Email: jwatanab@med.s.u-tokyo.ac.jp  
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano  
S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).  
Location/Qualifiers  
1. 500  
/organism="Plasmodium falciparum 3D7"  
/mol\_type="mRNA"  
/isolate="3D7"  
/db\_xref="taxon:36329"  
/clone="XFPn5652"  
/dev\_stage="erythrocytic stage"  
/clone\_lib="Sugano Malaria cDNA library"  
BASE COUNT 252 a 41 c 88 g 113 t 6 others  
ORIGIN

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Best Local Similarity 48.9%; Pred. No. 4.2;  
Matches 157; Conservative 0; Mismatches 162; Indels 2; Gaps 1;

Db 1270 AAAGAATTCGTAACCTAGAGAAAGACTGGAGAACTTGAACAAGATGGAAGACGGG 1329  
76 AAAAAAAGAAAAAATAAGTTATGATTAATAAATAATATTCAAAAAAGAAATTCGCTG 135  
1330 TTTCTAGATGCTGGACATCAATGCTGACCTTTTACTGCTGATGGAATGAGAGACA 1389  
136 CAAACATGAAATCAATATGCAATTAATCTGGAAGTGAATTCAGATGGAAAAATCAATA 195  
1390 CTGACCTTATGATTTATATGTCACAGAAATCTGATAGTAAGTCAGAAATGACCTGA-- 1447  
196 GTTCATATTTACGCTTGTCTATACAGTAATATGAGGAAGCAAGGAAGATGATCAAG 255  
1448 GAGACACGTCGAAGAACTGGAATGATGATTTTATGATTTTATGACAAATGATGATG 1507  
256 ATGAAATGAAAGATGAAAGATGAAATGCAATGCAAGTGAATGAAATGAAATGATGAG 315  
1508 AATGACATGATAGTGTGAAAAACGGACATATGATTAATCCCAAGTATGAAAGAGCTCA 1567  
316 AAGATGTGAAATGAAACAAATTAATAATATATGATCTGGAATATAAATTCACAAATTA 375  
1568 AACTAATTAAGTAATGAAATCA 1588  
376 ACATAAAAAGAAAAAATATTA 396

Tue Aug 12 10:28:18 2003

Search completed: August 10, 2003, 10:57:43  
Job time : 2740.47 secs

us-09-918-568-46.rst

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penCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 18:45:33 ; Search time 2858.63 Seconds

(without alignments)  
16242.876 Million cell updates/sec

Title: US-09-918-568-49

Perfect score: 1135

Sequence: 1 CTGCAAAAGCGGGTAT.....AACACCTGTGTCTGCTAG 1135

Scoring table: IDENTITY\_NNC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vi:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_hiv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pn:\*  
35: em\_htg\_rpd:\*  
36: em\_htg\_mim:\*  
37: em\_htg\_vtl:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1135	100.0	1135	6 AR181964	AR181964 Sequence
2	1135	100.0	1135	6 E08993	E08993 DNA encodin
3	1135	100.0	1135	6 I32529	I32529 Sequence 49
4	1135	100.0	1135	6 I43474	I43474 Sequence 49
5	908.8	80.1	1783	6 AR181961	AR181961 Sequence
6	908.8	80.1	1783	6 I32526	I32526 Sequence 46
7	908.8	80.1	1783	6 I43471	I43471 Sequence 46
8	887.6	78.2	1773	14 FLAHAJ3055	L20407 Influenza A
9	887.6	78.2	1773	14 FLAHA5157A	L20410 Influenza A
10	887.6	78.2	1773	14 FLAKRA59HA	L11134 Influenza A
11	886	78.1	1773	14 FLAHA3055J	L20406 Influenza A
12	884.4	77.9	1773	6 AX399727	AX399727 Sequence
13	884.4	77.9	1773	14 FLAHA1K	J02127 Influenza A
14	884.4	77.9	1773	14 FLAHA1557	L20408 Influenza A
15	884.4	77.9	1773	14 FLASIN57HA	L11142 Influenza A
16	882.8	77.8	1773	14 FLAHA575RI	L20409 Influenza A
17	879.6	77.5	1773	14 AB056699	AB056699 Influenza A
18	869.2	76.6	1773	14 FLAKOR68HA	L11133 Influenza A
19	866.8	76.4	1773	14 FLAIBNG4HA	L11126 Influenza A
20	860.4	75.8	1773	14 FLAHA1ZU	D13579 Influenza A
21	858.8	75.7	1773	14 FLAHA1ZR	D13580 Influenza A
22	852.4	75.1	1773	14 FLABER68HA	L11125 Influenza A
23	838	73.8	1728	6 E07248	E07248 Haemaggluti
24	838	73.8	1728	6 I32508	I32508 Sequence 28
25	838	73.8	1728	6 I32508	I32508 Sequence 28
26	838	73.8	1728	6 I43453	I43453 Sequence 28
27	814	71.7	1773	14 FLAHDR72HA	L11129 Influenza A
28	808.4	71.2	1773	14 FLAMT61HA	L11136 Influenza A
29	799.6	70.4	1773	14 FLAPOT83HA	L11139 Influenza A
30	799.6	70.4	1773	14 FLAPOT84HA	L11127 Influenza A
31	798	70.3	1773	14 FLAPOT85HA	L11140 Influenza A
32	793.2	69.9	1772	14 FLAENG78HA	L11128 Influenza A
33	793.2	69.9	1773	14 FLADE88HA	L11132 Influenza A
34	791.6	69.7	1772	14 FLAPRA76HA	L11141 Influenza A
35	761.8	67.1	1717	14 AF290440	AF290440 Influenza
36	760.2	67.0	1717	14 AF290441	AF290441 Influenza
37	760.2	67.0	1717	14 AF290442	AF290442 Influenza
38	758.6	66.8	1717	14 AF290439	AF290439 Influenza
39	698.8	61.6	1772	14 FLAONT76HA	L11138 Influenza A
40	698.8	61.6	1773	14 FLANY78HA	L11137 Influenza A
41	697.2	61.4	1773	14 FLANU91HA	L11131 Influenza A
42	689.2	60.7	1772	14 FLAAL888HA	L11135 Influenza A
43	687.6	60.6	1772	14 FLAND77HA	L11130 Influenza A
44	651.4	57.4	1723	14 AF116201	AF116201 Influenza
45	551.8	48.6	1768	14 INFHA12	X07869 Influenza A

#### ALIGNMENTS

RESULT 1  
LOCUS AR181964 1135 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 49 from patent US 6337070.  
ACCESSION AR181964  
VERSION AR181964.1 GI:20224880  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1135)  
AUTHORS Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.  
TITILE Polypeptides for use in generating anti-human influenza virus  
antibodies  
JOURNAL Patent: US 6337070-A 49 08-JAN-2002;

FEATURES  
 source  
 BASE COUNT 395 a 197 c 265 g 278 t  
 ORIGIN

Query Match 100.0%; Score 1135; DB 6; Length 1135;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-260;  
 Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTAGAAAAAGGAGGTTATACCATAGAAACCAAAAGCAAAACAAATGGCCATCATTTAT 60  
 1 CTAGAAAAAGGAGGTTATACCATAGAAACCAAAAGCAAAACAAATGGCCATCATTTAT 60  
 61 CTCATTCCTCTGTTACAGACAGTGAAGGGGACCAAGATTCATTCGATACCATGCCAAT 120  
 61 CTCATTCCTCTGTTACAGACAGTGAAGGGGACCAAGATTCATTCGATACCATGCCAAT 120  
 121 AATTCCACAGAGAGGTGCACACATTTAGAGCGGACGTCAGTGTGATGCGCAAG 180  
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 481 GGTGATGATGATACCATCAGCAATGACAGGATGATGACAGCAAGAA 540  
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 841 TTTTATACAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
 841 TTTTATACAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
 901 CCCAAGTATGAGAGAGGTCTAAACTAAATGAATGAATGAATGAATGAATGAAT 960  
 901 CCCAAGTATGAGAGAGGTCTAAACTAAATGAATGAATGAATGAATGAATGAAT 960

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RESULT 2  
 E08993  
 LOCUS  
 DEFINITION  
 DNA encoding an immunogenic peptide derived from human Influenza A virus haemagglutinin that doesn't have globular region.  
 ACCESSION  
 E08993  
 VERSION  
 E08993.1 GI:22024631  
 KEYWORDS  
 JP 1995089992-A/3.  
 SOURCE  
 unidentified  
 ORGANISM  
 unclassified.  
 REFERENCE  
 1 (bases 1 to 1135)  
 Okuno, Y., Isekawa, Y., Sasao, F. and Ueda, S.  
 IMMUNOGENIC ARTIFICIAL POLYPEPTIDE  
 Patent: JP 1995089992-A 3 04-APR-1995;  
 TAKARA SHUZO CO LTD  
 OS  
 None  
 COMMENT  
 Artificial sequences.  
 PN JP 1995089992-A/3  
 PD 04-APR-1995  
 PE 16-MAR-1994 JP 1994070194  
 PF 20-APR-1993 JP 93P 115216  
 PI OKUNO YOSHINOBU, ISEKAWA YUYU, SASAO FUYOKO, UEDA SHIGEHARU PC  
 C07K1/08, A61K39/145, C12N15/44, C12P21/02, C12N15/06, C12P21/08, PC  
 (C12P21/02)  
 PC C12R1:91), (C12P21/08, C12R1:91), C07K99:00;  
 CC strandedness: Double;  
 CC topology: linear;  
 FH key  
 FT source  
 FT 46.1092  
 FT 46.1092  
 FT 46.1092

FEATURES  
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 sig\_peptide 46.90  
 Location/Qualifiers  
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 BASE COUNT 395 a 197 c 265 g 278 t  
 ORIGIN

Query Match 100.0%; Score 1135; DB 6; Length 1135;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-260;  
 Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 1 CTAGAAAAAGGAGGTTATACCATAGAAACCAAAAGCAAAACAAATGGCCATCATTTAT 60  
 61 CTCATTCCTCTGTTACAGACAGTGAAGGGGACCAAGATTCATTCGATACCATGCCAAT 120  
 61 CTCATTCCTCTGTTACAGACAGTGAAGGGGACCAAGATTCATTCGATACCATGCCAAT 120  
 121 AATTCCACAGAGAGGTGCACACATTTAGAGCGGACGTCAGTGTGATGCGCAAG 180  
 121 AATTCCACAGAGAGGTGCACACATTTAGAGCGGACGTCAGTGTGATGCGCAAG 180  
 121 AATTCCACAGAGAGGTGCACACATTTAGAGCGGACGTCAGTGTGATGCGCAAG 180

181 GACATCCTTGAGAG ACCCATACGGAAGTTATGCAAACTAAACGATCCGGATGATG 240  
181 GACATCCTTGAGAG ACCCATACGGAAGTTATGCAAACTAAACGATCCGGATGATG 240  
241 AAAACAGAGAGAAC TTGAGAACTGTGAGACCAATGCGCAACTCTTTGGAGCAATA 300  
241 AAAACAGAGAGAAC TTGAGAACTGTGAGACCAATGCGCAACTCTTTGGAGCAATA 300  
301 AATCAACATTACCT TTTCACAAATGTCACCCACGACAAATAGGTGATGCCCAATAT 360  
301 AATCAACATTACCT TTTCACAAATGTCACCCACGACAAATAGGTGATGCCCAATAT 360  
361 GTAAATCGAGAGAG TTGCTCTAGCAACAGAGTAAGAAATGTTCCCAATGTAATCA 420  
361 GTAAATCGAGAGAG TTGCTCTAGCAACAGAGTAAGAAATGTTCCCAATGTAATCA 420  
421 AGAGAGTTGTTGGG SCATATAGCTGCTTTTATAGAGAGAGATGGCAAGAAATGTTGAC 480  
421 AGAGAGTTGTTGGG SCATATAGCTGCTTTTATAGAGAGAGATGGCAAGAAATGTTGAC 480  
481 GGTGGTATGATAC ATCACAGCAATGACAGGATCAGGATATGACAGCAAGAAAGAA 540  
481 GGTGGTATGATAC ATCACAGCAATGACAGGATCAGGATATGACAGCAAGAAAGAA 540  
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541 TTCACTCAAAAGGCA TTGATGAAATCACAAGGTAAATTCCTGATGAAAAGATA 600  
541 TTCACTCAAAAGGCA TTGATGAAATCACAAGGTAAATTCCTGATGAAAAGATA 600  
601 AACCCCAATTTGAA TCTGTTGGGAAAGATTCGGTAACTTAGAGAAAAGACTGGAAGAC 660  
601 AACCCCAATTTGAA TCTGTTGGGAAAGATTCGGTAACTTAGAGAAAAGACTGGAAGAC 660  
601 AACCCCAATTTGAA TCTGTTGGGAAAGATTCGGTAACTTAGAGAAAAGACTGGAAGAC 660  
661 TTGAACAAAAAGATG TGAAGACGGGTTCTAGATGTGGACATCAATGGCAGCTTTTA 720  
661 TTGAACAAAAAGATG TGAAGACGGGTTCTAGATGTGGACATCAATGGCAGCTTTTA 720  
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721 GTTCTGATGAAAAAT TGAAGACCACTTACCTTATCTATGTCAGAAATCTGTAT 780  
721 GTTCTGATGAAAAAT TGAAGACCACTTACCTTATCTATGTCAGAAATCTGTAT 780  
781 AGTAAATCGAATG TGAAGACCACTTACCTTATCTATGTCAGAAATCTGTAT 780  
781 AGTAAATCGAATG TGAAGACCACTTACCTTATCTATGTCAGAAATCTGTAT 780  
781 AGTAAATCGAATG TGAAGACCACTTACCTTATCTATGTCAGAAATCTGTAT 780  
841 TTTTATCACAAAATG TATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
841 TTTTATCACAAAATG TATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
901 CCCAAGTATGAGAA TGTCTAAACTAAATAGAAATGAAATCAAGGGGTAAATTCAGC 960  
901 CCCAAGTATGAGAA TGTCTAAACTAAATAGAAATGAAATCAAGGGGTAAATTCAGC 960  
961 AGCATGGGGGTTTAT TAAATCCTTGCATTTATGCTACAGTACAGAGTTCTATGCTACTG 1020  
961 AGCATGGGGGTTTAT TAAATCCTTGCATTTATGCTACAGTACAGAGTTCTATGCTACTG 1020  
1021 GCATTCATGATGCT TGGATCTCTTCTGGGTGCTGCCAAGGGGTCTCTGCAATGAGAG 1080  
1021 GCATTCATGATGCT TGGATCTCTTCTGGGTGCTGCCAAGGGGTCTCTGCAATGAGAG 1080  
1081 ATCTGCATATGATTA TATGATATTTTAAATTAACACCCCTTGTCTGCTAG 1135  
1081 ATCTGCATATGATTA TATGATATTTTAAATTAACACCCCTTGTCTGCTAG 1135

RESULT 3  
132529  
LOCUS 132529  
DEFINITION Sequence 49 from patent US 5589174.  
ACCESSION 132529  
VERSION 132529.1 GI:182320  
KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1135)  
AUTHORS Okuno, Y., Isegawa, Y., Sasao, F. and Ueda, S.  
TITLE Anti-human influenza virus antibody  
JOURNAL Patent: US 5589174-A 49 31-DEC-1996;  
FEATURES  
source location/Qualifiers  
1. 1135  
BASE COUNT 395 a 197 c 265 g 278 t  
ORIGIN  
Query Match 100.0%; Score 1135; DB 6; Length 1135;  
Best Local Similarity 100.0%; Pred. No. 2, 2e-260;  
Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CTACCAAAAGCAGGGGTTATACATAGAAAACCAAAAGCAAAACAAATGCCATCATTTAT 60  
1 CTACCAAAAGCAGGGGTTATACATAGAAAACCAAAAGCAAAACAAATGCCATCATTTAT 60  
61 CTCAATTCCTGTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120  
61 CTCAATTCCTGTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120  
121 AATTCACAGAGAGAGTGCACACAAATCTAGAGCGGAACGTCACTGTACTCATGCCAAG 180  
121 AATTCACAGAGAGAGTGCACACAAATCTAGAGCGGAACGTCACTGTACTCATGCCAAG 180  
181 GACATCCTTGAGAGAGCCCATACGGAAGTTATGCAAACTAAACGATCCGGATCATG 240  
181 GACATCCTTGAGAGAGCCCATACGGAAGTTATGCAAACTAAACGATCCGGATCATG 240  
241 AAAACAGAGAGAACTTGAAGTGTGAGAGCAAAATGCCAAATCCTTTGGAGCAATA 300  
241 AAAACAGAGAGAACTTGAAGTGTGAGAGCAAAATGCCAAATCCTTTGGAGCAATA 300  
301 AATCAACATTACCTTTTCAACATGTCACCACTGACCAATAGGTGATGCCCAATAT 360  
301 AATCAACATTACCTTTTCAACATGTCACCACTGACCAATAGGTGATGCCCAATAT 360  
361 GTAAATCGAGAAAGTTGGTCTTAGCAACAGAGACTAAGAAATGTTCCCGAGATTGAATCA 420  
361 GTAAATCGAGAAAGTTGGTCTTAGCAACAGAGACTAAGAAATGTTCCCGAGATTGAATCA 420  
421 AGAGAGTTGTTGGGCAATAGCTGTTTATAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
421 AGAGAGTTGTTGGGCAATAGCTGTTTATAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
481 GGTGGTATGATACATCACAGCAATGACAGGATCAGGATATGACAGCAAGAAAGAA 540  
481 GGTGGTATGATACATCACAGCAATGACAGGATCAGGATATGACAGCAAGAAAGAA 540  
541 TCCACTCAAAAGGCAATTTGATGAAATCAACCAAGGTAAATTCCTGATGAAAAGATA 600  
541 TCCACTCAAAAGGCAATTTGATGAAATCAACCAAGGTAAATTCCTGATGAAAAGATA 600  
601 AACCCCAATTTGAGAGCTGTTGGGAAAGAAATTCGTAATTTAGAGAAAGCTGGAGAC 660  
601 AACCCCAATTTGAGAGCTGTTGGGAAAGAAATTCGTAATTTAGAGAAAGCTGGAGAC 660  
661 TTGAACAAAAAGATGAGAGAGGGGTTCTAGATGTGAGACATCAATGCTGAGACTTTTA 720  
661 TTGAACAAAAAGATGAGAGAGGGGTTCTAGATGTGAGACATCAATGCTGAGACTTTTA 720  
721 GTTCTGATGAAAAATGAGAGAGCACTTTCATGATCTTAATGTCAGAAATCTGTAT 780  
721 GTTCTGATGAAAAATGAGAGAGCACTTTCATGATCTTAATGTCAGAAATCTGTAT 780  
781 AGTAAATCGAATGAGCTGAGAGAGACAGTCAAAAGCAATAGAGAAATGAGAGAGAG 840  
781 AGTAAATCGAATGAGCTGAGAGAGACAGTCAAAAGCAATAGAGAAATGAGAGAGAG 840  
841 TTTTATCACAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900

D <sub>b</sub>	841	TTTTATCCAAATGTGATGATGCATGCATGATAGTGTGAAAACGGGACATATGATAT	900
Q <sub>Y</sub>	901	CCCAAGTGTGAAGAAAGCTTAAACTAAATAGAAATGAATCAAGGGGTAAATTTGAGC	960
D <sub>b</sub>	901	CCCAAGTGTGAAGAAAGCTTAAACTAAATAGAAATGAATCAAGGGGTAAATTTGAGC	960
Q <sub>Y</sub>	961	AGCATGGGGTTTATCAAAATCCTTGCCTTTATGCTACAGTAGCAGGTTCTATGTCACTG	1020
D <sub>b</sub>	961	AGCATGGGGTTTATCAAAATCCTTGCCTTTATGCTACAGTAGCAGGTTCTATGTCACTG	1020
Q <sub>Y</sub>	1021	GCATTCATGATGGCGTGGGATCTCTTTCGGGTGTCCTCAACGGGTCTCTGACGACAG	1080
D <sub>b</sub>	1021	GCATTCATGATGGCGTGGGATCTCTTTCGGGTGTCCTCAACGGGTCTCTGACGACAG	1080
Q <sub>Y</sub>	1081	ATTCGCATATGATATATAGTCATTTTATATATTAATAAACACCCCTGTTCCTCTG	1135
D <sub>b</sub>	1081	ATTCGCATATGATATATAGTCATTTTATATATTAATAAACACCCCTGTTCCTCTG	1135

RESULT 4					
LOCUS	143474	1135 bp			
DEFINITION	Sequence 49 from patent US 5631350.				
ACCESSION	143474				
VERSION	143474.1	GI:2468718			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1135)				
TITLE	Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.				
JOURNAL	Anti-human Influenza virus antibody				
FEATURES	Patent: US 5631350-A 49 20-MAY-1997;				
source	Location/Qualifiers				
	1..1135				
	/organism="unknown"				
BASE COUNT	395 a	197 c	265 g	278 t	
ORIGIN					

Query Match	100.0%;	Score 1135;	DB 6;	Length 1135;
Best Local Similarity	100.0%;	Pred. No. 2.2e-260;		
Matches 1135; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

QY	1	CTAGCAAAAGCAGGGGTTATACCAATGAAACCAAAAGCAAAACATGGCCATCTTAT	60
Db	1	CTAGCAAAAGCAGGGGTTATACCAATGAAACCAAAAGCAAAACATGGCCATCTTAT	60
QY	61	CTCATCTTCCTGTTACAGCAGCTGAGAGGGGACAGATTCATTTGGATTCACATGGCCAT	120
Db	61	CTCATCTTCCTGTTACAGCAGCTGAGAGGGGACCAATATTCATTTGGATTCACATGGCCAT	120
QY	121	AATTCACAGAGAAAGGTGCAGACAAATTCATGAGCGGAACGTCTGACTCATGCGCAAG	180
Db	121	AATTCACAGAGAAAGGTGCAGACAAATTCATGAGCGGAACGTCTGACTCATGCGCAAG	180
QY	181	GACATCTCTTGAGAAAGACCCATTAACGAAAGTTATGCAACTAAACCGATCCGGATCATG	240
Db	181	GACATCTCTTGAGAAAGACCCATTAACGAAAGTTATGCAACTAAACCGATCCGGATCATG	240
QY	241	AAAACAGAGAAACATTTGAGAACTGTGAGACCAATGCCAAATCTCTTTGGAGACAATA	300
Db	241	AAAACAGAGAAACATTTGAGAACTGTGAGACCAATGCCAAATCTCTTTGGAGACAATA	300
QY	301	AATACCAACATTACTTTTCACAAATGCCACCACCTGACAAATAGTGAGTGCCCCCAATAT	360
Db	301	AATACCAACATTACTTTTCACAAATGCCACCACCTGACAAATAGTGAGTGCCCCCAATAT	360
QY	361	GTAATAATCGAGAAAGTTGGTCTTTAGCAACAGGACTAAGGAATGTTCCCGAGATTGATCA	420
Db	361	GTAATAATCGAGAAAGTTGGTCTTTAGCAACAGGACTAAGGAATGTTCCCGAGATTGATCA	420
QY	421	AGAGAGATTGTTGGGGCAATAGACTGTTTATAGAAGAGAGATGGCCAGAAATGTTGAC	480

Db	421	AGAGGATGTTGGGCAATAGCTGTTTATAGAGGAGATGCGAAGAAATGGTTGAC	480
OY	481	GGTTGGATGATACCATCACAGCAATGACCGGATCGGGTATGCGACGACAAAGAA	540
Db	481	GGTTGGATGATACCATCACAGCAATGACCGGATCGGGTATGCGACGACAAAGAA	540
OY	541	TCCACATCAAAAGGCATTGTATGGATTCACCAACAAGTAAATTCGTGATGTAAGAAAGTA	600
Db	541	TCCACATCAAAAGGCATTGTATGGATTCACCAACAAGTAAATTCGTGATGTAAGAAAGTA	600
OY	601	AACACCAATTTGAAGCTTTGGGAAAGAAATTCGGTAACTTAGAGAAAGACTCGGGAGAC	660
Db	601	AACACCAATTTGAAGCTTTGGGAAAGAAATTCGGTAACTTAGAGAAAGACTCGGGAGAC	660
OY	661	TTGACAAAAAGATGGAGACGGGTTTCTAGATGTGGACATACAAATGCTGACGTTTTTA	720
Db	661	TTGACAAAAAGATGGAGACGGGTTTCTAGATGTGGACATACAAATGCTGACGTTTTTA	720
OY	721	GTTCTGATGGAATATGAGAGACACTTTCATCTTATATCTATATGTCAAGAATCTGTTAT	780
Db	721	GTTCTGATGGAATATGAGAGACACTTTCATCTTATATCTATATGTCAAGAATCTGTTAT	780
OY	781	AGTAAAGTCAGATGCGAGCTGAGACACAAAGCTCAAAAGAACTAGAGAAATGGATGTTTGA	840
Db	781	AGTAAAGTCAGATGCGAGCTGAGACACAAAGCTCAAAAGAACTAGAGAAATGGATGTTTGA	840
OY	841	TTTTATCAGAAATGTGATGATGAATGCATGAATAGTGTGAAAAACGGGACATATGATTTAT	900
Db	841	TTTTATCAGAAATGTGATGATGAATGCATGAATAGTGTGAAAAACGGGACATATGATTTAT	900
OY	901	CCCAATATGAGAGAGAGCTTAACATAATATGAATATAATCAAAAGGGTAAATTTGAGC	960
Db	901	CCCAATATGAGAGAGAGCTTAACATAATATGAATATAATCAAAAGGGTAAATTTGAGC	960
OY	961	AGCATGGGGTTATCAAAATCCCTTCCATTAATCTACAGTACAGGTTCTATGTCACAG	1020
Db	961	AGCATGGGGTTATCAAAATCCCTTCCATTAATCTACAGTACAGGTTCTATGTCACAG	1020
OY	1021	GCAATCATGATGCGATGCGATCTTTCTGGGTGTGCTCAAGCGGTTCTGCAATGTCAGG	1080
Db	1021	GCAATCATGATGCGATGCGATCTTTCTGGGTGTGCTCAAGCGGTTCTGCAATGTCAGG	1080
OY	1081	ATCTGATATGATTAATAGTCAATTTTAAATTAATAAACACCTTTGTTCTGCTAG	1135
Db	1081	ATCTGATATGATTAATAGTCAATTTTAAATTAATAATAAACACCTTTGTTCTGCTAG	1135

RESULT	5
LOCUS	AR181961
DEFINITION	AR181961 Sequence 46 from patent US 6337070.
ACCESSION	AR181961
VERSION	AR181961.1 GI:20224877
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified. 1 (bases 1 to 1783) Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S. antibodies patent: US 6337070-A 46 08-JAN-2002; Location/Qualifiers 1..1783 '/organism='unknown'
JOURNAL FEATURES	
BASE COUNT	610 a     323 c     424 g     426 t
ORIGIN	

Query Match	80.1%;	Score 908.8;	DB-6;	Length 1783;
Best Local Similarity	98.7%;	Pred. No. 2.2e-206;		
Matches 916; Conservative	0;	Mismatches 12;	Indels 0;	Gaps 0;

Oy	208	AAATTATGCAAACTTAAACGATCCGGATCATGAAAACAGAAAGAACACTTGAGAACTGT	267
Db	853	AAAATATCGAAAAGTGGTAGTTTACAGCATCATGAAAACAGAAAGAACACTTGAGAACTGT	912
Oy	268	GAGACCAATGCGCAATCTCTTGGGAGCAATTAATTAACAATTAACCTTTTACAAATGTC	327
Db	913	GAGACCAATGCGCAATCTCTTGGGAGCAATTAATTAACAATTAACCTTTTACAAATGTC	972
Oy	328	CACCCACTGACAAATGCTGAGTGGCCCCCAATATGTAATTAATGGAAGAACTGGTCTTACCA	387
Db	973	CACCCACTGACAAATGCTGAGTGGCCCCCAATATGTAATTAATGGAAGAACTGGTCTTACCA	1032
Oy	388	ACAGACTTAAGCAATGTTCCCAATGTAATCAAGAGGATTTGGGGCAATAGCTGT	447
Db	1033	ACAGACTTAAGCAATGTTCCCAATGTAATCAAGAGGATTTGGGGCAATAGCTGT	1092
Oy	448	TTTATAGAGGAGGTTGGCAAGGAATGGTGAACGGTTGGTATGATACCATCACAGCAAT	507
Db	1093	TTTATAGAGGAGGTTGGCAAGGAATGGTGAACGGTTGGTATGATACCATCACAGCAAT	1152
Oy	508	GACCAAGGATCAGCTTATGACAGACAAAGATCCACTCAAAAGCATTTGATGATGATC	567
Db	1153	GACCAAGGATCAGCTTATGACAGACAAAGATCCACTCAAAAGCATTTGATGATGATC	1212
Oy	568	ACCAACAAGGTAAATCTGTGATTTGAAAAGATAAACACCCCAATTTGAAGCTGTGGAAA	627
Db	1213	ACCAACAAGGTAAATCTGTGATTTGAAAAGATAAACACCCCAATTTGAAGCTGTGGAAA	1272
Oy	628	GAATTCGGTAACTTGGCAAAAAGCTGAGAACTTGAACAAAAGATGGAAGACGGGTT	687
Db	1273	GAATTCGGTAACTTGGCAAAAAGCTGAGAACTTGAACAAAAGATGGAAGACGGGTT	1332
Oy	688	CTAGATGTGTGACCTTACAAATGCTGAGCTTTAGTTCTGATGAAAATGAGAGACACTT	747
Db	1333	CTAGATGTGTGACCTTACAAATGCTGAGCTTTAGTTCTGATGAAAATGAGAGACACTT	1392
Oy	748	GACTTTTCATGATTCATATGCAAGATCTGTATAGTAAAGTCAAGTCAAGCTGAGAGAC	807
Db	1393	GACTTTTCATGATTCATATGCAAGATCTGTATAGTAAAGTCAAGTCAAGCTGAGAGAC	1452
Oy	808	AACGTCAAAGAACTTGGAAATGGAATGTTTGAATTTTATCAAAATGATGATGAAGAC	867
Db	1453	AACGTCAAAGAACTTGGAAATGGAATGTTTGAATTTTATCAAAATGATGATGAAGAC	1512
Oy	868	ATGATAGTGTGAAATTAACGGGACATATGATTTCCCAAGTATGAAGAAGATCTAAACTA	927
Db	1513	ATGATAGTGTGAAATTAACGGGACATATGATTTCCCAAGTATGAAGAAGATCTAAACTA	1572
Oy	928	AATAGAAATGAATTAAGAGGGGTAAATTTGAGCAGCATGGGGGTTTATCAAACTCTTGGC	987
Db	1573	AATAGAAATGAATTAAGAGGGGTAAATTTGAGCAGCATGGGGGTTTATCAAACTCTTGGC	1632
Oy	988	ATTATAGTGTGAAATTAAGAGGGGTAAATTTGAGCAGCATGGGGGTTTATCAAACTCTTGGC	1047
Db	1633	ATTATAGTGTGAAATTAAGAGGGGTAAATTTGAGCAGCATGGGGGTTTATCAAACTCTTGGC	1692
Oy	1048	TGGGTGTCTCCCAATGGGCTCTCTCAGTGCAGATCTGCATATGATTAATAGCATTTTA	1107
Db	1693	TGGGTGTCTCCCAATGGGCTCTCTCAGTGCAGATCTGCATATGATTAATAGCATTTTA	1752
Oy	1108	TAATTTAAACACCTTTGTTTCTGCTAG	1135
Db	1753	TAATTTAAACACCTTTGTTTCTGCTAG	1780

ORGANISM		Unknown.	
REFERENCE		Unclassified.	
AUTHORS		1 (bases 1 to 1783)	
TITLE		Okuno, Y., Isegawa, Y., Sasao, F. and Ueda, S.	
JOURNAL		Anti-human influenza virus antibody	
FEATURES		Patent: US 5589174-A 46 31-DEC-1996;	
source		Location/Qualifiers	
		1..1783	
BASE COUNT		610 a 323 c 424 g 426 t	
ORIGIN		/organism="unknown"	
Query Match		80.1%; Score 908.8; DB 6; Length 1783;	
Best Local Similarity		98.7%; Pred. No. 2.2e-206;	
Matches		916; Conservative 0; Mismatches 12; Indels 0; Gaps 0;	
Oy	208	AAATTATGCAAACTTAAACGATCCGGATCATGAAAACAGAAAGAACACTTGAGAACTGT	267
Db	853	AAAATATCGAAAAGTGGTAGTTTACAGCATCATGAAAACAGAAAGAACACTTGAGAACTGT	912
Oy	268	GAGACCAATGCGCAATCTCTTGGGAGCAATTAATTAACAATTAACCTTTTACAAATGTC	327
Db	913	GAGACCAATGCGCAATCTCTTGGGAGCAATTAATTAACAATTAACCTTTTACAAATGTC	972
Oy	328	CACCCACTGACAAATGCTGAGTGGCCCCCAATATGTAATTAATGGAAGAACTGGTCTTACCA	387
Db	973	CACCCACTGACAAATGCTGAGTGGCCCCCAATATGTAATTAATGGAAGAACTGGTCTTACCA	1032
Oy	388	ACAGACTTAAGCAATGTTCCCAATGTAATCAAGAGGATTTGGGGCAATAGCTGT	447
Db	1033	ACAGACTTAAGCAATGTTCCCAATGTAATCAAGAGGATTTGGGGCAATAGCTGT	1092
Oy	448	TTTATAGAGGAGGATGGCAAGGAATGGTGAACGGTTGGTATGATACCATCACAGCAAT	507
Db	1093	TTTATAGAGGAGGATGGCAAGGAATGGTGAACGGTTGGTATGATACCATCACAGCAAT	1152
Oy	508	GACCAAGGATCAGGTTATGACAGCAACAAAGATCCACTCAAAAGCATTTGATGATGATC	567
Db	1153	GACCAAGGATCAGGTTATGACAGCAACAAAGATCCACTCAAAAGCATTTGATGATGATC	1212
Oy	568	ACCAACAAGGTAAATCTGTGATTTGAAAAGATAAACCCCAATTTGAAGCTGTGGAAA	627
Db	1213	ACCAACAAGGTAAATCTGTGATTTGAAAAGATAAACCCCAATTTGAAGCTGTGGAAA	1272
Oy	628	GAATTCGGTAACTTGGCAAAAAGCTGAGAACTTGAACAAAAGATGGAAGACGGGTTT	687
Db	1273	GAATTCGGTAACTTGGCAAAAAGCTGAGAACTTGAACAAAAGATGGAAGACGGGTTT	1332
Oy	688	CTAGATGTGTGACATTCGAATGCTGAGCTTTAGTTCTGATGAAAATGAGAGACACTT	747
Db	1333	CTAGATGTGTGACATTCGAATGCTGAGCTTTAGTTCTGATGAAAATGAGAGACACTT	1392
Oy	748	GACTTTTCATGATTCATATGCAAGAACTGTATAGTAAAGTCAAGTCAAGCTGAGAGAC	807
Db	1393	GACTTTTCATGATTCATATGCAAGAACTGTATAGTAAAGTCAAGTCAAGCTGAGAGAC	1452
Oy	808	AACGTCAAAGAACTAGGAAATGGAATGTTTGAATTTTATCAAAATGATGATGAATGC	867
Db	1453	AACGTCAAAGAACTAGGAAATGGAATGTTTGAATTTTATCAAAATGATGATGAATGC	1512
Oy	868	ATGAAATGTGTGAAAAACGGGACATATGATTTTCCCAAGTATGAAGAAGATCTAAACTA	927
Db	1513	ATGAAATGTGTGAAAAACGGGACATATGATTTTCCCAAGTATGAAGAAGATCTAAACTA	1572
Oy	928	AATAGAAATGAATTAAGAGGGGTAAATTTGAGCAGCATGGGGGTTTATCAAAATCTTGGC	987
Db	1573	AATAGAAATGAATTAAGAGGGGTAAATTTGAGCAGCATGGGGGTTTATCAAAATCTTGGC	1632
Oy	988	ATTATAGTGTACAGTAGAGGTTCTATGTCACTGGCAATCATGATGCGTGGGATCTCTTC	1047
Db	1633	ATTATAGTGTACAGTAGAGGTTCTATGTCACTGGCAATCATGATGCGTGGGATCTCTTC	1692
Oy	1048	TGGGTGTGCTCCAAACGGGCTCTGCACTGCAGATCTGCATATGATTAATAGCATTTTA	1107

RESULT 6  
LOCUS I32526 1783 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 46 from patent US 5589174.  
ACCESSION I32526  
VERSION I32526.1 GI:182.317  
KEYWORDS  
SOURCE Unknown.

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Db 1693 TGGGTGCTCCCAACGGGCTCTCTGCGATGCGAGGATCTGCATATGATTAATGTCATTTTA 1752
Qy 1108 TAATTAACACACCTTTCTTCTGCTAG 1135
Db 1753 TAATTAACACACCTTTCTTCTGCTAG 1780

RESULT 7
LOCUS 143471 1783 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 46 from patent US 5631350.
ACCESSION 143471
VERSION 143471.1 GI:2468715
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1783)
AUTHORS Okuno,Y., Iseigawa,Y., Sasao,F. and Ueda,S.
TITLE Anti-human influenza virus antibody
JOURNAL Patent: US 5631350-A 46 20-MAY-1997;
FEATURES
Source
1. 1783
BASE COUNT 610 a 323 c 424 g 426 t
ORIGIN

Query Match 80.1%; Score 908.8; DB 6; Length 1783;
Best Local Similarity 98.7%; Pred. No. 2.2e-206;
Matches 916; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 208 AAGTTATGCAAACTAAACGATCCGGATCATGAAACAGAGACACCTTGAGACTGT 267
Db 853 AAATATCGAAAAGAGGTAGTTCAGGATCTGAAAACAGAGACACCTTGAGACTGT 912
Qy 268 GAGACCAAAATGCCAAACTCTTTGGAGCAATAATACACATTACCTTTGACAAATGTC 327
Db 913 GAGACCAAAATGCCAAACTCTTTGGAGCAATAATACACATTACCTTTGACAAATGTC 972
Qy 328 CACCCACTGCATAGGTGAGTGCCCAATATGTAATAATCGAGAGAGTGGCTTAGCA 387
Db 973 CACCCACTGCATAGGTGAGTGCCCAATATGTAATAATCGAGAGAGTGGCTTAGCA 1032
Qy 388 ACAGACTAAGAGATGTTCCCGATGATGATCAAGAGAGATGTTGGGCAATAGCTGCT 447
Db 1033 ACAGACTAAGAGATGTTCCCGATGATGATCAAGAGAGATGTTGGGCAATAGCTGCT 1092
Qy 448 TTTATAGAGAGAGATGCGCAAGAGATGTTGACGGTGTATGATACATACACAGCAAT 507
Db 1093 TTTATAGAGAGAGATGCGCAAGAGATGTTGACGGTGTATGATACATACACAGCAAT 1152
Qy 508 GACACAGGATCAGGGTATGCGACAGACAAAGATCCATCAAAAGCATTTGATGATC 567
Db 1153 GACACAGGATCAGGGTATGCGACAGACAAAGATCCATCAAAAGCATTTGATGATC 1212
Qy 568 ACCAACAAGGTAAATCTGTGATTGAAAGATAAACCAATTTGAGCTGTTGGAAA 627
Db 1213 ACCAACAAGGTAAATCTGTGATTGAAAGATAAACCAATTTGAGCTGTTGGAAA 1272
Qy 628 GAATTCGGTAACTTAGAGAAAAGACTGGAGAACTTGACAAAAGATGAGAGCGGTTT 687
Db 1273 GAATTCGGTAACTTAGAGAAAAGACTGGAGAACTTGACAAAAGATGAGAGCGGTTT 1332
Qy 688 CAGAGTGTGTCGACATACATGCTGAGCTTTTGTCTGTATGTAAGAAATGAGAGACACTT 747
Db 1333 CAGAGTGTGTCGACATACATGCTGAGCTTTTGTCTGTATGTAAGAAATGAGAGACACTT 1392
Qy 748 GACTTTCATGATTTATATGCAAGATCTGTATAGTAAGTGCAGATGCAAGCTGAGAGAC 807
Db 1393 GACTTTCATGATTTATATGCAAGATCTGTATAGTAAGTGCAGATGCAAGCTGAGAGAC 1452
Qy 808 AACGTCAAGAACTAGAGAAATGATGTTTGAATTTATACAAATGTATGATGAATGC 867
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Db 1453 AACGTCAAGAACTAGAGAAATGATGTTTGAATTTATACAAATGTATGATGAATGC 1512
Qy 868 ATGAATAGTGTGAAGAAACGGGACATATGATATCCAGATGTGAAGAAAGTCTAACTA 927
Db 1513 ATGAATAGTGTGAAGAAACGGGACATATGATATCCAGATGTGAAGAAAGTCTAACTA 1572
Qy 928 AATGAAATGAAATCAAGGGGTAAATTTGAGACATGAGGGGTTTATCAAACTCTGCC 987
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Qy 988 ATTATGCTACAGTAGCAGGTTTCTATGCTACCTGCATCATGATGCTGGAGTCTTTTC 1047
Db 1633 ATTATGCTACAGTAGCAGGTTTCTATGCTACCTGCATCATGATGCTGGAGTCTTTTC 1692
Qy 1048 TGGGTGCTCCCAACGGGCTCTCTGAGTGCAGATGTCGATATGATTAATGATTTTA 1107
Db 1693 TGGGTGCTCCCAACGGGCTCTCTGAGTGCAGATGTCGATATGATTAATGATTTTA 1752
Qy 1108 TAATTAACACACCTTTCTTCTGCTAG 1135
Db 1753 TAATTAACACACCTTTCTTCTGCTAG 1780
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RESULT 8
LOCUS FLAHUJ3055 1773 bp RNA linear VRL 27-MAR-1995
DEFINITION Influenza A/Japan/305-/57 (H2N2) haemagglutinin (seg 4) gene,
complete cds.
ACCESSION L20407
VERSION L20407.1 GI:305154
KEYWORDS haemagglutinin.
SOURCE Influenza A virus
ORGANISM Viruses: ssRNA negative-strand viruses: Orthomyxoviridae; Influenza
A (bases 1 to 1773)
AUTHORS Connor,R.J., Kawaoaka,Y., Webster,R.G. and Paulson,J.C.
TITLE Receptor specificity in human, avian, and equine H2 and H3
JOURNAL Virology 205 (1), 17-23 (1994)
MEDLINE 95065649
PUBMED 7975212
COMMENT Original source text: Influenza virus type A (individual)_isolate
A/Japan/305-/57) RNA.
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BASE COUNT 608 a 320 c 421 g 424 t
ORIGIN

Query Match 78.2%; Score 887.6; DB 14; Length 1773;
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Best Local Similarity 97.4%; Pred. No. 2.6e-201; Matches 902; Conservative 0; Mismatches 24; Indels 0; Gaps 0;			
Qy	208	AAGTTATGCAACATCAACGATCCGGATCATATGAAACAGAGAACACTTGAGAACTGT	267
Db	848	AAATATTCGAAAGACATGAGTTCAGGATCTGTGAAACAGAGAACACTTGAGAACTGT	907
Qy	268	GAGACCAATGCGCAACCTCTTTGGGAGCAATAATACACATACCTTTTCCAGATGTC	327
Db	908	GAGACCAATGCGCAACCTCTTTGGGAGCAATAATACACATACCTTTTCCAGATGTC	967
Qy	328	CACCACTGACAAATAGTGAAGTCCCAATATATTAATCGGAGAGTTGGTCTTAGCA	387
Db	968	CACCACTGACAAATAGTGAAGTCCCAATATATTAATCGGAGAGTTGGTCTTAGCA	1027
Qy	388	ACAGACTAAGGAATTTTCCCAATGGAATCAAGAGATTTGGGGCAATAGCTGCT	447
Db	1028	ACAGACTAAGGAATTTTCCCAATGGAATCAAGAGATTTGGGGCAATAGCTGCT	1087
Qy	448	TTTATAGAGGAGATGCGCAAGAAATGTTGACGGTTGTATGATACCATCACAGCAAT	507
Db	1088	TTTATAGAGGAGATGCGCAAGAAATGTTGATGTTGATGATGATACCATCACAGCAAT	1147
Qy	508	GACCAAGGATCAGGGTATGCGACGACAGACAAGATCCACTCAAAAGCATTTGATGAAATC	567
Db	1148	GACCAAGGATCAGGGTATGCGACGACAGACAAGATCCACTCAAAAGCATTTGATGAAATC	1207
Qy	568	ACCAACAAGGTAATTTCTGTGATGTAAGAAAGTAACACCAATTTGAAAGCTTTGGGAAA	627
Db	1208	ACCAACAAGGTAATTTCTGTGATGTAAGAAAGTAACACCAATTTGAAAGCTTTGGGAAA	1267
Qy	628	GAATTCGTAACCTTAAGAAAGACGAGAACTTGAACAAAGATGGAAGACGGGTTT	687
Db	1268	GAATTCGTAACCTTAAGAAAGACGAGAACTTGAACAAAGATGGAAGACGGGTTT	1327
Qy	688	CTAGATCTGTGACAAATGATCTGAGCTTTTACTTGTATGGAAGATGAGAGACACTT	747
Db	1328	CTAGATCTGTGACAAATGATCTGAGCTTTTACTTGTATGGAAGATGAGAGACACTT	1387
Qy	748	GACCTTATGATCTTATGTCACAAGATCTGATATGAAGTCAAGATGCAAGCTGAGAGAC	807
Db	1388	GACCTTATGATCTTATGTCACAAGATCTGATATGAAGTCAAGATGCAAGCTGAGAGAC	1447
Qy	808	AACGTCAAGAACTAAGAAATGATGTTTGAATTTTATCAACAATGATGATGAATGC	867
Db	1448	AACGTCAAGAACTAAGAAATGATGTTTGAATTTTATCAACAATGATGATGAATGC	1507
Qy	868	ATGATATGCTGAAAACGGGACATATGATTTCCCAAGTATGAAGAGACTTAAACTA	927
Db	1508	ATGATATGCTGAAAACGGGACATATGATTTCCCAAGTATGAAGAGACTTAAACTA	1567
Qy	928	AATGAATGATGAATCAAGGGGTAAATTTGAGCAGCATGGGGGTTTCAAAATCCTTGCC	987
Db	1568	AATGAATGATGAATCAAGGGGTAAATTTGAGCAGCATGGGGGTTTCAAAATCCTTGCC	1627
Qy	988	ATTATGCTCAAGTAAGAGTTCTATGCTCACTGGCAATCATGATGGCTGATCTTTTC	1047
Db	1628	ATTATGCTCAAGTAAGAGTTCTCTGCTCACTGGCAATCATGATGGCTGATCTTTTC	1687
Qy	1048	TGGGTGTGCTCAACAGGTCTCTGAGTGCAGAGATCTGCATATGATTAAGTATTTTA	1107
Db	1688	TGGGTGTGCTCAACAGGTCTCTGAGTGCAGAGATCTGCATATGATTAAGTATTTTA	1747
Qy	1108	TAATTAATAACACCCCTGTTTCTGCT 1133	
Db	1748	TAATTAATAACACCCCTGTTTCTACT 1773	

RESULT 9  
FLAHAS157A  
LOCUS  
DEFINITION Influenza A/Singapore/1/57 (H2N2) haemagglutinin (seg 4) gene,  
complete cds.

ACCESSION L20410 VERSION GI:305170 KEYWORDS haemagglutinin. SOURCE Influenza A virus ORGANISM Influenza A virus REFERENCE A viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A. 1 (bases 1 to 1773) AUTHORS Connor, R.J., Kawakita, Y., Webster, R.G. and Paulson, J.C. TITLE Receptor specificity in human, avian, and equine H2 and H3 JOURNAL Virology 205 (1), 17-23 (1994) MEDLINE 95065649 PUBMED 7975212 COMMENT Original source text: Influenza virus type A (individual isolate A/Singapore/1/57) RNA. FEATURES Source Location/Qualifiers 1..1773. /organism="Influenza A virus" /mol_type="genomic RNA" /isolate="A/Singapore/1/57" /db_xref="taxon:11320" 44..1732 /gene="HA" 44..1732 /gene="HA" /codon_start=1 /product="haemagglutinin" /protein_id="JAA64366.1" /db_xref="GI:305171" /translation="MAITVYLLETFARVGDICIGYHANNSTKVDLTLENNVTHA KDIETKHNKIKLKLNGIPIPLELDCSIAGLILNPECDRLSYSPMSYIMKRNPD GLCYPSKFNDEBELKHLSSVYKHEKXILPKMDHTHTTGSRACVAGSNPFEN MVLTKRESNPVPAKGSYNNSTSGROMILINCHHPNDERTRLTYOVAVGYVSGCT LNKSTPDIDATRPVNLGSRMEFWLLDMMDTINESTGNLAIPEYGRKISRGS GIMKEGTLENCETKQPLGALNTLTPFHVHPLTIGECRPYKSEKLVATLNV POLESRLFGAIEAGIEGWGVGYHNSDQSGVAADSEYKQKAFDGTITNV NSYLEKNTQFEAVGEFNSLERLENLNKMEGFDLDVYNAELVLVLENNETLD HDSVKNLIDYKRMQLNDVYKELNGCFEFYHKCDDCMNSVKNGTYDYPYEESEKL NRNRIKIVKLSSMGVYQIILAIYATVAGSLSLAIMMAGISFMCSNGSLQRCIC"			
BASE COUNT 612 a 319 c 417 g 425 t			
ORIGIN			
Query Match 78.2%; Score 887.6; DB 14; Length 1773; Best Local Similarity 97.4%; Pred. No. 2.6e-201; Matches 902; Conservative 0; Mismatches 24; Indels 0; Gaps 0;			
Qy	208	AAGTTATGCAAAATGATGATCCGGATCATGTAAGAAACAGAGAACACTTGAGAACTGT	267
Db	848	AAATATTCGAAAGACATGAGTTCAGGATCTGAAACAGAGAACACTTGAGAACTGT	907
Qy	268	GAGACCAATGCGCAACCTCTTTGGGAGCAATAATACACATACCTTTTCCAGATGTC	327
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Qy	328	CACCACTGACAAATAGTGAAGTCCCAATATGTAAGTGAAGAGTTGGTCTTAGCA	387
Db	968	CACCACTGACAAATAGTGAAGTCCCAATATGTAAGTGAAGAGTTGGTCTTAGCA	1027
Qy	388	ACAGACTAAGGAATTTTCCCAATGGAATCAAGAGATTTGGGGCAATAGCTGCT	447
Db	1028	ACAGACTAAGGAATTTTCCCAATGGAATCAAGAGATTTGGGGCAATAGCTGCT	1087
Qy	448	TTTATAGAGGAGATGCGCAAGAAATGTTGACGGTTGTATGATACCATCACAGCAAT	507
Db	1088	TTTATAGAGGAGATGCGCAAGAAATGTTGATGTTGATGATACCATCACAGCAAT	1147
Qy	508	GACCAAGGATCAGGGTATGCGACGACAGACAAGATCCACTCAAAAGCATTTGATGAAATC	567
Db	1148	GACCAAGGATCAGGGTATGCGACGACAGACAAGATCCACTCAAAAGCATTTGATGAAATC	1207
Qy	568	ACCAACAAGGTAATTTCTGTGATGTAAGAAAGTAACACCAATTTGAAAGCTTTGGGAAA	627

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Db      1208 ACCAACAGTAATTCTGTGATTGAAAGATGAGACCCCAATTTGAGCTGTGGGAAA 1267
OY      628 GATTGGTAACTTAGAGAAAAGCTGAGAACTTGAACAAAAGATGAGACGGGTTT 687
Db      1268 GAATTCAGTAACTTAGAGAGAAAGCTGAGAACTTGAACAAAAGATGAGACGGGTTT 1327
OY      688 CTAGATGTGTGACATACATGCTGAGCTTTTGTGTTCTGTATGAGAAAATGAGAGACATT 747
Db      1328 CTAGATGTGTGACATACATGCTGAGCTTTCTGATTTCTGTATGAGAAAATGAGAGACATT 1387
OY      748 GACTTCATGATTTCTATGTGACAGATCTGTATAGTAAGTGAAGTGCAGCTGAGAGAC 807
Db      1388 GACTTCATGATTTCTATGTGACAGATCTGTATAGTAAGTGAAGTGCAGCTGAGAGAC 1447
OY      808 AACGTCAGAACTAGGAATGATGATTTGATTTATACAAATGTGATGATGATG 867
Db      1448 AACGTCAGAACTAGGAATGATGATTTGATTTATACAAATGTGATGATGATG 1507
OY      868 ATGATAGTGTGAAAAAGCGGACATATGATTTATCCAGATGAGAGAGATGTAAC 927
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OY      928 AATAGAAATGAATCAAAAGGGGTAATGAGAGAGATGGGGTTTATCAATCCCTTGC 987
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Db      1628 ATTTATGCTACAGTACAGAGTTCTCTGTCTGCTGCTGATGATGATGCTGGGATCTTTC 1687
OY      1048 TGGGTGTGCTCCAGCGGTTCTGCGAGTGCAGATCTGCATATGATTTATAGTCATTTTA 1107
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OY      1108 TAATTAACAAACCCCTGTGTTCTGCT 1133
Db      1748 TAATTAACAAACCCCTGTGTTCTACT 1773

RESULT 10
FLAKRA59HA      1773 bp ss-RNA      linear      VRL_13-OCT-2000
LOCUS      Influenza A virus (A/Krasnodar/101/59 (H2N2)) hemagglutinin (HA)
DEFINITION      gene, complete cds.
ACCESSION      L11134.1 GI:408524
KEYWORDS      haemagglutinin.
SOURCE      Influenza A virus (A/Krasnodar/101/59 (H2N2))
ORGANISM      Influenza A virus (A/Krasnodar/101/59 (H2N2))
VIRUSES: sRNA negative-strand viruses: Orthomyxoviridae; Influenza
A viruses; Influenzavirus A; Influenza A virus; H2N2 subtype.
Schäfer, J. R., Kawasaka, Y., Bean, W. J., Suss, J., Senne, D. and
Webster, R. G.
TITLE      Origin of the pandemic 1957 H2 influenza A virus and the
JOURNAL      persistence of its possible progenitors in the avian reservoir
MEDLINE      93276567
PUBMED      7684877
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BASE COUNT      608 a 321 c 420 g 424 t
ORIGIN
Query Match      78.2% Score 887.6; DB 14; Length 1773;
Best Local Similarity 97.4%; Pred. No. 2.6e-201;
Matches 902; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
OY      208 AACTTATGCAAACTAAGCGATCCGGATCATGAAACAGAGAACTTGAGAACTGT 267
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OY      328 CACCACATGACATAGTGTAGTCCCAATATATGTAATGCGAGAACTTGCTTTAGCA 387
Db      968 CACCACATGACATAGTGTAGTCCCAATATATGTAATGCGAGAACTTGCTTTAGCA 1027
OY      388 ACAGACTAAGGAAGTTCGCCAGATGATGATCAAGAGATTTGGGGCAATATCTGT 447
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Db      1088 TTTATGAGGAGGAGTGAAGGAATGTTGAGCGTGTGATNGATACCATCAGCAAT 1147
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Db      1268 GAATTCGTTACCTTGAAGAAAGCTGGAGACTTGACCAAAAGATGGAAGACGGGTT 1327
OY      688 CTAGATGTGTGACATACATGCTGAGCTTTTGTGATGAGAAAATGAGAGACACTT 747
Db      1328 CTAGATGTGTGACATACATGCTGAGCTTTTGTGATGAGAAAATGAGAGACACTT 1387
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Db      1448 AACGTCAGAACTAGGAATGATGATTTGATTTATACAAATGTGATGATGATG 1507
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OY      928 AATAGAAATGAATCAAAAGGGGTAATGAGAGAGATGGGGTTTATCAATCCCTTGC 987
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[illegible]

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Dd		1028	ACAGGACTAAGCAATGTTTCCCACATTTGAATCAAAGAGATTGTTGGGGCATAGCTGT	1087
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Dd		1088	TTTTATAGNAGGAGATGGCAGAAGAAAGTGTTGATGTTGATGTGATACCATCACAGCAAT	1147
OY		508	GACCAAGGATCAGGGTATGCAAGCAGACAAGAATCCACTCAAAAAGCATTTGATGCAATC	567
Dd		1148	GACCAAGGATCAGGGTATGCAAGCAGACAAGAATCCACTCAAAAAGCATTTGATGCAATC	1207
OY		568	ACCAACAAGGAAATTTCTGTGATTCGAAGAATAAACGCCAATTTTGAAGCTGTGGGAAA	627
Dd		1208	ACCAACAAGGAAATTTCTGTGATTCGAAGAATAAACGCCAATTTTGAAGCTGTGGGAAA	1267
OY		628	GAATTCGGTAACCTTAGAGAAAAAGACTGAGAACCTTGGAACAAAAAGATGGAAGAGCGGTTT	687
Dd		1268	GAATTCAGTAACCTTAGAGAAAAAGACTGAGAACCTTGGAACAAAAAGATGGAAGAGCGGTTT	1327
OY		688	CTAAGTGTGTGGACATACAAATGCTGAGCTTTTACTTCTGATGGAAATAGNAGGACACTT	747
Dd		1328	CTAAGTGTGTGGACATACAAATGCTGAGCTTTTACTTCTGATGGAAATAGNAGGACACTT	1387
OY		748	GACTTTCATGATTCCTAATGCTCAAGAATCTGTATAGTAAGTCAGAAATGCAGCTGAGAGAC	807
Dd		1388	GACTTTCATGATTCCTAATGCTCAAGAATCTGTATAGTAAGTCAGAAATGCAGCTGAGAGAC	1447
OY		808	AACGTCAAAGAACATAGAGAAATGATGTTTTGAATTTTATCACAAAATGTGATGAATGATGC	867
Dd		1448	AACGTCAAAGAACATAGAGAAATGATGTTTTGAATTTTATCACAAAATGTGATGAATGATGC	1507
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Dd		1628	ATTATATGCTACATGACGAGTTTCTCTGCTCACTGGCAATCATGATAGCTGGGATCTCTTTC	1687
OY		1048	TGGGTGTCCTCCAACGGGCTCTCTGAGTGCAGGATCTGCATATGATTTATAGTCATTTTA	1107
Dd		1688	TGGGTGTCCTCCAACGGGCTCTCTGAGTGCAGGATCTGCATATGATTTATAGTCATTTTA	1747
OY		1108	TAATTAANAACACCCCTTGTCTCTGCT	1133
Dd		1748	TAATTAANAACACCCCTTGTCTCTACT	1773
RESULT 12				
LOCUS	AX399727	1773 bp	DNA	linear
DEFINITION	Sequence 4 from Patent W00224876.			PAT 06-JUN-2002
ACCESSION	AX399727			
VERSION	AX399727.1	GI:2135485		
KEYWORDS				
SOURCE				
ORGANISM				
		Influenza A virus (STRAIN A/SINGAPORE/1/57)		
		Influenza A virus (STRAIN A/SINGAPORE/1/57)		
		Viruses: ssRNA negative-strand viruses; Orthomyxoviridae; Influenzavirinae		
		A viruses; Influenzavirus A; Influenza A virus; unidentified		
		subtype.		
REFERENCE				
AUTHORS	Ferko, B., Egorov, A., Romanova, J., Kalinge, D. and Kalinge, H.			
JOURNAL	Live vaccine and method of manufacture			
	Patent: WO 0224876-A 4 28-MAR-2002;			
	POLYMUR SCIENT IMMUNOBIOT FORSCH (AT)			
FEATURES				
source		Location/Qualifiers		
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QY	388	ACAGAGCTAAGGAAT	BTTCGCCAGATTGAATCAAGAGATTGTTGGGGCAATAGCTGT	447
Db	1028	ACAGAGCTAAGGAAT	BTTCGCCAGATTGAATCAAGAGATTGTTGGGGCAATAGCTGT	1087
QY	448	TTTATAGAGAGGA	TGGCAAGGAATGGTGGAGGTGTATGATACCATCAGCAAT	507
Db	1088	TTTATAGAGAGGA	TGGCAAGGAATGGTGGAGGTGTATGATACCATCAGCAAT	1147
QY	508	GACCCAGGATCAGGG	TATGCGACAGACAAGATCCACTCAAAAGGCAATTTGATGATC	567
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QY	568	ACCAACAAGTAAAT	CTGTGATTGAAAGATAAACCCCAATTTGAAGCTGTTGGGAA	627
Db	1208	ACCAACAAGTAAAT	CTGTGATTGAAAGATAAACCCCAATTTGAAGCTGTTGGGAA	1267
QY	628	GAATTCGTACTA	TGAGAAAGCTGAGAACTTGAAACAAAGATGGAAGACGGTTT	687
Db	1268	GAATTCGTACTA	TGAGAAAGCTGAGAACTTGAAACAAAGATGGAAGACGGTTT	1327
QY	688	CTAGATGTGACAA	TCAATGCTGACCTTTTACTGTGATGAAATGAGAGACACTT	747
Db	1328	CTAGATGTGACAA	TCAATGCTGACCTTTTACTGTGATGAAATGAGAGACACTT	1387
QY	748	GACTTTCATGATCT	TATGTCAGAACTCTGTATAGTAAGTCAAGATGCAAGCTGAGAC	807
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QY	808	AACGTCAAGACTAG	GAAATGATGATTTTGAATTTATCACAATGTGATGATGATG	867
Db	1448	AACGTCAAGACTAG	GAAATGATGATTTTGAATTTATCACAATGTGATGATGATG	1507
QY	868	ATGAATAGTGA	ACGGGACATATGATTTATCCCAATGATGAAGAGTCTAACTA	927
Db	1508	ATGAATAGTGA	ACGGGACATATGATTTATCCCAATGATGAAGAGTCTAACTA	1567
QY	928	AATGAAATGAAT	CTAAGGGTAAATTGACAGCATGGGGTTTATCAATCTCTGCC	987
Db	1568	AATGAAATGAAT	CTAAGGGTAAATTGACAGCATGGGGTTTATCAATCTCTGCC	1627
QY	988	ATTATGCTACAGT	AGAGTTCATGCTACATGCAATGATGCGTGGGATCTCTTC	1047
Db	1628	ATTATGCTACAGT	AGAGTTCATGCTACATGCAATGATGCGTGGGATCTCTTC	1687
QY	1048	TGGGTGTCTCACA	CGGGTCTCTGACATGCAAGATGCAATGATGATTAAGTCAATTTA	1107
Db	1688	TGGGTGTCTCACA	CGGGTCTCTGACATGCAAGATGCAATGATGATTAAGTCAATTTA	1747
QY	1108	TAATTAATAAC	CCCTTGTTCTGCT 1133	
Db	1748	TAATTAATAAC	CCCTTGTTCTGCT 1773	

RESULT 14  
FLAHARIS57 1773 bp RNA linear VRL 27-MAR-1995  
DEFINITION Influenza A/R/5+/57 (H2N2) haemagglutinin (seg 4) gene, complete cds.  
ACCESSION L20408  
VERSION L20408.1 GI:305162  
KEYWORDS haemagglutinin.  
SOURCE Influenza A virus  
ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A.  
REFERENCE Connor, R.J., Kawachi, Y., Webster, R.G. and Paulson, J.C. 1 (bases 1 to 1773)  
TITLE Receptor specificity in human, avian, and equine H2 and H3

JOURNAL	Influenza virus isolates			
MEDLINE	Virology 205 (1), 17-23 (1994)			
PUBMED	95065649			
COMMENT	7975212			
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 ACCESSION L11142  
 VERSION L11142.1 GI:408676  
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 SOURCE Influenza A virus (A/Singapore/1/57 (H2N2))  
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 Schaefer, J.R., Kawakita, Y., Bean, W.J., Suss, J., Senne, D. and Webster, R.G.  
 Origin of the pandemic 1957 H2 influenza A virus and the persistence of its possible progenitors in the avian reservoir.  
 JOURNAL Virology 194 (2), 781-788 (1993)  
 MEDLINE 93276567  
 PUBMED 7684877

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Query Match 77.9%; Score 884.4; DB 14; Length 1773;  
 Best Local Similarity 97.2%; Pred. No. 1.5e-200;  
 Matches 900; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Tue Aug 12 10:28:19 2003

us-09-918-568-49.rge

Page 13

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-09-918-568-46

Perfect score: 1783

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Gapop 10.0 ,  
Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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and is derived by analysis of the total score distribution.

## SUMMARIES

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4	695.6	39.0	1754	US-09-918-568-27	Sequence 27, Appl
5	400	22.4	400	US-09-918-568-33	Sequence 33, Appl
6	397	22.3	409	US-09-918-568-34	Sequence 34, Appl
7	382.4	21.4	410	US-09-918-568-35	Sequence 35, Appl
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10	291	16.3	1711	US-10-099-619-1	Sequence 1, Appl
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12	251.6	13.6	442	US-09-918-568-29	Sequence 29, Appl
13	241.8	13.1	424	US-09-918-568-32	Sequence 32, Appl
14	233.6	13.1	424	US-09-918-568-30	Sequence 30, Appl
15	233.6	13.1	424	US-09-918-568-31	Sequence 31, Appl
16	125.2	7.0	334	US-09-918-568-38	Sequence 38, Appl

17	123.6	6.9	329	9	US-09-918-568-39	Sequence 39, Appl
18	123.6	6.9	334	9	US-09-918-568-40	Sequence 40, Appl
19	121	6.8	329	9	US-09-918-568-37	Sequence 37, Appl
20	118.8	6.7	329	9	US-09-918-568-41	Sequence 41, Appl
21	44.4	2.5	1115	14	US-10-184-644-440	Sequence 440, App
22	44.4	2.5	1115	14	US-10-184-634-440	Sequence 440, App
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26	41.8	2.3	3441	9	US-09-880-192-41	Sequence 41, Appl
27	41.8	2.3	3444	13	US-10-114-893-126	Sequence 126, App
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34	40	2.2	2843	11	US-09-822-846-421	Sequence 421, App
35	40	2.2	3058	14	US-10-106-698-468	Sequence 468, App
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## ALIGNMENTS

RESULT 1  
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Sequence 46, Application US/09918568  
Patent No. US20020054882A1  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/918,568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200  
 TELEFAX: 202-721-8250  
 INFORMATION FOR SEQ ID NO: 46:  
 SEQUENCE CHARACTERISTICS:  
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 1141 CATCAGCAGATGACAGGAGTACAGGATGTGAGAGAGCAAGAAATGCACTCAAAAGGCA 1200  
 1141 CATCAGCAGATGACAGGAGTACAGGATGTGAGAGAGCAAGAAATGCACTCAAAAGGCA 1200  
 1201 TTTGATGAGATACCAACAAAGTAAATCTGATTTGAAAGAGATTAACACCAATTTGAA 1260  
 1201 TTTGATGAGATACCAACAAAGTAAATCTGATTTGAAAGAGATTAACACCAATTTGAA 1260  
 1261 GCTGTTGGGAAGAAATTCGGTAACTTAAGAGAAAACCTGAGAACTTAACAAAAGATG 1320  
 1261 GCTGTTGGGAAGAAATTCGGTAACTTAAGAGAAAACCTGAGAACTTAACAAAAGATG 1320  
 1321 GAAGACGGGTTCTGATATGTGACATACATGCTGAGCTTTAGTTCTGATGAGAAAT 1380  
 1321 GAAGACGGGTTCTGATATGTGACATACATGCTGAGCTTTAGTTCTGATGAGAAAT 1380

OY	1381	GAGAGGACACTGGAC	TTTCATGATCTTCAATGTCAGAGATCGTATAGTAAAGTCAGATG	1440
Db	1381	GAGAGGACACTGGAC	TTTCATGATCTTCAATGTCAGAGATCTGTATAGTAAAGTCAGATG	1440
OY	1441	CAGCTGAGAGACAAC	TTCAAAAGACTAGGAATGATGTTTGATTTATACAAATGT	1500
Db	1441	CAGCTGAGAGACAAC	TTCAAAAGACTAGGAATGATGTTTGATTTATACAAATGT	1500
OY	1501	GATATGATGATGATG	AATAGTGTAAAAACGGGACATATGATTATCCCAAGTATGAGAA	1560
Db	1501	GATATGATGATGATG	AATAGTGTAAAAACGGGACATATGATTATCCCAAGTATGAGAA	1560
OY	1561	GAGCTTAACCTAAAT	AGAAATGAATCAAAAGGGGTAAATTTGACACAGATGGGGTTAT	1620
Db	1561	GAGCTTAACCTAAAT	AGAAATGAATCAAAAGGGGTAAATTTGACACAGATGGGGTTAT	1620
OY	1621	CAATTCCTGGCCATT	TATGCTACACAGTACAGAGTTCTATGTCACAGGCAATCATATGCGT	1680
Db	1621	CAATTCCTGGCCATT	TATGCTACACAGTACAGAGTTCTATGTCACAGGCAATCATATGCGT	1680
OY	1681	GGGATCTCTTCTCGG	TTGATGCTCCCAAGGGGCTCTGCAGTGCAGAGATCTGCATATGATTA	1740
Db	1681	GGGATCTCTTCTCGG	TTGATGCTCCCAAGGGGCTCTGCAGTGCAGAGATCTGCATATGATTA	1740
OY	1741	TAACTCATTTTATAA	TTAAAAACCCCTTGTTTCTGCTAACCGG	1783
Db	1741	TAACTCATTTTATAA	TTAAAAACCCCTTGTTTCTGCTAACCGG	1783

RESULT 2  
US-09-918-568-28  
; Sequence 28, Application US/09918568  
; Patent No. US20020054882A1  
; GENERAL INFORMATION:

APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING

ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wendepoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street N.W.  
CITY: Washington, D.C. 20004

STATE: 2003 A Pierce, N.W., #800  
CITY: Washington  
STATE: D.C.

COUNTRY: U.S.A.  
ZIP: 20006

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; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
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;
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
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; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; ADDRESS: wordpa

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APPLICATION NUMBER: US/09/918,568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: ~~Unpub~~

CLASSIFICATION: UNCLASSIFIED  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422

FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862

FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/229,781

FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016

FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Chook

NAME: WALTER M. CREEK, JR.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <link>

TELECOMMUNICATION INFORMATION  
TELEPHONE: 202-721-8200

TELEFAX: 202-721-8225  
TELEX: <Unknown>

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; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:

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1 LENGTH: 1728 base pairs
2 TYPE: nucleic acid
3 STRANDEDNESS: double
4 TOPOLOGY: linear
5 MOLECULE TYPE: cDNA to genomic RNA
6 HYPOTHETICAL: <unknown>
7 ANTI-SENSE: <unknown>
8 FRAGMENT TYPE: <unknown>
9 ORIGINAL SOURCE:
10 ORGANISM: A/12um1/5/65
11 STRAIN: <unknown>
12 INDIVIDUAL ISOLATE: <unknown>
13 DEVELOPMENTAL STAGE: <unknown>
14 HAPLOTYPE: <unknown>
15 TISSUE TYPE: <unknown>
16 CELL TYPE: <unknown>
17 CELL LINE: <unknown>
18 ORGANELLE: <unknown>
19 IMMEDIATE SOURCE:
20 LIBRARY: <unknown>
21 CLONE: <unknown>
22 POSITION IN GENOME:
23 CHROMOSOME/SEGMENT: <unknown>
24 MAP POSITION: <unknown>
25 UNITS: <unknown>
26 FEATURE:
27 NAME/KEY:
28 LOCATION:
29 IDENTIFICATION METHOD:
30 OTHER INFORMATION:
31 PUBLICATION INFORMATION:
32 AUTHORS:
33 TITLE:
34 JOURNAL:
35 VOLUME:
36 ISSUE:
37 PAGES:
38 DATE:
39 DOCUMENT NUMBER:
40 FILING DATE:
41 PUBLICATION DATE:
42 RELEVANT RESIDUES IN SEQ ID NO:
43 SEQUENCE DESCRIPTION: SEQ ID NO: 28:
44 US-09-918-568-28
45
46 Query Match          90.1%;   Score 1606.4;   DB 9;   Length 1728;
47 Best Local Similarity 95.6%;   Pred. No. 0;
48 Matches 1652;   Conservative 0;   Mismatches 76;   Indels 0;   Gaps 0

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; RELEVANT RESIDUES IN SEQ ID NO:
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-918-568-28

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Query Match	90.1%	Score 1606.4	DB 9	Length 1728
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Best Local Similarity 95.0%; PRed. NO. 0;  
Matches 1652; Conservative 0; Mismatches 76; Indels 0; Gaps 0.

QY	27	ATAGAAAACCCAAAAGCAAAACAAATGGCCATCATTTATCTCATCTCTGTTCCAGACAGT	86
Db	1	ATGAGCAACCCAAAGCATTAACATGGCCATCATCTATCTCATCTCTGTTCCAGACAGT	60
QY	87	GAGAGGGGACACAGATATGCAATTGGATACCATGCAATATTTCCACAGAGAAAGTGCACAC	14
Db	61	GAGGGGGGACCAAGATATGCAATTGGATACCATGCAATATTTCCACAGAGAAAGTGCACAC	120
QY	147	AATTTAGAGCGGACAGTCAGCTGTCATGCTCATGCCAAGGACATCCCTTGGAGAGACCCATAA	209
Db	121	AATTTAGAGCGGAAAGTCAGCTGTCATGCTCATGCCAAGGACATCCCTTGGAGAGACCCACAA	189
QY	207	CGGAAAGTTATGCAAACTAAACGGAATCCCTCCACTTAAGTAGGGAGACTTAGACATTGC	266
Db	181	CGGAAAGCTATGCAAACTAAACGGAATCCCTCCACTTAGACTAGGGAGACTTAGACATTGC	240
QY	267	CGGATGGCTCCTTGGAAATCCAAAATGTGATAGCCTTAAAGTGTGCCAGAACGGTCCCTA	322
Db	241	CGGATGGCTCCTTGGAAATCCAGAATGTGATAGCCTTAAAGGGTGCCAGAAATGGTCCCTA	300
QY	327	TATATTTGGGAAAAGAAAACCCGAGAGACGCTTTGTGTATATCCAGGACAGCTTCATGATTA	388
Db	301	TATATTTGGGAAAAGAAAACCCGAGATATACGTTTATGTTATCCAGGACAGCTTCATGATTA	360

387 TGAAGATTGAACATCTCTCTGACAGCGTGAAACATTTGCGAAGATAAGATTCTGCC 446  
|||||  
361 TGAAGATTGAACATCTCTCTGACAGCGTGAAACATTTGCGAAGATAAGATTCTGCC 420  
447 CAAAGATAGATGACACAGCATCAACAACTGAGGTTACGGGCTGGCGGCTGTGG 506  
|||||  
421 CAAAGATAGATGACACAGCATCAACAACTGAGGTTCAAGGCCCTGGCGAGTGTAGG 480  
507 TAATCATCATTTTTCAGCAACATGCTGCTGACAAAGAGAGATCAGATTATCCGGT 566  
|||||  
481 TAACCATCATTTCTTCTGAGCAACATGCTGCTGACAAAGAGAGATCAGATTATCCGGT 540  
567 TGCAGAGAGATGCTGACAAACATGCTGCTGACAAAGAGAGATCAGATTATCCGGT 626  
|||||  
541 TGCAGAGAGATGCTGACAAACATGCTGCTGACAAAGAGAGATCAGATTATCCGGT 600  
627 CCATCCCATTTGATGACAGCAAGCAACATTTGCTACAGATGCTGAGGAGCTATGTTTC 686  
|||||  
601 CCATCCCATTTGATGACAGCAAGCAACATTTGCTACAGATGCTGAGGAGCTATGTTTC 660  
687 CGTAGGCATCATCAACATTTGACAAAGGTCACCCGAGAAATAGCAACAGGCTTAAAGT 746  
|||||  
661 CGCAAGCATCATCAACATTTGACAAAGGTCACCCGAGAAATAGCAACAGGCTTAAAGT 720  
747 GAATGGACAGAGAGATGAGATGGAATTTCTTGGACCTCTTGGATATGTTGGACACCAT 806  
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721 GAATGGACAGAGATGAGATGGAATTTCTTGGACCTCTTGGATATGTTGGACACCAT 780  
807 AAATTTTGAAGATGATGATTAATCTAATTCACACAGATGATGATGATGATGATGATGATG 866  
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781 AAATTTTGAAGATGATGATTAATCTAATTCACACAGATGATGATGATGATGATGATGATG 840  
867 AGTGTGTCAGGATCATCAAAACAGAGAGACATTTGAGAACTGTGAGACCAATGCCA 926  
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841 AGTGTGTCAGGATCATCAAAACAGAGAGACATTTGAGAACTGTGAGACCAATGCCA 900  
927 AACCTCTTGGAGCAATTAATTAACATTTACCTTTTCAAAATGTCACCCCATGCAAT 986  
|||||  
901 AACCTCTTGGAGCAATTAATTAACATTTACCTTTTCAAAATGTCACCCCATGCAAT 960  
967 AGTGTGTCAGGATCATCAAAACAGAGAGATTTGCTTACCAACAGAGATGAGAA 1046  
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961 AGTGTGTCAGGATCATCAAAACAGAGAGATTTGCTTACCAACAGAGATGAGAA 1020  
1047 TGTTCCTCCAGATGATCAAGAGATTTGTTGGGCAATAGCTGTTTATGAGAGAGG 1106  
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1021 TGTTCCTCCAGATGATCAAGAGATTTGTTGGGCAATAGCTGTTTATGAGAGAGG 1080  
1107 ATGCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1166  
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1081 ATGCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140  
1167 GTATGACAGACAGCAAGATCCACTCAAAAGGATTTGATGATGATGATGATGATGATG 1226  
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1141 GTATGACAGACAGCAAGATCCACTCAAAAGGATTTGATGATGATGATGATGATGATG 1200  
1227 TTTCTGTGATTTGAAAAAGATTAACACCCCATTTGAACCTGTTGGGAAAGATTGGTAACTT 1286  
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1201 TTTCTGTGATTTGAAAAAGATTAACACCCCATTTGAACCTGTTGGGAAAGATTGAATTAATTT 1260  
1287 AGAGAAAAAGATGACAGCTGACCAAAAGATGAGAGAGGCTTTAGATGATGATGATG 1346  
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1261 AGAGAAAAAGATGACAGCTGACCAAAAGATGAGAGAGGCTTTAGATGATGATGATG 1320  
1347 ATACAAATGCTGAGCTTTAGTTGATGATGATGATGATGATGATGATGATGATGATG 1406  
|||||  
1321 ATACAAATGCTGAGCTTTAGTTGATGATGATGATGATGATGATGATGATGATGATG 1380  
1407 TAAATGTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1466  
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1381 TAAATGTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440  
1467 AGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1526

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1441 AGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500  
1527 AAACGGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1586  
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1501 AAACGGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560  
1587 CAAAGGGCTAAAAATGACAGCATGGGGGTTTATCAAAATCTTGCATTTATGATCAAGT 1646  
|||||  
1561 CAAAGGGCTAAAAATGACAGCATGGGGGTTTATCAAAATCTTGCATTTATGATCAAGT 1620  
1621 TGCAGGTTCTCTGCTCACTGCGCAATGATGATGATGATGATGATGATGATGATGATG 1680  
1647 AGCAGGTTCTATGCTCACTGCGCAATGATGATGATGATGATGATGATGATGATGATG 1706  
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1707 CGGCTCTGCTCACTGCGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1754  
1681 CGGCTCTGCTCACTGCGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1728

RESULT 3  
US-09-918-568-49  
; Sequence 49, Application US/09918568  
; Patent No. US20020054882A1  
; GENERAL INFORMATION:  
; APPLICANT: Yoshinobu OKUNO et al.  
; TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
; ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
; STREET: 2033 K Street, N.W., #800  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/918,568  
; FILING DATE: 02-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/004,422  
; FILING DATE: January 8, 1998  
; APPLICATION NUMBER: 08/443,862  
; FILING DATE: May 22, 1995  
; APPLICATION NUMBER: 08/229,781  
; FILING DATE: April 19, 1994  
; APPLICATION NUMBER: 08/054,016  
; FILING DATE: April 29, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER: <Unknown>  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-721-8200  
; TELEFAX: 202-721-8250  
; TELEX: <unknown>  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1135 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to genomic RNA  
; HYPOTHETICAL: <unknown>  
; ANTI-SENSE: <unknown>  
; FRAGMENT TYPE: <unknown>  
; ORIGINAL SOURCE:

	ORGANISM:	A/Oryza/57
	STRAIN:	<Unknown>
	INDIVIDUAL ISOLATE:	<Unknown>
	DEVELOPMENTAL STAGE:	<Unknown>
	HAPLOTYPE:	<Unk down>
	TISSUE TYPE:	<Unknown>
	CELL TYPE:	<Unk down>
	CELL LINE:	<Unk down>
	ORGANELLE:	<Unk down>
	IMMEDIATE SOURCE:	
	LIBRARY:	<Unknown>
	CLONE:	<Unknown>
	POSITION IN GENOME:	
	CHROMOSOME/SEGMENT:	<Unknown>
	MAP POSITION:	<Unknown>
	UNITS:	<Unknown>
	FEATURE:	
	NAME/KEY:	
	LOCATION:	
	IDENTIFICATION METHOD:	
	OTHER INFORMATION:	
	PUBLICATION INFORMATION:	
	AUTHORS:	
	TITLE:	
	JOURNAL:	
	VOLUME:	
	ISSUE:	
	PAGES:	
	DATE:	
	DOCUMENT NUMBER:	
	FILING DATE:	
	PUBLICATION DATE:	
	RELEVANT RESIDUES IN SEQ ID NO:	
	SEQUENCE DESCRIPTION:	SEQ ID NO: 49;
	US-09-918-568-49	
Query Match	51.9% Score 908.8; DB 9; Length 1135;	
Best Local Similarity	98.9%; Pred. No. 1.9e-242;	
Matches 916; Conservative	0; Mismatches 12; Indels 0; Gaps 0;	
OY	853 AAATATCGAAGAAACGCTACTTCAGGGGTGCATGAATAACAAGAAGAACACTTGAGAACTGT	912
Dd	208 AAGTTATGCCAACCATTACCCGATCCGGGATCATGAAAACGAAGGACACTTGGAGACTGT	267
OY	913 GAGACCAATGCCAACTCCTTTGGGAGCAATTAATACMACATTACCTTTTCACAAATGTC	972
Dd	268 GAGACCAAATGCCAACTCCTTTGGGAGCAATTAATACMACATTACCTTTTCACAAATGTC	327
OY	973 CACCACCTGACAAATGTGAGTGTCCCCCAAAATATGTAAAAATCGGAGAAATGGTGGCTTAGCA	1032
Dd	328 CACCACCTGACAAATGTGAGTGTCCCCCAAAATATGTAAAAATCGGAGAAATGGTGGCTTAGCA	387
OY	1033 ACAGGACTAAGGAATBTCCCACAGATTGAATCAAGAGGATGTTGGGGCAATAGCTGGT	1092
Dd	388 ACAGGACTAAGGAATBTCCCACAGATTGAATCAAGAGGATGTTGGGGCAATAGCTGGT	447
OY	1093 TTTATAGAGAGAGATGGCAAGGAATGTGACGGTTGGTATGTGATACCATCACAGCAAT	1152
Dd	448 TTTATAGAGAGAGATGGCAAGGAATGTGACGGTTGGTATGTGATACCATCACAGCAAT	507
OY	1153 GACCAGGATCVAGGGATGACGACGACAAAGAAATCCACTCAAAAAGGCACTTTGATGAGATC	1212
Dd	508 GACCAGGATCVAGGGATGACGACGACAAAGAAATCCACTCAAAAAGGCACTTTGATGAGATC	567
OY	1213 ACCAACAAGGTAATCTGTGATTTGAAAAGATAACCCAAATTTGAAGCGTGGGGGAAA	1272
Dd	568 ACCAACAAGGTAATCTGTGATTTGAAAAGATAACCCAAATTTGAAGCGTGGGGGAAA	627
OY	1273 GAATTCGTAACCTTATGAAAAGACTGTGAGAACTTGAACAAAGAAATGGAGACGGGTTTT	1332
Dd	628 GAATTCGTAACCTTATGAAAAGACTGTGAGAACTTGAACAAAGAAATGGAGACGGGTTTT	687
OY	1333 CTAGATGTGTGACATACATGTGTAGCTTTTACTTCTGATGAGAAAATGAGAGGACACTT	1392

Db	688	CTAGATGCTGTCAGATACCAATGCTGAGCTTTTAGTTCGTGATGGAATAATGAGAGCACACTT	747
Qy	1393	GACCTTTCATGATTCCTAATGTCACAAATCTGTATAGTAAAGTCAGAAATGCAGCTGAGAGAC	1452
Db	748	GACCTTCATGATTCCTAATGTCACAAATCTGTATAGTAAAGTCAGAAATGCAGCTGAGAGAC	807
Qy	1453	AACGTCAAAGACTAGAGAAATGATGTTTGGAAATTTATCCAAATGTGATGATGAATGC	1512
Db	808	AACGTCAAAGAACTAGAGAAATGATGTTTGGAAATTTATCCAAATGTGATGATGAATGC	867
Qy	1513	ATGAATAGTGTGAAGAAACGGGACATATGATTTATGCCAAGTATGAAAGAAAGACTTAAACTA	1572
Db	868	ATGAATAGTGTGAAGAAACGGGACATATGATTTATGCCAAGTATGAAAGAAAGACTTAAACTA	927
Qy	1573	AATGAAGATGAATTCAAAGGGGTAAATTTGAGCAGCATGGGGGTTTATCCAATCCTTGCC	1632
Db	928	AATGAAGATGAATTCAAAGGGGTAAATTTGAGCAGCATGGGGGTTTATCCAATCCTTGCC	987
Qy	1633	ATTATAGCTACAGTAGCAGGTTTCTATGTCACTGGCAATCATGATGGCTGGGATCTCTTTC	1692
Db	988	ATTATAGCTACAGTAGCAGGTTTCTATGTCACTGGCAATCATGATGGCTGGGATCTCTTTC	1047
Qy	1693	TGGGTGTGCTCCAAAGGGTCTCTTCGACGTGCAGGATCTGCATATGATTTAATAGCATTTTAA	1752
Db	1048	TGGGTGTGCTCCAAAGGGTCTCTTCGACGTGCAGGATCTGCATATGATTTAATAGCATTTTAA	1107
Qy	1753	TAATTAAGAACACGCTGTCTTCCTGTAAG	1780
Db	1108	TAATTAAGAACACGCTGTCTTCCTGTAAG	1135

RESULT 4  
 US-09-918-568-27  
 Sequence 27, Application US/09918568  
 Patent No. US20020054882A1  
 GENERAL INFORMATION:  
 APPLICANT: Yoshinobu OKUNO et al.  
 TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
 ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
 NUMBER OF SEQUENCES: 58  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
 STREET: 2033 K Street, N.W., #800  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20006  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/918,568  
 FILING DATE: 02-Aug-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/004,422  
 FILING DATE: January 8, 1998  
 APPLICATION NUMBER: 08/443,862  
 FILING DATE: May 22, 1995  
 APPLICATION NUMBER: 08/229,781  
 FILING DATE: April 19, 1994  
 APPLICATION NUMBER: 08/054,016  
 FILING DATE: April 29, 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warren M. Cheek, Jr.  
 REGISTRATION/DOCKET NUMBER: 33,367  
 TELECOMMUNICATION INFORMATION: <Unknown>  
 TELEPHONE: 202-721-8200  
 TELEFAX: 202-721-8250

TELEX: <Unknown>  
INFORMATION FOR SEQ. ID NO: 27 :  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1754 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOHETICAL: <Unknown>  
ANTI-SENSE: <Unknown>  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: A/Suila/1/89  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>  
CELL LINE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ. ID NO:  
SEQUENCE DESCRIPTION: SEQ. ID NO: 27:  
us-09-918-568-27

Query Match 39.0%; Score 695.6; DB 9; Length 1754;  
Best Local Similarity 64.0%; Pred. No. 5,9e-183;  
Matches 1068; Conservative 0; Mismatches 594; Indels 6; Gaps 1;

QY 76 TTCACAGCAGTAGAGGGGACCAAGATATGATGATACCCAGCAATATTCACAGAG 135  
DB 54 TTTCAGTACAGATGACACACATATGTATAGGCTACACGCAACTCAACCGAC 113  
QY 136 AAGTCGACACATTTCTAGAGCGGACGTCAGTGCATGACATGCCAAGACATCCTGAG 195  
DB 114 ACTGTGACACAGTACTTGAAGAAAGCGACAGTACACACTCTGTCAACTACTTGGAG 173  
QY 196 AAGACCCATTAAGGAAAGTTATGCAAACTAAACGGAATCCCTCAGTTGAAGTAGGGAG 255  
DB 174 GACAGTACAAAGGAAACTATGTGACATAAAGGAAATGCCCACTACAAATTTGGGTAAAT 233  
QY 256 TGTAGCATTTGCCGGATGGCTCTTGGAATCCAAATGTGATAGGCTTAAAGTGTGCA 315  
DB 234 TGCAGCATTTGCCGGATGGATCTTAAAGAAACCGAATGCACTGTTTCTAAGAA 293  
QY 316 GAAGGCTCTATATTTGGAGAAAGAAACCGAGAGCGTTTGTGTTATCCAGGAC 375  
DB 294 TCATGGTCTCATTTGACAGAAACACCAACTCCGGAATGGAACATGTTACCCAGGCTAT 353  
QY 376 TTCAATGATATGAAGATTTGAACATCTCTCAGCAGCGTGAACATTTGAGAAAGTA 435

DB 354 TTGCCGACATATGAGGAACGTGAGGAGCAATTTGATTCAGATATCATTCATCGAGATTTC 413  
QY 436 AAGATTTGCCCCAAGATAGAT-----GGACACAGATATCAACACTGAGGTTACAGG 489  
DB 414 GAAATATTTCCCAAGAAAGCTCATGGCCCAACCAACCGTACCAAGAGGATACGGCA 473  
QY 490 GCCTGCGGGGTGTGTGTAATCATATTTTCAGAAACATGTGTGGCTGACAAAGAA 549  
DB 474 TCATGCTCCCATTAATGGGAAAGCAGTTTACGAAATTTGCTATGGCTGACGGGAG 533  
QY 550 GGATCAGATTTATCCGGTTGCCAAGAGTCTGACACATATCAAGCGGAGACAAATGCTA 609  
DB 534 AATGGCTTGACCAAACTGAGCAAGCTCTGATGTGAACCAAGAGAAAGATCTT 593  
QY 610 ATAATTTGGGGGTGCACCATCCATGATGAGACACAGAAAGAAACATTTACCGAAT 669  
DB 594 GTACTATGGGTGTTCATCAACCCGCTACATATAGGGACCAAAAGGCGCATCTATCA 653  
QY 670 GTGGGAACCTATGTTCCGTAGGCACATCAACATTTGAACAAAGGTCAACCCGAAATA 729  
DB 654 GAAATGCTTATGTCTGTAGTGTCTTACATTTATGACGAGATTTACCCCAATA 713  
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DB 714 GCAAAAAGCCCAAGATGAGAGTCAAGAAAGAAATTAACATCACTACATGACTGCTG 773  
QY 790 GATATGTGGACACCATTAATTTTGTAGAGTACTGTAATTAATTCACACAGATTTGA 849  
DB 774 GAACCCGGGACACAAATATTTTGAAGCAATATGAAATTTATACGCCATGATGCT 833  
QY 850 TTCAAATATGCAAAAGAGTACTTACGGATCATGAAACACAGAAAGCACTTGAAC 909  
DB 834 TTGCACTGATGAGGCTTTGGGTGAGATATCATCCTCAAAACCATCAATGATGA 893.  
QY 910 TGTGAGACCAATATGCCAAATCCTTTGGAGCAATTAATACATTTACTTTTCAAT 969  
DB 894 TGTGAGCGGAGTGTAAACACCCAGGAGCTATTAACAGATGCTCTCTTCCAGAT 953  
QY 970 GTCCACCACCTGACATAGTGTGAGTCCCAATATGTAATAATCGGAAAGTTGGCTTA 1029  
DB 954 GTACACCCAGTCAACATATGAGAGGTGTCCAAATATGTGAGAGTCAAAATTAAGATG 1013  
QY 1030 GCAACAGGACTAAGAAATGTTCCCAAGTTGAATCAAGAGATTTGTTGGCAATAGCT 1089  
DB 1014 GTTACAGGACTAAGAAATCCCATCATCAATCAAGAGTTGTTGGACCATTTGCC 1073  
QY 1090 GGTTTATGAAAGAGATGCGCAAGAAATGTTGACGTTGTTGATGATACATCAGAC 1149  
DB 1074 GGTTCATTTGAAAGGGGTGAGTGTGAATGATGATGATGATGATGATGATGATGATG 1133  
QY 1150 AATGACAGGATCAGGATATGACAGACAGCAAAAGATCACTCAAAAGGCAATTTGATGA 1209  
DB 1134 AATGAACAGGATCTGGTATGTGTGATGATCAAAAGACACCAAAATGCCATTAAAGCA 1193  
QY 1210 ATACCAACAGGTAATTTCTGTGATTAAGAAATTAACACCAATTTGAAGCTTTGG 1269  
DB 1194 ATTAACAAAGGTGATTTCTGTAAATCGAAATTAACACATCAATTCACACTGTGGC 1253  
QY 1270 AAGAAATTCGTACTTATGAGAAAGCTGAGAACTTGAAACAAAGATGGAAGACGG 1329  
DB 1254 AAGAAATTAACAAATTAAGAAAGAGATGATGATGATGATGATGATGATGATGATGATG 1313  
QY 1330 TTTTATGATGTGATACATACATCTGATTTAGTTTCTGATGGAATGAGAGCA 1389  
DB 1314 TTTCTGACATTTGGACATATATACAGATTTGTTGTTCTACTGGAATTAAGAGCT 1373  
QY 1390 CTTGACTTTCATGATTTCTAATGTCAAGATCTGTACTAAGTCAAGATCAGAGTGA 1449  
DB 1374 TTGGAATTTCTATGATCAAAATGTGAAGATCTGTATGAAAGTAAAGCAATTAAG 1433  
QY 1450 GACACGTCAAGACATGAGAAATGATGTTTGAATTTTATCAAAATGATGATGAA 1509

Db 1434 AATAATGCCAAGA/ATAGATACGGGTGTTTGAATCTACACAGCTGAACATGAA 1493  
QY 1510 TGCATGATAGTGTAAAAAGGGGACATATGATATCCAGTATGAGAGAGCTGAA 1569  
Db 1494 TGCAATGGAATGTGAAAAATGAGACTTATGACTATCCAAATATTCGAGGAATCAAG 1553  
QY 1570 CTAATATGAAATGATATCAAGGGGTAAATTTGAGCAGACATGGGGTTTATCAATCCCT 1629  
Db 1554 TTAACAGGGGAAAAATGATGATGAGTGAATTTGGAATCAATGGGAGCTCTATCAGATTCTG 1613  
QY 1630 GCCATTATGCTACATGACAGCTTCTATGTCACCTGCCAATCAGATGGCTGGGATCTCT 1689  
Db 1614 GCGATCTACTCAACTGTGCGCAGTTCACCTGCTTGTCTCTCCCTGGGGCAATCCAGC 1673  
QY 1690 TTCGTGGGTGCTCTCAACGGGTCTGTCAGTGCAGGATCGCATATGA 1737  
Db 1674 TTCTGATGTGTCTTAATGGGTCTTTGCAGTGTAAATATGCACTGA 1721

## RESULT 5

US-09-918-568-33  
Sequence 33, Application US/09918568  
Patent No. US20020054882A1

## GENERAL INFORMATION:

APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenceroth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/918,568

FILING DATE: 02-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/004,422

FILING DATE: January 8, 1998

APPLICATION NUMBER: 08/443,862

FILING DATE: May 22, 1995

APPLICATION NUMBER: 08/229,781

FILING DATE: April 19, 1994

APPLICATION NUMBER: 08/054,016

FILING DATE: April 29, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER: <Unknown>

TELEPHONE: 202-721-8200

TELEFAX: 202-721-8250

TELEX: <Unknown>

SEQUENCE CHARACTERISTICS:

LENGTH: 400 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to genomic RNA

HYPOTHETICAL: <Unknown>

ANTI-SENSE: <Unknown>

FRAGMENT TYPE: <Unknown>

ORIGINAL SOURCE:

ORGANISM: A/Okuda/57

STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>  
CELL LINE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-918-568-33

Query Match 22.4%; Score 400; DB 9; Length 400;  
Best Local Similarity 100.0%; Pred. No. 5.2e-101;  
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 940 GCATTAATACACATTCCTTTTCACATGTCACCCACGACATAGTGATGCCCC 999  
Db 1 GCAATTAATACACATTCCTTTTCACATGTCACCCACGACATAGTGATGCCCC 60  
QY 1000 AATATGTAAATGAGAGAGTGTCTTACACAGGACGATAGGAATGCCAGATT 1059  
Db 61 AATATGTAAATGAGAGAGTGTCTTACACAGGACGATAGGAATGCCAGATT 120  
QY 1060 GAATCAAGAGATTTGTTGGGGCAATAGCTGTTTATAGAAGAGATGCAAGGATG 1119  
Db 121 GAATCAAGAGATTTGTTGGGGCAATAGCTGTTTATAGAAGAGATGCAAGGATG 180  
QY 1120 GTTACGGTGTGATGATACCATCAGCATGACAGGATCAGGGTATGACAGCAG 1179  
Db 181 GTTACGGTGTGATGATACCATCAGCATGACAGGATCAGGGTATGACAGCAG 240  
QY 1180 AAAGATTCATCAAAAGGCAATTTGATGATTCACCAACAGGATTAATTTGATTTAA 1239  
Db 241 AAAGATTCATCAAAAGGCAATTTGATGATTCACCAACAGGATTAATTTGATTTAA 300  
QY 1240 AAGATTAACACCCATTTGAAGCTGTTGGGAAAGAAATTCGTAATGAGAAAAAGACTG 1299  
Db 301 AAGATTAACACCCATTTGAAGCTGTTGGGAAAGAAATTCGTAATGAGAAAAAGACTG 360  
QY 1300 GAGAACTTGAACAAAAGATGGAAGCGGTTCTTAGATG 1339  
Db 361 GAGAACTTGAACAAAAGATGGAAGCGGTTCTTAGATG 400

## RESULT 6

US-09-918-568-34  
Sequence 34, Application US/09918568  
Patent No. US20020054882A1  
GENERAL INFORMATION:

APPLICANT: Yoshinobu OKUNO et al.  
 TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
 ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
 NUMBER OF SEQUENCES: 58  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
 STREET: 2033 K Street, N.W., #800  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20006  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/918,568  
 FILING DATE: 02-Aug-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/004,422  
 FILING DATE: January 8, 1998  
 APPLICATION NUMBER: 08/443,862  
 FILING DATE: May 22, 1995  
 APPLICATION NUMBER: 08/229,781  
 FILING DATE: April 19, 1994  
 APPLICATION NUMBER: 08/054,016  
 FILING DATE: April 29, 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warren M. Cheek, Jr.  
 REGISTRATION NUMBER: 33,367  
 REFERENCE/DOCKET NUMBER: <Unknown>  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-721-8200  
 TELEFAX: 202-721-8250  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 34:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 409 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to genomic RNA  
 HYPOTHEetical: <Unknown>  
 ANTI-SENSE: <Unknown>  
 FRAGMENT TYPE: <Unknown>  
 ORIGINAL SOURCE:  
 ORGANISM: A/Adachi/2/57  
 STRAIN: <Unknown>  
 INDIVIDUAL ISOLATE: <Unknown>  
 DEVELOPMENTAL STAGE: <Unknown>  
 HAPLOTYPE: <Unknown>  
 TISSUE TYPE: <Unknown>  
 CELL TYPE: <Unknown>  
 CELL LINE: <Unknown>  
 ORGANELLE: <Unknown>  
 IMMEDIATE SOURCE:  
 LIBRARY: <Unknown>  
 CLONE: <Unknown>  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT: <Unknown>  
 MAP POSITION: <Unknown>  
 UNITS: <Unknown>  
 FEATURE:  
 NAME/KEY:  
 LOCATION:  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 PUBLICATION INFORMATION:  
 AUTHORS:  
 TITLE:  
 JOURNAL:

VOLUME:  
 ISSUE:  
 PAGES:  
 DATE:  
 DOCUMENT NUMBER:  
 FILING DATE:  
 PUBLICATION DATE:  
 RELEVANT RESIDUES IN SEQ ID NO:  
 SEQUENCE DESCRIPTION: SEQ ID NO: 34:  
 US-09-918-568-34  
 Query Match 22.3%; Score 397; DB 9; Length 409;  
 Best Local Similarity 98.8%; Pred. No. 3.6e-100;  
 Matches 400; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 935 TGGGAGCAATTAATACACATTCCTTTCACAAAGTCCACCACGACGACATAGGTGCT 994  
 Db 5 TTGGAGCAATTAATACACATTCCTTTCACAAAGTCCACCACGACGACATAGGTGCT 64  
 QY 995 GCCCAAAATATGTAATATCGAGAAAGTTGCTTACCAACAGAGACTAAGAAATGTTCCCC 1054  
 Db 65 GCCCAAAATATGTAATATCGAGAAAGTTGCTTACCAACAGAGACTAAGAAATGTTCCCC 124  
 QY 1055 AGATTGAATCAGAGAGATTGTTGGGCAATAGCTGTTTATAGAGAGAGATGGCAAG 1114  
 Db 125 AGATTGAATCAGAGAGATTGTTGGGCAATAGCTGTTTATAGAGAGAGATGGCAAG 184  
 QY 1115 GAATGTTGACGGTGTGATGATACCATCAGCAAGTACGAGGATCAGGTTGCGAG 1174  
 Db 185 GAATGTTGATGTTGATGATGATACCATCAGCAAGTACGAGGATCAGGTTGCGAG 244  
 QY 1175 CAGACAAGATTCACACTCAAAAGGCAATTTGATGATGATCACCACAAGGTAATTTCTGTA 1234  
 Db 245 CAGACAAGATTCACACTCAAAAGGCAATTTGATGATGATCACCACAAGGTAATTTCTGTA 304  
 QY 1235 TTGAAAAGATTAACACCCCAATTTGAAGCTGTTGGGAAGAATTGCGTAACCTAGAGAAA 1294  
 Db 305 TTGAAAAGATTAACACCCCAATTTGAAGCTGTTGGGAAGAATTGCGTAACCTAGAGAAA 364  
 QY 1295 GACTGGAGAACTTGAACAAAAGATGGAAGACGGGTTTCTAGATG 1339  
 Db 365 GACTGGAGAACTTGAACAAAAGATGGAAGACGGGTTTCTAGATG 409  
 RESULT 7  
 US-09-918-568-35  
 Sequence 35, Application US/09918568  
 Patent No. US20020054882A1  
 GENERAL INFORMATION:  
 APPLICANT: Yoshinobu OKUNO et al.  
 TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
 ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
 NUMBER OF SEQUENCES: 58  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
 STREET: 2033 K Street, N.W., #800  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20006  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/918,568  
 FILING DATE: 02-Aug-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/004,422  
 FILING DATE: January 8, 1998  
 APPLICATION NUMBER: 08/443,862



	FILING DATE:	MAY 22, 1995
	APPLICATION NUMBER:	08/229,781
	FILING DATE:	APRIL 19, 1994
	APPLICATION NUMBER:	08/054,016
	FILING DATE:	APRIL 29, 1993
	ATTORNEY/AGENT INFORMATION:	
	NAME:	MARLEN M. CHEEK, JR.
	REGISTRATION NUMBER:	33,367
	REFERENCE/DOCKET NUMBER:	<UNKNOWN>
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE:	202-721-8200
	TELEFAX:	202-741-8250
	TELEX:	<UNKNOWN>
	INFORMATION FOR SEQ ID NO: 35:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH:	410 base pairs
	TYPE:	nucleic acid
	STRANDEDNESS:	double
	TOPOLOGY:	linear
	MOLECULE TYPE:	cDNA to genomic RNA
	HYPOTHETICAL:	<UNKNOWN>
	ANTI-SENSE:	<UNKNOWN>
	FRAGMENT TYPE:	<UNKNOWN>
	ORIGINAL SOURCE:	
	ORGANISM:	A/KUHAMOTO/1/65
	STRAIN:	<UNKNOWN>
	INDIVIDUAL ISOLATE:	<UNKNOWN>
	DEVELOPMENTAL STAGE:	<UNKNOWN>
	HAPLOTYPE:	<UNKNOWN>
	TISSUE TYPE:	<UNKNOWN>
	CELL TYPE:	<UNKNOWN>
	CELL LINE:	<UNKNOWN>
	ORGANELLE:	<UNKNOWN>
	IMMEDIATE SOURCE:	
	LIBRARY:	<UNKNOWN>
	CLONE:	<UNKNOWN>
	POSITION IN GENOME:	
	CHROMOSOME/SEGMENT:	<UNKNOWN>
	MAP POSITION:	<UNKNOWN>
	UNITS:	<UNKNOWN>
	FEATURE:	
	NAME/KEY:	
	LOCATION:	
	IDENTIFICATION METHOD:	
	OTHER INFORMATION:	
	PUBLICATION INFORMATION:	
	AUTHORS:	
	TITLE:	
	JOURNAL:	
	VOLUME:	
	ISSUE:	
	PAGES:	
	DATE:	
	DOCUMENT NUMBER:	
	FILING DATE:	
	PUBLICATION DATE:	
	RELEVANT RESIDUES IN SEQ ID NO:	
	SEQUENCE DESCRIPTION: SEQ ID NO: 35:	
	US-09-918-568-35	
	Query Match	21.4%; Score 382.4; DB 9; Length 410;
	Best Local Similarity	96.1%; Pred. No. 4.2e-96;
	Matches 392; Conservative	0; Mismatches 16; Indels 0; Gaps 0;
OY	932	CTTTGGGCGCAATAAATACACATTACTCTTTCACAATGTCGCCACCACATGACAAATAGGTG 991
Dd	3	CTTTGGGCGCATATAATACCAACATTACCTTTTCACAATGTCGCCACCACATGACAAATAGGTG 62
OY	992	AGTCCGCCCAATATATTAAATCGGAGAAGTGCTTAGCAACAAGAGCATAAGGAATGTC 1051
Dd	63	AATGCCCAATATATTAAATCGGAGAAGTGTCTTAGCAACAAGAGCATAAGGAATGTC 122
OY	1052	CCGAGATTGAATCAAGAGATTGTTGGGCGCAATAGCTGTTTTATATAGAGAGAGATGC 11111

Db 123 CCCGATTGATCTAAGAGATTGTTGGGGCAATAGCTGGCTTTGTAGACAGAGATGCG 182  
 QY 1112 AAGGAATGCTTGAACGGTTGATGATACCATCAACAGCAATGACCGAGATCAGGTAATG 117U  
 Db 183 AAGGAATGATGATGATGTTGATGATACCATCAACAGCAATGATCAGGATCAGGTTTG 242  
 QY 1172 CAGCAGCAAAAGATTCACATCAAAAGCATTTGATGATATCCAAACAGGTAATTTCTG 123U  
 Db 243 CAGCAGCAAAAGATTCACATCAAAAGCATTTGATGATATCCAAACAGGTAATTTCTG 302  
 QY 1232 TGATGAAAGATTAACACCCATTTGAGCTGTTGGCAAGCAATTCGCTAATTAGGA 129U  
 Db 303 TGATGAAAGATTAACACCCATTTGAGCTGTTGGCAAGCAATTCGCTAATTTAGGA 362  
 QY 1292 AAAGACTGGAGAACTTGACAAAAAGATGGAAGACGGGTTCTGATG 1339  
 Db 363 AAAGACTGGAGAACTTGACAAAGATGGAAGACGGGTTCTGATG 410  
 RESULT 8  
 US-09-918-568-36  
 Sequence 36, Application US/09918568  
 Patent No. US20020054882A1  
 GENERAL INFORMATION:  
 APPLICANT: Yoshinobu OKUNO et al.  
 TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
 ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
 NUMBER OF SEQUENCES: 58  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
 STREET: 2033 K Street, N.W., #800  
 City: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20006  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/918,568  
 FILING DATE: 02-Aug-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/004,422  
 FILING DATE: January 8, 1998  
 APPLICATION NUMBER: 08/443,862  
 FILING DATE: May 22, 1995  
 APPLICATION NUMBER: 08/229,781  
 FILING DATE: April 19, 1994  
 APPLICATION NUMBER: 08/054,016  
 FILING DATE: April 29, 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warren M. Cheek, Jr.  
 REGISTRATION NUMBER: 33,367  
 REFERENCE/DOCKET NUMBER: <Unknown>  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-721-8200  
 TELEFAX: 202-721-8250  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 36:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 394 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to genomic RNA  
 HYPOTHEICAL: <Unknown>  
 ANTI-SENSE: <Unknown>  
 FRAGMENT TYPE: <Unknown>  
 ORIGINAL SOURCE:

ORGANISM: A/Kaizuka/2/65  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>  
CELL LINE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 36;  
US-09-918-568-36

Query Match 21.3%; Score 379.6; DB 9; Length 394;  
Best Local Similarity 97.7%; Pred. No. 2.5e-95;  
Matches 385; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 946 AATACACATTTACCTTTTCACATGTCACCCCTGACATAGTAGTCCCAATAT 1005  
DB 1 AATACACACTACCTTTTCACATGTCACCCCTGACATAGTAGTCCCAATAT 60  
QY 1006 GTAATATCGAGAGTGTGCTTTCAGCAGAGACTAAGAAATGTTCCCGATTTGATCA 1065  
DB 61 GTAATATCGAGAGTGTGCTTTCAGCAGAGACTAAGAAATGTTCCCGATTTGATCA 120  
QY 1066 AGAGATTGTTGGGCAATAGCTGTTTATGAAGAGAGATGCCAAGAAATGTTGAC 1125  
DB 121 AGAGATTGTTGGGCAATAGCTGTTTATGAAGAGAGATGCCAAGAAATGTTGAT 180  
QY 1126 GGTGGTATGATACCATCAGCATGACAGGGATCGAGGTATCAGACAGCAAGAA 1185  
DB 181 GGTGGTATGATACCATCAGCATGACAGGGATCGAGGTATCAGACAGCAAGAA 240  
QY 1186 TCCACTCAAAAGCAATTTGATGGAATCACCACAAGTAATCTGATTTGAAAGATA 1245  
DB 241 TCCACTCAAAAGCAATTTGATGGAATCACCACAAGTAATCTGATTTGAAAGATG 300  
QY 1246 AACACCCCAATTTGAAGCTGTTGGGAAAGAAATTCGTAAGTGAAGAAAGACTGGAAC 1305  
DB 301 AACACCCCAATTTGAAGCTGTTGGGAAAGAAATTCGTAAGTGAAGAAAGACTGGAAC 360  
QY 1306 TTGAACAAAAGATGGAAGCGGTTTCTAGATG 1339  
DB 361 TTGAACAAAAGATGGAAGCGGTTTCTAGATG 394

GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/918,568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/034,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1777 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL: <Unknown>  
ANTI-SENSE: <Unknown>  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: A2/Alchi/2/68  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>  
CELL LINE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:



QY 216 ATGCAACTAAACGGAATCCCTCCACTGTAAGGGGACTGTAGCATTTGCCGATGGCT 275  
 Db 187 CTGC---TCMAAAGGAAAAGGACAGTTGACCTCGGTCAATGAGACTTCTGGAAACAT 243  
 QY 276 CTTGAAATCCAAATGTGATAGCTTTAAGTGTGCCAAGAGCTCTATATATTGGA 335  
 Db 244 CACTGGGACCCCAATGTGACCAAGTCTCTAGAAATTTTCAGCCGATCTAATTTAGAG 303  
 QY 336 GAAAGAAAACCCGAGAGCGTTTGTATCCAGCAGCTTCAATGATTTAGAAACAT 395  
 Db 304 GCGAGAA-----GSAAGTGTCTGTTATCTCTGGAAATTCGTGAATGAAGAGCTCT 357  
 QY 396 GAACATCTCTCTGACAGCAGCTGAAACATTTGAGAAAAGTAAAGATTTGCCCAAGAT 455  
 Db 358 GAGCAAAATTTCTCAGGAGAGTCAAGCGGAATTTGACAGGAGCAATGGATTCACATAC 417  
 QY 456 ATGACACAGCATCAACACAGTGGATTCAGCGGCTCGCGGCTGTGGTAATTCATC 515  
 Db 418 CGGAATAGAACTAATGAAACACAGTACATGTAGAGATCAGATCTTCATTTCTATGC 477  
 QY 516 ATTTTTCAGAACATGTGTCTGTGACAAAGAAAGATCAGATTTCCGGTTCGCAAGG 575  
 Db 478 AGAG---ATGAAATGGCTCTGTCAAAACACAGACATGCTCTTCCGCAATGACTAA 534  
 QY 576 ATGTAACAATCAACAGCGGAGAAACAAATCTAATTAATTTGGGGGTGCACCATCCAT 635  
 Db 535 GTCTACAAAAACAAAGAAAGACCCAGCTCTGTAATATATGGGGATTCACCATTTCCG 594  
 QY 636 TGATGACACAGAAAGAACATTTGTACCAAGATGTGGAGCATTTTCCGTAGACAC 695  
 Db 595 ATCAACTACAGAACAGCAACAGTATATGGAGTGGAAACAACTGATTAACAGTTGGAG 654  
 QY 696 ATCAACTTAACAAAAGGTCAACCCAGAAATAGCAACAGGCTTAAGTAATGACGA 755  
 Db 655 TTCTAATTAACACAGCTCTTGTGACCGATCCAGAGAGAGACACCAAGTAATGGCCA 714  
 QY 756 AGGAGTAGAATGGAATTTCTTGAGCCCTCTTGATATGTGGACACCATTAATTTGA 815  
 Db 715 ATCTGGAAGATGACTTCTTATGCTGATGTAAACCCCAATGACACAGTCACTTTGAG 774  
 QY 816 GAGTACTGTAACTAATTTGACACAGATGTGATTAATAATTCGAAAAGAGTACTTC 875  
 Db 775 TTTCATTTGGGCTTCATAGCTCAGACCTGCA---AGTTTCTGTAGAGGAGTCTAT 831  
 QY 876 AGGATCATGAAACAAAGAAAGAACTGTGAACTGTGAGACCAAAATGCCAACTCTTT 935  
 Db 832 GGGGATTCAGAGTGGAGTACAGGTGATGCCAATTTGGAAGAGATTGCTATACAGTGG 891  
 QY 936 GGGACCAATTAATTAACAACTTACCTTTTCAATGTCACCCACTGACAAATAGGTGATG 995  
 Db 892 AGGACCAATTAATTAATTTGCCCTTTGAGAACTAATTAATAGCAGGCACTAGGAAATG 951  
 QY 996 CCCCATAATTAATTAATTCGAGAAAGTGTCTTGAACAGAGCACTAAGAAATTTCCCA 1055  
 Db 952 TCCGAGATATGTTAAGCAAGAGTGTGCTGCGCAACAGGATGAGAGATTTCCCA 1011  
 QY 1056 GATTAAATCA-----AGAGGATTTGTTGGGCAATAGCTGTTTATAGA 1100  
 Db 1012 AATTCCAAAAAGAGTGCCTGTGAGAGAGGCTAATTTGGTATAGCGGTTTCAATTA 1071  
 QY 1101 AGGAGATGCGAAGATGTGAGGTTGTGATGATACCATCACAGCAATGACAGGG 1160  
 Db 1072 AAATGATGGAGAGGTCTGATTTGATGGGTGATAGGCTTCAGGCATCAAAATGACAGAG 1131  
 QY 1161 ATCAGGGTATGACAGAGAAAGATTCATCAAAAGCATTTGATGGAATGACCAACA 1220  
 Db 1132 AGAGGGAAGTCTGTGAGATTACAAAGACCAACCAATTTGATCAAGTAAACAGGAA 1191  
 QY 1221 GGTAAATTTCTGATTAAGAAATTAACACCAATTTGAAGCTTTGGAAAGAAATTCGG 1280  
 Db 1192 ATTGAACCGGCTTATAGAAAAAATTAACCAATTTGATTAATAGACAATGAAATTCAC 1251  
 QY 1281 TAACTTAGAGAAAGAGTGGAGAACTTAACAAAAAGATGGAAGAGGGGTTTCTAGATGT 1340

Db 1252 TGAGTTGAAAACCAATTTGGCAATGTGTAATTTGACACAGAGTTCATGACAGAGT 1311  
 QY 1341 GTGACATCAATGCTGAGCTTTTACTGTGTGTAAGAAATGAGAGACACTTGACTTTCA 1400  
 Db 1312 GTGTCTCTTAAGCTGTAAGTCTTTGTAGCAATGGAGAACGACATTAATTTGATCTGAC 1371  
 QY 1401 TGATTTAATGTCAGAAATCTGTATAGTAAGTCAAGAAATGACGTGAGAGCAACGTCA 1460  
 Db 1372 CGACTCAGAAATGAACAACTATACGAACGACTGAAGAGACTACTGAGAGAAATCTGA 1431  
 QY 1461 AGACATGAGAAATGATGTTTGAATTTTATACAAATGTATGATGATGATGATGATG 1520  
 Db 1432 AGAAGTGGACACTGTGCTTCAAAATTTTCACAAAGTGTATGATGATGATGATGATG 1491  
 QY 1521 TGTAAGAAACGAGACATATGATTTATCCCAAGTATGAAGAGTCAATTAATTAACAA 1580  
 Db 1492 TATTGAAACCAACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1551  
 QY 1581 TGAATTCAAAGGCTTAATTAATGACAGCATGGGGGTTATTCAAATCTTGCCATTTATG 1640  
 Db 1552 ACAGATTAACCCAGTCAAACTAAGACAGCGGCTTACAAAGATGTGATGATGATGAT 1611  
 QY 1641 TACAGTACAGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1700  
 Db 1612 CGGGCATCATGTTTCACTTCTGCGCATTTGCAATGGCCCTGCTTCAATGATGATGATG 1671  
 QY 1701 CTCACAGGCTCTCTGAGTGTGAGATCTGCATGATGATGATGATGATGATGATGAT 1741  
 Db 1672 --AATGGAACAAATCGCGTCTCACTATTTGATTAATGATTT 1709

RESULT 11  
 US-09-918-568-57  
 ; Sequence 57, Application us/0918568  
 ; Patent No. US20020054882A1  
 GENERAL INFORMATION:  
 APPLICANT: Yoshinobu OKUNO et al.  
 TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
 ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
 NUMBER OF SEQUENCES: 58  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Mendelsohn, Lind & Ponack, L.L.P.  
 STREET: 2033 K Street, N.W., #800  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20006  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: us/09/918, 568  
 FILING DATE: 02-Aug-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/004,422  
 FILING DATE: January 8, 1998  
 APPLICATION NUMBER: 08/443,862  
 FILING DATE: May 22, 1995  
 APPLICATION NUMBER: 08/229,781  
 FILING DATE: April 19, 1994  
 APPLICATION NUMBER: 08/054,016  
 FILING DATE: April 29, 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warren M. Cheek, Jr.  
 REGISTRATION NUMBER: 33,367  
 REFERENCE/DOCKET NUMBER: <Unknown>  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-721-8200  
 TELEFAX: 202-721-8250



FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8250  
TELEFAX: 202-721-8250  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 442 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL: <Unknown>  
ANTI-SENSE: <Unknown>  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: A/PR/8/34  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>  
CELL LINE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-918-568-29

Query Match 14.1%; Score 251.6; DB 9; Length 442;  
Best Local Similarity 73.1%; Pred. No. 1.2e-59;  
Matches 323; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 958 CCTTTCACAAATGTCACCACTGACAAATAGTGTGCGCCCAAAATATGTAAATGGAG 1017  
DB 1 CCTTTCAGAAATATACACCAGCTACAAATAGAGAGTGTGCCAAAATACGTGAGAGTGC 60

QY 1018 AAGTGTGCTTGTAGCAAGAGACTAAGAGATGTTCCCAATGATGAATCAAGAGATTGTT 1077  
DB 61 AATTTGAGATGCTTACAGAGACTAAGAGAAATCCCGTCATTCATCCAGAGGCTTATTT 120

QY 1078 GGGGCAATAGCTGTTTATAGAGAGAGATGCAAGAAATGTTGACGTTGTATGGA 1137  
DB 121 GGAGCAATGCGCGTTTATATGAGGGGAGTGTGACATGGAATGATGATGATGTATGT 180

QY 1138 TACCATCACAGCATGACCAGGAGATCAGGATGACAGCAGACAAGATCCACTCAAG 1197

DB 181 TATCATCATCAGATGACAGAGGATGAGCTATGACGCGATCAAAAAAGCACACAAAT 240  
QY 1198 GCATTTGATGATATCAACCAAGAGTAATTCGTGATTTGAAAAGATAACCAATTT 1257  
DB 241 GGCATTAACGGGATTAACCAAGGTAAGTGAATGCAAAATGAACTCAATTC 300  
QY 1258 GAAGCTGTGGGAAATTCGGTACTAGAGAAAGAGCTGAGAGAACTTGAACAAAAG 1317  
DB 301 ACAGCTGTGGGTAAGAAATTCACCAATTTAGAAAAAGAGATGAAATTTAATATAAAA 360  
QY 1318 ATGGAAGACGGGTTTCTAGATGTGTGACATACAAATGCTGAGCTTTTACTGTGATGAA 1377  
DB 361 GTTGATGATGATTTCTGACATTTGACATATATATGACAGAAATGTATGTTACTGTGAA 420  
QY 1378 AATGAGAGCACTTACCTTC 1399  
DB 421 AATGAAAGAGCTCTGTGATTTCC 442

RESULT 13  
US-09-918-568-32  
Sequence 32, Application US/09918568  
Patent No. US2002005482A1  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/918,568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 429 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL: <Unknown>  
ANTI-SENSE: <Unknown>  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:



## OTHER INFORMATION:

PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 30;  
US-09-918-568-30

Query Match 13.1%; Score 233.6; DB 9; Length 424;  
Best Local Similarity 71.9%; Pred. No. 1.2e-54;  
Matches 305; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 958 CCTTTTCACATGCTCCACCCACTGACAAATAGTGAGTGCCTCCAAATATGTAAATCGGAG 1017  
DB 1 CCTTTCAGAAATGTACACCCAGTCAATAGAGAGTGCCTCCAAAGTACGTGAGAGTACA 60  
QY 1018 AATTGGCTTTACCAACAGAGACTAGGAATGTTCCCGAGATGATCAAGAGATGTTT 1077  
DB 61 AATTGAAGATGTTACAGAGACTAGGAATGTTCCCGAGATGATCAAGAGATGTTT 120  
QY 1078 GGGGCAATAGCTGTTTATAGAAAGAGATGGCAAGTATGTTGAGGTTGATGGA 1137  
DB 121 GGGGCAATAGCTGTTTATAGAAAGAGATGGCAAGTATGTTGAGGTTGATGGA 180  
QY 1138 TACCATCAGCAATGACAGGATGAGGATGATGACAGCAAAAGATCCACTCAAAAG 1197  
DB 181 TATCATCATCAGATGAAACAGAGATGCTGCTATGCTCGGATCAAAAAGACACAAAT 240  
QY 1198 GGATTTGATGATTCACCAACAGGATTAATTCGTGTTGAAAAGATTAACCCCAATTT 1257  
DB 241 GCCATTACGGGATTCACCAACAGGATTAATTCGTGTTGAAAAGATTAACCCCAATTT 300  
QY 1258 GAAGCTGTTGGGAAAGATTCGTTAATTAAGAAAAGACTGGAAGATTAAGAAAAG 1317  
DB 301 ACAGCTGTTGGGAAAGATTCGTTAATTAAGAAAAGACTGGAAGATTAAGAAAAG 360  
QY 1318 ATGGAAGAGGGTTTCTAGATGTTGACATTAATGCTGAGCTTTAGTTGATGAA 1377  
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QY 1378 AATG 1381  
DB 421 AATG 424

## RESULT 15

US-09-918-568-31  
Sequence 31, Application us/09918568  
Patent No. US20020054882A1

## GENERAL INFORMATION:

APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS

## SOFTWARE: wordperfect 5.1

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/918,568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995

APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993

ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250

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TELECOMMUNICATION INFORMATION:  
REFERENCE/DOCKET NUMBER: <Unknown>

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TELEPHONE: 202-721-8200  
TELECOMMUNICATION INFORMATION:  
REFERENCE/DOCKET NUMBER: <Unknown>

TELEFAX: 202-721-8250  
TELEPHONE: 202-721-8200  
TELECOMMUNICATION INFORMATION:  
REFERENCE/DOCKET NUMBER: <Unknown>

## US-09-918-568-31

Query Match 13.1%; Score 233.6; DB 9; Length 424;  
Best Local Similarity 71.9%; Pred. No. 1.2e-54;  
Matches 305; Conservative 0; Mismatches 119; Indels 0; Gaps 0;



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OY 958 CCTTTCACATGTCACCCACTGACATAGTGTGCGCCCAATATGTAAATCGGAG 1017
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 CCTTCCAGATGTATACCCAGTCACATAGGAGAGTGCCTCAAGTATGTCAGAGTACA 60
OY 1018 AAGTTGGCTTAGCAACAGGACTAAGAAATGTTCCCAATGTAATCAAGAGATGTTT 1077
    || || || || || || || || || || || || || || || || || || || || ||
Db 61 AAATTAGGATGGTTACAGGACTAAGGAACATCCCATCAATTCATCCAGAGTGTGTTT 120
OY 1078 GGGGCATAGCTGGTTTATAGAGGAGATGSCAAGAAATGTTGACGGTTGATGGA 1137
    || || || || || || || || || || || || || || || || || || || || ||
Db 121 GGAGCCATGCGCGGTTTCATTTGAAGGGGGGTGACTGSAATGATGATGGATGGTATGT 180
OY 1138 TACCATCAGACGAATACCCAGGATCAGGGATGTCAGACAGACAAGAAATCCACTCAAAAG 1197
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Db 181 TATCATCATCAGATTAACAAGATCTGGCTATGCTCGGATCAAAAAAGCACACAAAT 240
OY 1198 GCATTGATGGAATCACCAACAGGTAAATTCTGTGATGAAAAGATTAACACCCCAATT 1257
    || || || || || || || || || || || || || || || || || || || || ||
Db 241 GCCATTACGGGATTAACAACAAAGTGAATCTGTAAATCGAATAATGAACACTCAATTTC 300
OY 1258 GAAGCTGTGGGAATTAATGCTTAAGTGAAGAAAGACTGSAAGTGAACAAAG 1317
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Db 301 ACAGCTGTGGCAATTAATTCACAAATTGAAAGAAAGATGAAACCTTAATTAAGAAA 360
OY 1318 ATGGAAGACGGGTTTATAGATGCTGTGACATACAAATGCTGATTTAGTTCTGATGAA 1377
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Db 361 GTTGATGATGATTTTGTGACATTTGACATATATATGACAGATTTGTTGTTCTACTGGA 420
OY 1378 AATG 1381
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Db 421 AATG 424
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Job time : 289.395 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 19:23:49 ; Search time 57.7644 Seconds  
(without alignments)  
8672.640 Million cell updates/sec

Title: US-09-918-568-49

Perfect score: 1135

Sequence: 1 CTAGCAAGACGGGGTAT.....AACACCCCTGTTCTCTAG 1135

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 120691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued\_Patents\_NA:

1: /cgn2\_6/p10data/2/1na/5A\_COMB.seq:\*  
2: /cgn2\_6/p10data/2/1na/5B\_COMB.seq:\*  
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4: /cgn2\_6/p10data/2/1na/5B\_COMB.seq:\*  
5: /cgn2\_6/p10data/2/1na/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/p10data/2/1na/backfill1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1135	100.0	1135	1	US-08-229-781-49 Sequence 49, Appl
2	1135	100.0	1135	1	US-08-630-918-49 Sequence 49, Appl
3	1135	100.0	1135	1	US-09-004-422-49 Sequence 49, Appl
4	908.8	80.1	1783	1	US-08-229-781-46 Sequence 46, Appl
5	908.8	80.1	1783	1	US-08-630-918-46 Sequence 46, Appl
6	908.8	80.1	1783	1	US-09-004-422-46 Sequence 46, Appl
7	838	73.8	1728	1	US-08-229-781-28 Sequence 28, Appl
8	838	73.8	1728	1	US-08-630-918-28 Sequence 28, Appl
9	838	73.8	1728	1	US-09-004-422-28 Sequence 28, Appl
10	461.2	40.6	1721	3	US-08-686-968C-226 Sequence 226, App
11	451	39.7	1766	2	US-08-453-848-8 Sequence 8, Appl
12	451	39.7	1766	2	US-09-169-027-8 Sequence 8, Appl
13	448.6	39.5	1724	3	US-09-197-679A-1 Sequence 1, Appl
14	447.8	39.5	1754	1	US-08-229-781-27 Sequence 27, Appl
15	447.8	39.5	1754	1	US-08-630-918-27 Sequence 27, Appl
16	447.8	39.5	1754	1	US-09-004-422-27 Sequence 27, Appl
17	443	39.0	1701	3	US-09-232-468A-13 Sequence 13, Appl
18	443	39.0	1701	3	US-09-784-984B-11 Sequence 11, Appl
19	400	35.2	400	1	US-08-229-781-33 Sequence 33, Appl
20	400	35.2	400	1	US-08-630-918-33 Sequence 33, Appl
21	400	35.2	400	1	US-09-004-422-33 Sequence 33, Appl
22	397	35.0	409	1	US-08-229-781-34 Sequence 34, Appl
23	397	35.0	409	1	US-08-630-918-34 Sequence 34, Appl
24	397	35.0	409	1	US-09-004-422-34 Sequence 34, Appl
25	382.4	33.7	410	1	US-08-229-781-35 Sequence 35, Appl
26	382.4	33.7	410	1	US-08-630-918-35 Sequence 35, Appl
27	382.4	33.7	410	1	US-09-004-422-35 Sequence 35, Appl

28	379.6	33.4	394	1	US-08-229-781-36 Sequence 36, Appl
29	379.6	33.4	394	1	US-08-630-918-36 Sequence 36, Appl
30	379.6	33.4	394	4	US-09-004-422-36 Sequence 36, Appl
31	373	32.9	924	5	PCT-US94-01149-15 Sequence 15, Appl
32	372.6	32.8	810	5	PCT-US94-01149-19 Sequence 19, Appl
33	368.2	32.4	670	5	PCT-US94-01149-5 Sequence 5, Appl
34	361.4	31.8	912	5	PCT-US94-01149-31 Sequence 31, Appl
35	263.8	23.2	729	5	PCT-US94-01149-17 Sequence 17, Appl
36	263	23.2	1777	1	US-08-229-781-54 Sequence 54, Appl
37	263	23.2	1777	1	US-08-630-918-54 Sequence 54, Appl
38	263	23.2	1777	4	US-09-004-422-54 Sequence 54, Appl
39	259.2	22.8	630	5	PCT-US94-01149-21 Sequence 21, Appl
40	256.4	22.6	474	5	PCT-US94-01149-33 Sequence 33, Appl
41	254.6	22.4	1762	1	US-08-105-483-284 Sequence 284, App
42	254.6	22.4	1762	1	US-08-709-209-284 Sequence 284, App
43	254.6	22.4	1762	1	US-08-458-101-284 Sequence 284, App
44	253.6	22.3	1793	2	US-08-453-848-6 Sequence 6, Appl
45	253.6	22.3	1793	3	US-09-169-027-6 Sequence 6, Appl

## ALIGNMENTS

RESULT 1  
US-08-229-781-49  
Sequence 49, Application US/08229781  
Patent No. 5589174  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/229,781  
FILING DATE: April 19, 1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1135 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: A/Okuda/57  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:

HAFLTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELL:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-229-781-49

Query Match 100.0%; Score 1135; DB 1; Length 1135;  
Best Local Similarity 100.0%; Pred. No. 6.4e-315;  
Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGCAAAAGCAGGGGTTTATACCATGAAACCAAAAGCAAAATGGCCATCATTTAT 60  
DB 1 CTAGCAAAAGCAGGGGTTTATACCATGAAACCAAAAGCAAAATGGCCATCATTTAT 60  
QY 61 CTCATTCCTGCTGTCACAGCAGTGAAGGGGACCATGATGCTTGGATACCATGCAAT 120  
DB 61 CTCATTCCTGCTGTCACAGCAGTGAAGGGGACCATGATGCTTGGATACCATGCAAT 120  
QY 121 AATTCACAGAGAGAGGTCGACACAAATTTAGACGGAGCTCATGCTCATGCGCAAG 180  
DB 121 AATTCACAGAGAGAGGTCGACACAAATTTAGACGGAGCTCATGCTCATGCGCAAG 180  
QY 181 GACATCCTTGAGAAAGCCCATTAACGAAAGTTATGCAAACTAAACGATCCGGGATCATG 240  
DB 181 GACATCCTTGAGAAAGCCCATTAACGAAAGTTATGCAAACTAAACGATCCGGGATCATG 240  
QY 241 AAAACAGAGAGACCTTGAGAACTGTGAGACCAATGCCAAATCCTTTGGGAGACATA 300  
DB 241 AAAACAGAGAGACCTTGAGAACTGTGAGACCAATGCCAAATCCTTTGGGAGACATA 300  
QY 301 AATACACATTAACCTTTTACAAATGTCCACCACTGACAAATAGTGGCCCAATAT 360  
DB 301 AATACACATTAACCTTTTACAAATGTCCACCACTGACAAATAGTGGCCCAATAT 360  
QY 361 GTAATATGGAGAAAGTTGCTTTAGCAACAGACTAAGAAATTTCCCAAGATTGATCA 420  
DB 361 GTAATATGGAGAAAGTTGCTTTAGCAACAGACTAAGAAATTTCCCAAGATTGATCA 420  
QY 421 AGAGATTTGTTGGGCAATAGCTGTTTATAGAGAGAGATGGCAAGATGTTGAC 480  
DB 421 AGAGATTTGTTGGGCAATAGCTGTTTATAGAGAGAGATGGCAAGATGTTGAC 480  
QY 481 GGTGTATGATACCATCAGACAAATGACAGGGATGAGGATGACAGACAAAGAA 540  
DB 481 GGTGTATGATACCATCAGACAAATGACAGGGATGAGGATGACAGACAAAGAA 540  
QY 541 TCCACTCAAAAGGCAATTTGATGATCACCACAAAGTAAATTTCTGTGATGAAAAGATA 600  
DB 541 TCCACTCAAAAGGCAATTTGATGATCACCACAAAGTAAATTTCTGTGATGAAAAGATA 600

DB 541 TCCACTCAAAAGGCAATTTGATGATCACCACAAAGTAAATTTCTGTGATGAAAAGATA 600  
QY 601 AACACCAATTTGAACCTTTGGGAAAGAAATTCGGTAATTTAGAAAAAGCTGAGAAC 660  
DB 601 AACACCAATTTGAACCTTTGGGAAAGAAATTCGGTAATTTAGAAAAAGCTGAGAAC 660  
QY 661 TTGACAAAAAGATGAGACAGGCTTCTAGATGTGTGACATACAAATGCTGAGCTTTA 720  
DB 661 TTGACAAAAAGATGAGACAGGCTTCTAGATGTGTGACATACAAATGCTGAGCTTTA 720  
QY 721 GTTCTGATGAAAAATGAGAGACACTTCTCATGATTTATATGCAAGAACTGTAT 780  
DB 721 GTTCTGATGAAAAATGAGAGACACTTCTCATGATTTATATGCAAGAACTGTAT 780  
QY 781 AGTAAAGTCAGATGAGCTGAGAGACACGTCACAAAGAACTGAAATGATGTTTGA 840  
DB 781 AGTAAAGTCAGATGAGCTGAGAGACACGTCACAAAGAACTGAAATGATGTTTGA 840  
QY 841 TTTTATCACAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
DB 841 TTTTATCACAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
QY 901 CCCAAGTATGAGAGAGCTCTAAGTAACTAATGAAATGAAATGAAATGAAATGAGC 960  
DB 901 CCCAAGTATGAGAGAGCTCTAAGTAACTAATGAAATGAAATGAAATGAAATGAGC 960  
QY 961 AGCATGGGGTTTATCAATTCCTTGCATTTTGTCTAGAGACAGGTTCTATGTCATG 1020  
DB 961 AGCATGGGGTTTATCAATTCCTTGCATTTTGTCTAGAGACAGGTTCTATGTCATG 1020  
QY 1021 GCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080  
DB 1021 GCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080  
QY 1081 ATCTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1135  
DB 1081 ATCTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1135

## RESULT 2

US-08-630-918-49  
Sequence 49, Application US/08630918  
Patent No. 5631350  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,918  
FILING DATE: April 5, 1996  
CLASSIFICATION: 530  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8830  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1135 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
ORIGINAL SOURCE:  
ORGANISM: A/Okuda/57  
US-08-630-918-49

Query Match 100.0%; Score 1135; DB 1; Length 1135;  
Best Local Similarity 100.0%; Pred. No. 6, 4e-315;  
Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGCAAAAGCAGGCTTATACCATAGAAAACCAAAAGCAAAACATGCGCATCTTAT 60  
DB 1 CTAGCAAAAGCAGGCTTATACCATAGAAAACCAAAAGCAAAACATGCGCATCTTAT 60  
QY 61 CTCATTCTCCTGTTCTACAGAGTGAAGGGGACAGATATGCATTGGATACATGCCAAT 120  
DB 61 CTCATTCTCCTGTTCTACAGAGTGAAGGGGACAGATATGCATTGGATACATGCCAAT 120  
QY 121 AATTCACAGAGAGGTTCACACAAATTTAGAGCGGACGTCATCTGACTATGCCAAG 180  
DB 121 AATTCACAGAGAGGTTCACACAAATTTAGAGCGGACGTCATCTGACTATGCCAAG 180  
QY 181 GACATCCTTGAGAGAGCCCATACGGAAGTTATGCAAACTAACGATCCGGATCATG 240  
DB 181 GACATCCTTGAGAGAGCCCATACGGAAGTTATGCAAACTAACGATCCGGATCATG 240  
QY 241 AAAACGAAAGAACACCTGAGAACTGTGAGACCAATGCCAACTCTTTGGAGACAATA 300  
DB 241 AAAACGAAAGAACACCTGAGAACTGTGAGACCAATGCCAACTCTTTGGAGACAATA 300  
QY 301 AATACAACTTACCTTTTCACATGTCACCCACATGCAATAGTGTAGAGCCCAATAT 360  
DB 301 AATACAACTTACCTTTTCACATGTCACCCACATGCAATAGTGTAGAGCCCAATAT 360  
QY 361 GTAATAATCGAGAGAGTGTGCTTTAGCAACAGAGCTAAGGATGTTCCAGATTGATCA 420  
DB 361 GTAATAATCGAGAGAGTGTGCTTTAGCAACAGAGCTAAGGATGTTCCAGATTGATCA 420  
QY 421 AGAGATTTGTTGGGGTAATAGCTGTTTATAGAAAGAGATGCGAAGATGTTGAC 480  
DB 421 AGAGATTTGTTGGGGTAATAGCTGTTTATAGAAAGAGATGCGAAGATGTTGAC 480  
QY 481 GGTGGTATGATACCATACAGCAATGACCGAGGATGCAAGGATGACACAGCAAGAA 540  
DB 481 GGTGGTATGATACCATACAGCAATGACCGAGGATGCAAGGATGACACAGCAAGAA 540  
QY 541 TCCACTCAAAAGGCATTTGATGGAATCACCACAAAGTAATTTCTGTGATTGAAAGATA 600  
DB 541 TCCACTCAAAAGGCATTTGATGGAATCACCACAAAGTAATTTCTGTGATTGAAAGATA 600  
QY 601 AACACCCCAATTTGAGTTGTTGGGAAAGAAATTCGGAATCTTGAAGAAAGACTGAGAAC 660  
DB 601 AACACCCCAATTTGAGTTGTTGGGAAAGAAATTCGGAATCTTGAAGAAAGACTGAGAAC 660  
QY 661 TTGAACAAAAGATGAGAGCGGTTTCTAGATGTGTGACATACATGCTGAGCTTTTA 720  
DB 661 TTGAACAAAAGATGAGAGCGGTTTCTAGATGTGTGACATACATGCTGAGCTTTTA 720  
QY 721 GTTCTGATGAAATGAGAGCACTTGAATTCATGATTTAATGCAAGATCTGAT 780  
DB 721 GTTCTGATGAAATGAGAGCACTTGAATTCATGATTTAATGCAAGATCTGAT 780  
QY 781 AGTAAAGTGAATGCTGAGAGCAAGCTCAAAAGAACTGGAAGATGATGTTTGA 840  
DB 781 AGTAAAGTGAATGCTGAGAGCAAGCTCAAAAGAACTGGAAGATGATGTTTGA 840

DB 781 AGTAAAGTGAATGCTGAGAGCAAGCTCAAAAGAACTGGAAGATGATGTTTGA 840  
QY 841 TTTTATCACAATGTGATGTAATGCATGATGATGTAATGTAATGTAATGTAAT 900  
DB 841 TTTTATCACAATGTGATGTAATGCATGATGTAATGTAATGTAATGTAAT 900  
QY 901 CCCAATGAGAGAGCTTAACTAAATAGAAATGAAATCAAGGGGTAATGAGC 960  
DB 901 CCCAATGAGAGAGCTTAACTAAATAGAAATGAAATCAAGGGGTAATGAGC 960  
QY 961 AGCATGGGGTTTATCAATCTTCCATTTATGCTACAGTAGCAGTTCTATGTCAG 1020  
DB 961 AGCATGGGGTTTATCAATCTTCCATTTATGCTACAGTAGCAGTTCTATGTCAG 1020  
QY 1021 GCAATCATATGCTGGGATCTTCTGCGTGTCCAGCGGTCCTGCAAGTCAG 1080  
DB 1021 GCAATCATATGCTGGGATCTTCTGCGTGTCCAGCGGTCCTGCAAGTCAG 1080  
QY 1081 ATCTGATATGATTAATGATTTATTAATTAATTAATTAATTAATTAATTAAT 1135  
DB 1081 ATCTGATATGATTAATGATTTATTAATTAATTAATTAATTAATTAATTAAT 1135

RESULT 3  
US-09-004-422-49  
Sequence 49, Application US/09004422  
Patent No. 6337070  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/004,422  
FILING DATE: January 8, 1998  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1135 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL:

ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: A/Okuda/57  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-09-004-422-49

Query Match 100.0%; Score 1135; DB 4; Length 1135;  
Best Local Similarity 100.0%; Pred. No. 6.4e-315;  
Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGCAAAAGCGGGGTTATACCATAGAAAACCAAAAGCAAAACCAATGGCCATCATTTAT 60  
DB 1 CTAGCAAAAGCGGGGTTATACCATAGAAAACCAAAAGCAAAACCAATGGCCATCATTTAT 60  
QY 61 CTCATTCCTCTGTCACAGCAGTGAAGGGGACCATGATTCGATTCGATACCATGCCAT 120  
DB 61 CTCATTCCTCTGTCACAGCAGTGAAGGGGACCATGATTCGATTCGATACCATGCCAT 120  
QY 121 AATTCACAGAGAAGGTGACACAAATTCAGAGCGGAACGTCAGTGTGATGATGCCAAG 180  
DB 121 AATTCACAGAGAAGGTGACACAAATTCAGAGCGGAACGTCAGTGTGATGATGCCAAG 180  
QY 181 GACATCCTTGAGAGAACCCATAGCGAAAGTTATGCAAACTAAACGGATCCGGGATCATG 240  
DB 181 GACATCCTTGAGAGAACCCATAGCGAAAGTTATGCAAACTAAACGGATCCGGGATCATG 240  
QY 241 AAAACAGAGAACCTTGAGAGACCTGTGAGACCAATGCCAAATCCTTTGGAGACAATA 300  
DB 241 AAAACAGAGAACCTTGAGAGACCTGTGAGACCAATGCCAAATCCTTTGGAGACAATA 300  
QY 301 AATACACATTAACCTTTTACAAATGCCACCACTGACAAATAGTGAGTGGCCCAATAT 360  
DB 301 AATACACATTAACCTTTTACAAATGCCACCACTGACAAATAGTGAGTGGCCCAATAT 360  
QY 361 GTAAATGAGAGAACTGTGCTTACCAACAGGACTAAGGAATGTTCCCGAGATTGATCA 420  
DB 361 GTAAATGAGAGAACTGTGCTTACCAACAGGACTAAGGAATGTTCCCGAGATTGATCA 420  
QY 421 AGAGATGTTTGGGGCAATAGCTGTGTTTATAGAGAGAGATGGCAAGGAATGTTGAC 480  
DB 421 AGAGATGTTTGGGGCAATAGCTGTGTTTATAGAGAGAGATGGCAAGGAATGTTGAC 480

QY 481 GGTGGTATGATACCATCAGCAATGACCGAGGATCGGGTATGACAGACAAGAA 540  
DB 481 GGTGGTATGATACCATCAGCAATGACCGAGGATCGGGTATGACAGACAAGAA 540  
QY 541 TCCACTCAAAAGCATTTGATGGAATCACAACAAGGTAATTTCTGTATGAAAGATA 600  
DB 541 TCCACTCAAAAGCATTTGATGGAATCACAACAAGGTAATTTCTGTATGAAAGATA 600  
QY 601 AACACCAATTTGAAGCTGTTGGGAAGAAATTCGTAATCTAGACAAAAGCTGAGAAC 660  
DB 601 AACACCAATTTGAAGCTGTTGGGAAGAAATTCGTAATCTAGACAAAAGCTGAGAAC 660  
QY 661 TTGAACAAAAGATGGAAGAGCGGTTCTAGATGTGAGACATCAATGCTGACTTTTA 720  
DB 661 TTGAACAAAAGATGGAAGAGCGGTTCTAGATGTGAGACATCAATGCTGACTTTTA 720  
QY 721 GTTCGTATGAAATGAGAGACACTTGACATTTCAATGATTCATGTCAGAAATCTGTAT 780  
DB 721 GTTCGTATGAAATGAGAGACACTTGACATTTCAATGATTCATGTCAGAAATCTGTAT 780  
QY 781 AGTAAAGTGAATGACGCTGAGAGACAACGTCAAAGACTAGCAATGATGTTTGA 840  
DB 781 AGTAAAGTGAATGACGCTGAGAGACAACGTCAAAGACTAGCAATGATGTTTGA 840  
QY 841 TTTTATCACAATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
DB 841 TTTTATCACAATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
QY 901 CCCAAGTATGAAGAGTCTAACTAAATGAATGAATGAATGAATGAATGAATGAAT 960  
DB 901 CCCAAGTATGAAGAGTCTAACTAAATGAATGAATGAATGAATGAATGAATGAAT 960  
QY 961 ACATGAGGGTTATCAAAATCTTCCCATTTATGCTAAGTAGAGAGTTCTATGCTG 1020  
DB 961 ACATGAGGGTTATCAAAATCTTCCCATTTATGCTAAGTAGAGAGTTCTATGCTG 1020  
QY 1021 GCAATCATGATGCTGCGGATCTCTTCTGGGTCCTCAACGGGTCCTGCAATGAGG 1080  
DB 1021 GCAATCATGATGCTGCGGATCTCTTCTGGGTCCTCAACGGGTCCTGCAATGAGG 1080  
QY 1081 ATCTGCATATGATTAAGTCAATTTTAAATTAATAAACACCCCTGTTCTGCTAG 1135  
DB 1081 ATCTGCATATGATTAAGTCAATTTTAAATTAATAAACACCCCTGTTCTGCTAG 1135

RESULT 4  
US-08-229-781-46  
; Sequence 46, Application US/08229781  
; Patent No. 5589174  
; GENERAL INFORMATION:  
; APPLICANT: Yoshinobu OKUNO et al.  
; TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/229,781  
; FILING DATE: April 19, 1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/054,016  
; FILING DATE: April 29, 1993

ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 83,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8860  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1783 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cdna to genomic RNA  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: A/Okuda/57  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-229-781-46

Query Match 80.1%; Score 908.8; DB 1; Length 1783;  
Best Local Similarity 98.7%; Pred. No. 3.7e-250;  
Matches 916; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 208 AAGTATGCAACTAAACGATCCGGATCATGAAAAAGAGAGAACACTTGAGAACTGT 267  
DB 853 AAGATATCGAAAAAGAGTAGTGTGAGGAGCAATTAATACACATTACCTTTTCAAAATGTC 912  
QY 268 GAGACCAAAATGCCAACTCCTTTGGGAGCAATAAACAACATTACCTTTTCACATGTC 327  
DB 913 GAGACCAAAATGCCAACTCCTTTGGGAGCAATTAATACACATTACCTTTTCAAAATGTC 972  
QY 328 CACCCACTGCAATAGTGTAGTCCCAAAATATGTAATCGAGAGAGTGTGCTTAGCA 387  
DB 973 CACCCACTGCAATAGTGTAGTCCCAAAATATGTAATCGAGAGAGTGTGCTTAGCA 1032  
QY 388 ACAGGACTAAGAAATGTTCCCGAGATTGAATCAAGAGAGATTGTTGGGGCAATAGCTGCT 447  
DB 1033 ACAGGACTAAGAAATGTTCCCGAGATTGAATCAAGAGAGATTGTTGGGGCAATAGCTGCT 1092

QY 448 TTTATAGAGAGATGCAAGGAATGTTGACGGTTGTATGGATACCATCAGCAAT 507  
DB 1093 TTTATAGAGAGATGCAAGGAATGTTGACGGTTGTATGGATACCATCAGCAAT 1152  
QY 508 GACCAGGATCAGGGATGTCAGCAGACACAAGAAATCCACTCAAAAGCATTTGATGAATC 567  
DB 1153 GACCAGGATCAGGGATGTCAGCAGACACAAGAAATCCACTCAAAAGCATTTGATGAATC 1212  
QY 568 ACCAACAAGTAAATTTGTGATTGTAAGATAACACCCAAATTTGAAGCTGTTGGGAAA 627  
DB 1213 ACCAACAAGTAAATTTGTGATTGTAAGATAACACCCAAATTTGAAGCTGTTGGGAAA 1272  
QY 628 GAATTCGTAAGTATAGAGAAAAGACTGAGAACTTGAACAAAAGATGGAAGAGCGGTTT 687  
DB 1273 GAATTCGTAAGTATAGAGAAAAGACTGAGAACTTGAACAAAAGATGGAAGAGCGGTTT 1332  
QY 688 CTAGATGTGTGACATCAATGCTGACCTTTTACTGTGATGGAATAAGAGAGACACTT 747  
DB 1333 CTAGATGTGTGACATCAATGCTGACCTTTTACTGTGATGGAATAAGAGAGACACTT 1392  
QY 748 GACTTTGATGATCTAATGTCAGAAATCTGTATAGTAAGTCAGAAATGCAAGAGAC 807  
DB 1393 GACTTTGATGATCTAATGTCAGAAATCTGTATAGTAAGTCAGAAATGCAAGAGAC 1452  
QY 808 AACGTCAAGACATGAGAAATGATGTTTGAATTTATCAAAATGATGATGATGTC 867  
DB 1453 AACGTCAAGACATGAGAAATGATGTTTGAATTTATCAAAATGATGATGATGTC 1512  
QY 868 ATGAATAGTGTGAAAAAGGAGCATATGATATCCCAAGTATGAAAGAGATCAAACTA 927  
DB 1513 ATGAATAGTGTGAAAAAGGAGCATATGATATCCCAAGTATGAAAGAGATCAAACTA 1572  
QY 928 AATAGAAATGAATCAAAAGGGGTAAATTTGAGCAGCATGGGGTTTATCAAAATCCTTGGC 987  
DB 1573 AATAGAAATGAATCAAAAGGGGTAAATTTGAGCAGCATGGGGTTTATCAAAATCCTTGGC 1632  
QY 988 ATTTATGCTCAGTACAGGAGTTCATGTCACTGCAATCATGATGCTGGGATCTTTTC 1047  
DB 1633 ATTTATGCTCAGTACAGGAGTTCATGTCACTGCAATCATGATGCTGGGATCTTTTC 1692  
QY 1048 TGGGTGTGTCCAACGGGCTCTGCACTGCAAGATGCAATGATGATTAAGTCAATTTTA 1107  
DB 1693 TGGGTGTGTCCAACGGGCTCTGCACTGCAAGATGCAATGATGATTAAGTCAATTTTA 1152  
QY 1108 TAATTAATAACACCTTGTCTGCTAG 1135  
DB 1753 TAATTAATAACACCTTGTCTGCTAG 1780

RESULT 5  
US-08-630-918-46  
Sequence 46, Application US/08630918  
Patent No. 5631350  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
City: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,918  
FILING DATE: April 5, 1996





FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: A/Okuda/57  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-09-004-422-46

Query Match 80.1%; Score 908.8; DB 4; Length 1783;  
Best Local Similarity 98.7%; Pred. No. 3.7e-250;  
Matches 916; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 208 AAGTATGCAACTAAAGGATCGGGATGATGAAAAAGAGAGACACTTGAAGCTGT 267  
DB 853 AAATATGCAAGAAAGAGTGTAGTTCAGGGATGATGAAAAAGAGAGACACTTGAAGCTGT 912  
QY 268 GAGACCAATGCCAATCTCTTGGGAGCAATAATCAACATTACTCTTTCACAAATGTC 327  
DB 913 GAGACCAATGCCAATCTCTTGGGAGCAATAATCAACATTACTCTTTCACAAATGTC 972  
QY 328 CACCACTGCAATAGGTGAGTCCCCCAATATGTAATCGGAGAGTGGCTTTAGCA 387  
DB 973 CACCACTGCAATAGGTGAGTCCCCCAATATGTAATCGGAGAGTGGCTTTAGCA 1032  
QY 388 ACAGGACTAAGAAATTTCCCAAGATTGAATCAAGAGATTGTTGGGGCAATAGCTGT 447  
DB 1033 ACAGGACTAAGAAATTTCCCAAGATTGAATCAAGAGATTGTTGGGGCAATAGCTGT 1092  
QY 448 TTTATGAAGAGAGATGCGAAGATGCGTGGATGATGATACATCAGCAAT 507  
DB 1093 TTTATGAAGAGAGATGCGAAGATGCGTGGATGATGATACATCAGCAAT 1152  
QY 508 GACCAAGGATCAGGATGATGCGAGAGACAAAGATCCACTAAAAGCATTTGATGCAATC 567  
DB 1153 GACCAAGGATCAGGATGATGCGAGAGACAAAGATCCACTAAAAGCATTTGATGCAATC 1212  
QY 568 ACCAACAAGTAAATTTGATGATGAAAGATTAACACCAATTTGAAGCTGTGGGAAA 627  
DB 1213 ACCAACAAGTAAATTTGATGATGAAAGATTAACACCAATTTGAAGCTGTGGGAAA 1272  
QY 628 GAATTCGTAACCTTAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 687  
DB 1273 GAATTCGTAACCTTAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1332

QY 688 CTAGATGTGCGACATACAAATGCTGAGCTTTTACTGTGATGAAATGAGAGACACTT 747  
DB 1333 CTAGATGTGCGACATACAAATGCTGAGCTTTTACTGTGATGAAATGAGAGACACTT 1392  
QY 748 GACTTTCATGATTTTATGTCACAAATCTGATAGTAAAGTCACAAATGCTGAGAGC 807  
DB 1393 GACTTTCATGATTTTATGTCACAAATCTGATAGTAAAGTCACAAATGCTGAGAGC 1452  
QY 808 AACGTCAAG 867  
DB 1453 AACGTCAAG 1512  
QY 868 ATGATAGTGTGAAAAACGGGACATATGATTTATCCAGATGAAAGAGAGAGAGAGAG 927  
DB 1513 ATGATAGTGTGAAAAACGGGACATATGATTTATCCAGATGAAAGAGAGAGAGAGAG 1572  
QY 928 AATGAAATGAAATCAAGGGGTAAATTTGAGCAGATGGGGGTTTATCAATCTTGGC 987  
DB 1573 AATGAAATGAAATCAAGGGGTAAATTTGAGCAGATGGGGGTTTATCAATCTTGGC 1632  
QY 988 ATTTATGCTACAGTACAGGAGTCTGATGTCACATGCAATGATGAGCTGGGATCTTTC 1047  
DB 1633 ATTTATGCTACAGTACAGGAGTCTGATGTCACATGCAATGATGAGCTGGGATCTTTC 1692  
QY 1048 TGGGTGTCTCCAAAGGGTCTCTGACATGAGATGCAATGATGATTAAGTCAATTTTA 1107  
DB 1693 TGGGTGTCTCCAAAGGGTCTCTGACATGAGATGCAATGATGATTAAGTCAATTTTA 1752  
QY 1108 TAATTAATAAACACCTTGTCTGCTAG 1135  
DB 1753 TAATTAATAAACACCTTGTCTGCTAG 1780

RESULT 7  
US-08-229-781-28  
Sequence 28, Application US/08229781  
Patent No. 5589174  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/229,781  
FILING DATE: April 19, 1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SRO ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1728 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double





CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-09-004-422-28

Query Match 73.8%; Score 838; DB 4; Length 1728;  
Best Local Similarity 95.6%; Pred. No. 6,5e-230;  
Matches 862; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 208 AAGTATGCAAACTAAACGATCCGGATCATGAAACAGAGAGACACTTGAGACTGT 267  
DB 827 AAATATCGAAAGAGAGTAGTTCAGGATCATGAAAGACAGAGACACTTGAGACTGT 886  
QY 268 GAGACCAAAATGCCAACTCTTTGGGAGCAATAATACACATTACCTTTTACAAATGTC 327  
DB 887 GAGACCAAAATGCCAACTCTTTGGGAGCAATAATACACACTACCTTTTACAAATGTC 946  
QY 328 CACCCACTGACAAATAGTGTAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 387  
DB 947 CACCCACTGACAAATAGTGTAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1006  
QY 388 AAGGACTAAGGAAATGTTCCCGCATTTGAATCAAGAGAGATTTGGGGCAATAGCTGT 447  
DB 1007 AAGGACTAAGGAAATGTTCCCGCATTTGAATCAAGAGAGATTTGGGGCAATAGCTGT 1066  
QY 448 TTTATGAGAGAGATGCGAAGAGATGTTGAGGTTGATGATACATACATGATGATG 507  
DB 1067 TTTATGAGAGAGATGCGAAGAGATGTTGAGGTTGATGATACATACATGATGATG 1126  
QY 508 GACCAAGGATCAAGGATGATGACAGACAGAAAGATCCACTCAAAAGCATTTGATGATG 567  
DB 1127 GACCAAGGATCAAGGATGATGACAGACAGAAAGATCCACTCAAAAGCATTTGATGATG 1186  
QY 568 ACCAACAAGTAAATCTGATGATGAAAGATTAACACCAATTTGAGCTGTGGGAAA 627  
DB 1187 ACCAACAAGTAAATCTGATGATGAAAGATTAACACCAATTTGAGCTGTGGGAAA 1246  
QY 628 GAATTCGTAAGTGAAGAAAGACTGAGAACTTAACAAAAGATGGAAGCGGGTTT 687  
DB 1247 GAATTCGTAAGTGAAGAAAGACTGAGAACTTAACAAAAGATGGAAGCGGGTTT 1306  
QY 688 CTAGATGCTGACATACAAATCTGAGCTTTAGTTCTGATGGAAGATGAGAGACATT 747  
DB 1307 CTAGATGCTGACATACAAATCTGAGCTTTAGTTCTGATGGAAGATGAGAGACATT 1366  
QY 748 GACTTCGTAAGTGAAGAAAGACTGAGAACTTAACAAAAGATGGAAGCGGGTTT 807  
DB 1367 GACTTCGTAAGTGAAGAAAGACTGAGAACTTAACAAAAGATGGAAGCGGGTTT 1426  
QY 808 AAGCTCAAGAACTGGAAGATGTTGAAATTTATCACAATGATGATGATGATGATG 867  
DB 1427 AAGCTCAAGAACTGGAAGATGTTGAAATTTATCACAATGATGATGATGATGATG 1486  
QY 868 ATGATAGTGTGAAAAACGGGACATATGATTTCCAGATGAGAGAGAGCTTAACCTA 927

DB 1487 ATGATAGTGTGAAAAACGGGACATATGATTTATCCAGATGAGAGAGAGCTTAACCTA 1546  
QY 928 AATGAAATGAAATCAAGGGGTAAATTTGAGAGCATGAGGGGTTTATCAATCTTCC 987  
DB 1547 AATGAAATGAAATCAAGGGGTAAATTTGAGAGCATGAGGGGTTTATCAATCTTCC 1606  
QY 988 ATTATGCTAGATGAGAGTTCATGCTACCTGCAATCATGATGAGCTGATCTCTTC 1047  
DB 1607 ATTATGCTAGATGAGAGTTCATGCTACCTGCAATCATGATGAGCTGATCTCTTC 1666  
QY 1048 TGGGTGCTCCACAGGCTCTGCAATGAGATGCTGCAATGATGATGATGATGATG 1107  
DB 1667 TGGGTGCTCCACAGGCTCTGCAATGAGATGCTGCAATGATGATGATGATGATG 1726  
QY 1108 TA 1109  
DB 1727 TA 1728

RESULT 10  
US-08-686-968C-226  
Sequence 226, Application US/08686968C  
Patent No. 6221361  
GENERAL INFORMATION:  
APPLICANT: Cochran, Mark D.  
APPLICANT: Junker, David E.  
TITLE OF INVENTION: Recombinant Swinepox Virus  
FILE REFERENCE: 39119-H/JML  
CURRENT APPLICATION NUMBER: US/08/686, 968C  
CURRENT FILING DATE: 1996-07-25  
NUMBER OF SEQ ID NOS: 231  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 226  
LENGTH: 1721  
TYPE: DNA  
ORGANISM: Swinepox virus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1707)  
US-08-686-968C-226

Query Match 40.6%; Score 461.2; DB 3; Length 1721;  
Best Local Similarity 70.5%; Pred. No. 3.7e-122;  
Matches 616; Conservative 0; Mismatches 258; Indels 0; Gaps 0;

QY 226 GATCCGGGATCATGAAACAGAGAGACACTTGAGAACTGTGAGACCAATGCCAACT 285  
DB 844 GATCCGGGATCATGAAACAGAGAGACACTTGAGAACTGTGAGACCAATGCCAACT 903  
QY 286 CTTTGGGAGCAATAATACACATTCCTTTTCAATGTCACCCACTGCANTAGT 345  
DB 904 CTTTGGGAGCAATAATACACATTCCTTTTCAATGTCACCCACTGCANTAGT 963  
QY 346 GATGCCCAATATGTAATTCGAGAACTGCTTACCAACAGCACTAAGAACTT 405  
DB 964 GATGCCCAATATGTAATTCGAGAACTGCTTACCAACAGCACTAAGAACTT 1023  
QY 406 CCCAGATTAAGTCAAGAGATGTTGGGGCAATGCTGTTTATGAGAGAGATG 465  
DB 1024 CCCAGATTAAGTCAAGAGATGTTGGGGCAATGCTGTTTATGAGAGAGATG 1083  
QY 466 CAAGAAATGTTGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATG 525  
DB 1084 CAAGAAATGTTGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATG 1143  
QY 526 GAGAGACAAAGATTCATCAAAAGCATTTGATGATGATGATGATGATGATGATGATG 585  
DB 1144 GAGAGACAAAGATTCATCAAAAGCATTTGATGATGATGATGATGATGATGATGATG 1203  
QY 586 GTGATGAAAGATTAACACCAATTTGAACTGTGGGAAAGATTCGTAACCTTAC 645  
DB 1204 GTGATGAAAGATTAACACCAATTTGAACTGTGGGAAAGATTCGTAACCTTAC 1263

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QY 646 AAAAGACTGAGAACTTGACAAAAGATGAGAACGGGTTTCTAGATGTGAGACTAC 705
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1264 AAAAGATAGAGAACTTAAACAAAAGCTGATGATGTTTCTGATGTTTGGACTTAC 1323
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 706 AATGCTGAGCTTTTATTTCTGATGAGAAATGAGAGACACTTACTTTCATGATTCAT 765
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1324 AATGCCGAAGCTTTGTTTCTATGAGAAATGAGAAAGCTTGGATATATCAGATTCAT 1383
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 766 GTCAAGATCTGTATAGTAAGTCAGATTCAGCTGAGAGACACGTCAGAACTAGCA 825
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1384 GTGAAGAACTTAATATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1443
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 826 AATGATGTTTGAATTTTATCACAATGTGATGATGATGATGATGATGATGATGATG 885
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1444 AATGCGCTGCTTGAATTTTACACAAATGTGATGACAGCGTGTGAGAGCGTCACAAAT 1503
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 886 GGGACATGATGATTTATCCCAAGTATGAGAGAGCTTAACCTAAATGAGAAATCMAA 945
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1504 GGGACTTATGATTAACCAAAATCTCAGAGAGAGAGAGAGAGAGAGAGATGAT 1563
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 946 GGGGTAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1005
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1564 GGGGTAAGCTGGAATCAACAGAGATTTACAGATTTGGGAGATCAATCAACTGTCCGC 1623
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1006 GGTCTATGCTCACTGCAATCATGATGAGCTGGATCTCTTCTGGGAGTGTCCAGAGGG 1665
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1624 AGTTCATGCTACTGTAGTCTCTCCCTGGGGCAATCGTTTCTGAGATGTCTCAATGGG 1683
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1066 TCTCTGAGAGTGCAGAGATCTGCAATGATGATTAAG 1099
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1684 TCTTTACAGTGAGAGATATGATTTTAAATTAAG 1717
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 11
US-08-453-848-8
; Sequence 8, Application US/08453848
; Patent No. 5858368
; GENERAL INFORMATION:
; APPLICANT: Smith, Gale Eugene
; APPLICANT: Voikovitz, Franklin
; APPLICANT: Wilkinson, Bithanie Eident
; APPLICANT: Voznesensky, Andrei I.
; APPLICANT: Hackett, Craig Stanley
; TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA
; TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Babst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; City: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA
; APPLICATION NUMBER: US/08/453,848
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/120,607
; FILING DATE: 13-SEPT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Babst, Patrea L.
; REGISTRATION NUMBER: 1,284
; REFERENCE/DOCKET NUMBER: MGS101CIP
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1766 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Influenza virus
; INDIVIDUAL ISOLATE: A/Texas/36/91 rHA
; FEATURE:
; NAME/KEY: polyhedrin mRNA leader (partial)
; LOCATION: 1 to 18
; FEATURE:
; NAME/KEY: coding region for AcNPV 61k protein signal
; NAME/KEY: peptide
; LOCATION: 19 to 72
; FEATURE:
; NAME/KEY: SmaI restriction site
; LOCATION: 76 to 81
; FEATURE:
; NAME/KEY: KpnI restriction site
; LOCATION: 82 to 87
; FEATURE:
; NAME/KEY: SmaI restriction site
; LOCATION: 88 to 93
; FEATURE:
; NAME/KEY: coding region for mature rHA
; LOCATION: 73 to 1734
; FEATURE:
; NAME/KEY: KpnI restriction site
; LOCATION: 1744 to 1749
; FEATURE:
; NAME/KEY: BglII restriction site
; LOCATION: 1750 to 1755
; FEATURE:
; NAME/KEY: universal translation termination signal
; LOCATION: 1756 to 1766
; US-08-453-848-8

Query Match 39.7%; Score 451; DB 2; Length 1766;
Best Local Similarity 70.0%; Pred. No. 3,1e-119;
Matches 607; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

QY 226 GATCCGGGATCATGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 285
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 877 GGGTCAGAGATCATCTCAACGATCATGATGATGATGATGATGATGATGATGATGATG 936
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 286 CCTTTGGAGAGATTAATACACATTACCTTTTACAGATGTCACCCACTGACAAATAGT 345
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 937 CCCAGGAGAGCTATAACAGTAGTCTTCTTCCAGAAATGTACACCCAGACACATAGCA 996
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 346 GAGTGGCCCAATATGTAAATGCGAGAGAGTGTGTTAGCAACAGAGACTAAGCAATGT 405
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 997 GAGTGTCCAAAGTATCTGAGAGATACAAATTAAGATGTTTACAGACTTAAGAAATC 1056
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 406 CCCAGATGATGATGAGAGAGATGTTTGGGCAATAGCTGTTTATGAGAGAGAGATG 465
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1057 CCATCCATTCATCCAGAGAGGTTTGTGAGAGCCATTCGCGTTTCAATGAGAGAGG 1116
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 466 CAAGATGCTGAGAGGTTGATATGATACCATCAGAGCAATGACAGAGAGATCAGGAT 525
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1117 ACTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1176
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 526 GCAGCAGACAAAGATCCATCAAAAGGCAATTTGATGATGATGATGATGATGATGATG 585
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1177 GCTGCGGACCAAAAAGACACACAAATGCCATTAAAGGATGATGATGATGATGATGAT 1236
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 586 GTGATGAAAGATATAACACCCCAATTTGAAGCTGTTGGAAGAGAAATTCGTAATTAAG 645
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 1237 GTAATCGAGAAATTAACACTCAATTCACAGCTGTGGCCAAAGAAATTAACAATTAGAA 1296  
Qy 646 AAAACAGCGAGAACTTGAAACAAAAGATGAAAGCGGTTTCTTATATGTGGACATAC 705  
Db 1297 AGAAGATGAGAAACTTAATAAAGAGTTGATGATGATTTCTTGACATTTGACATATAT 1356  
Qy 706 AATGCTGAGCTTTTACTGATGAGAAATGAGAGACACTTGACTTTCATGATCTTAAT 765  
Db 1357 AATGAGATTTGTTGTTCTTACTGGAATGAGAGACTTTGATTTTCTGACTCAAT 1416  
Qy 766 GTCAAGAAATCTGTATAGTAAGTCAAGATGCACTGAGACACAGCTCAAGAAGTACA 825  
Db 1417 GTGAAGAAATCTGTATAGTAAGTAAGAAAGCCAAATGAAATAGCCAAAGAAATAGCG 1476  
Qy 826 AATGATGTTTGAATTTTATCAAAATGTGATGATGATGATGATGATGATGATGATGAT 885  
Db 1477 AAGGCTGTTTGAATTTCTATCAAAAGTGTAAAGTAAGTAAGTAAGTAAGTAAGTAAG 1536  
Qy 886 GGAACATATGATTTATCCCAAGTATGAGAGAGTCAATTAATTAATGAATGAATCAAA 945  
Db 1537 GGAACATATGATTTATCCCAAGTATGAGAGAGTCAATTAATTAAGCGGGAATTAAT 1596  
Qy 946 GGGGTAATTTGAGCAGATGGGGTTTATCAATCTTCCATTTATGCTACAGTAGCA 1005  
Db 1597 GGAGGAATTTGGAATCAATGAGAGTCAATGATGATGATGATGATGATGATGATGATG 1656  
Qy 1006 GGTTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1065  
Db 1657 AGTTCACGTGCTGCTTTTGTCTCCCTGGGGGCAATCAGCTTCTGATGATGATGATG 1716  
Qy 1066 TCTTCGAGTGCAGAGATGCTGATGCA 1092  
Db 1717 TCTTCGAGTGCAGAGATGATGATGCA 1743

## RESULT 12

US-09-169-027-8

Sequence 8, Application US/09169027

Patent No. 6245532

GENERAL INFORMATION:

APPLICANT: Smith, Gale Eugene

APPLICANT: Volvovitz, Franklin

APPLICANT: Wilkinson, Bethanie Eident

APPLICANT: Voznesensky, Andrei I.

TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESS: Patrea L. Pabst

STREET: 2800 One Atlantic Center

STREET: 1201 West Peachtree Street

CITY: Atlanta

STATE: GA

COUNTRY: USA

ZIP: 30309-3450

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/169,027

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/453,848

FILING DATE: 30-MAY-1995

APPLICATION NUMBER: 08/120,607

FILING DATE: 13-SEPT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: MGS101CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-873-8794  
TELEFAX: (404)-873-8795  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1766 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Influenza virus  
INDIVIDUAL ISOLATE: A/Texas/36/91 rHA  
FEATURE:  
NAME/KEY: polynuclein mRNA leader (partial)  
LOCATION: 1 to 18  
FEATURE:  
NAME/KEY: coding region for ACPV 61k protein signal  
LOCATION: 19 to 72  
FEATURE:  
NAME/KEY: SmaI restriction site  
LOCATION: 76 to 81  
FEATURE:  
NAME/KEY: KpnI restriction site  
LOCATION: 82 to 87  
FEATURE:  
NAME/KEY: SmaI restriction site  
LOCATION: 88 to 93  
FEATURE:  
NAME/KEY: SmaI restriction site  
LOCATION: 94 to 100  
FEATURE:  
NAME/KEY: coding region for mature rHA  
LOCATION: 101 to 1766  
FEATURE:  
NAME/KEY: KpnI restriction site  
LOCATION: 1744 to 1749  
FEATURE:  
NAME/KEY: BglII restriction site  
LOCATION: 1750 to 1755  
FEATURE:  
NAME/KEY: universal translation termination signal  
LOCATION: 1756 to 1766

## Query Match

39.7%; Score 451; DB 3; Length 1766;

Best Local Similarity 70.0%; Pred. No. 3,1e-119;

Matches 607; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

Qy 226 GATTCGGGATCATCAAAAACAGAGACACTTGAGAACTGTGACCAATGCAACT 285  
Db 877 GGTGAGAGATCATCACTCAAGCAATGATGATGATGATGATGATGATGATGATG 936  
Qy 286 CTTTGGAGCAATTAATCAACATTAATCAATGATGATGATGATGATGATGATGATG 345  
Db 937 CCCCAGGAGCATATAACAGTAGTCTTCCAGATGTACACCCAGTCACATAGGA 996  
Qy 346 GAGTCCCAATATGTAATAATCGAGAGTTGGTCTTACGACAGAGCACTAAGCAATGT 405  
Db 997 GAGTCCCAATATGTAATAATCGAGAGTTGGTCTTACGAGAGCACTAAGCAATGT 1056  
Qy 406 CCCCAGATGTAATCAAGAGATTTGTTGGGCAATACGTGTTTATAGAAGAGATGG 465  
Db 1057 CATTCCATTAATCAAGAGATTTGTTGGGCAATACGTGTTTATAGAAGAGATGG 1116  
Qy 466 CAAGGATGTTGAGAGTTGATGATGATGATGATGATGATGATGATGATGATGATG 525  
Db 1117 ACTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1176  
Qy 526 GCAGCAGCAAAAGATCCACTCAAAAGCAATTTGATGATGATGATGATGATGATGAT 585

Db 1177 GCTGCGGACCAAAAAGCACAACAAATGCCATTACGGGATTTACAAACAGTGAAATCT 1236  
QY 586 GTGATTTGAAAAGATTAACACCAATTTGAAGCTGTGGGAAAGATTTGGTAACCTTAGAG 645  
Db 1237 GTATGAGAAAATGAAACACTCAATTCACAGCTGTGGGCAAAAGATTTCAAAATTTAGAA 1296  
QY 646 AAAAGACTGGAGAACTTGAACAAAAGATGGAAGAGCGGTTTCTAGATGTGTGAGACATAC 705  
Db 1297 AGAAGATGGAACCTTAATAAATAAGATGATGATGATTTCTGGACATTTGACATAT 1356  
QY 706 AATGCTGAGCTTTTAAATTTGATGAGAAATGAGAGCACTTGACTTTCAATTTCTAAT 765  
Db 1357 AATGCGAAATTTGTTGTTCTTACTAGAAAATGGAAGCACTTTGGATTTTCATGACTCAAT 1416  
QY 766 GTCAAGATCTGTATAGTAAGTCAGATGACAGTGGAGCAACGCAAGCAAGCAAGCA 825  
Db 1417 GTGAGAGATCTGTATAGTAAGTAAGTAAGCAATTTGAAGATATATGCAAGAAATAGGG 1476  
QY 826 AATGAGATTTTGAATTTTATCAAAATGTATGATGAATGATGAATAGTGAATAAC 885  
Db 1477 AAGGGGTGTTTGAATTTCTATCAAGATGTATACAAATGATGATGAAAGTGTGAATAAT 1536  
QY 886 GGAACATATGATTTATCCAAATGTGAAGAAAGACTTAACATAATGAAATGAATCAAA 945  
Db 1537 GGAACCTATGACTATCAAAATATTCGGAAGATCAAAAGTTAAACAGGGGAAATTTGAT 1596  
QY 946 GGGGTAAATTTAGCAATGATGGGTTTATCAATGCTTGGCATTTATGCTAGAGTACGA 1005  
Db 1597 GGAATGAAATTTGAAATCAATGAGATCTATCAAGATTTGCGATGCTACTCACTGCGC 1656  
QY 1006 GGTATGATGCTACTGCAATCATGATGCTGCGATGCTTCTGCGGTGCTGCCAAGCGG 1065  
Db 1657 AGTTCACTGGTCTTGTGCTCCCGGAGGCAATCAGCTTCTGATGTTCTTAATGGG 1716  
QY 1066 TCTCTGCAAGCGAGGTTCTGCAATATGA 1092  
Db 1717 TCTTTGCAAGTCAGAAATATGAATCTGA 1743

## RESULT 13

US-09-197-679A-1  
Sequence 1, Application US/9197679A  
Patent No. 6287570

## GENERAL INFORMATION:

APPLICANT: Foley, Patricia L.  
TITLE OF INVENTION: Vaccine Against Swine Influenza  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Hendricks and Associates  
STREET: P.O. Box 2509  
City: Fairfax  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22031

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/197,679A  
FILING DATE: 23-Nov-6287570-1998  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hendricks, Patricia  
REFERENCE/DOCKET NUMBER: foley

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 425-8405  
TELEFAX: (703) 425-8406  
INFORMATION FOR SEQ ID NO: 1:

## SEQUENCE CHARACTERISTICS:

LENGTH: 1724 base pairs  
Type: nucleic acid

STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-197-679A-1

Query Match 39.5%; Score 448.6; DB 3; Length 1724;  
Best Local Similarity 70.38; Pred. No. 1.3e-118;  
Matches 615; Conservative 0; Mismatches 259; Indels 1; Gaps 1;

QY 226 GGATCCGGGATCATGAAACAGAGGAAACACTTGAGAACTGTGAGACCAATGCCAACT 285  
Db 835 GGATCTGGTATTTTCATTTTCAATTCAGATACACGTCACAGATTTGTAATACAGCTGTCAACCA 894  
QY 286 CCTTTGGAGACATAAATATACACATTACCTTTTCACAATGTCACACCCTAGCAATAGGT 345  
Db 895 CCCAAAGGTGCTATTAACACACACCTCCCTATTCAGAAATATACATCCAGTCACAAATTTGA 954  
QY 346 GAGTCCGCCCAATATGTAAATGCGAGAACTGTGCTTACACAGAGCACTAAGGAATGT 405  
Db 955 GAATGTCCAAAATATGTCAAAATATGACAAATTTGAGAAATGCTACAGGATTAAGGAATTC 1014  
QY 406 CCCCAAGATTAATCAAGAGATTTGTTGGGCAATAGCTGTTTATAGAGAGGATGG 465  
Db 1015 CCGTCTATTCAATCTAGGGGCTGTTTGGAGCCATTGCTGCTTTATTTGAGGGGGGTGG 1074  
QY 466 CAAAGATGTTGACGGTGTGATGATATACATCAGACAAATGACAGGATCAGGGAT 525  
Db 1075 ACAGAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1134  
QY 526 GCAGCAGCAAAATATCCATCAAAAGCAATTTGATGATGATGATGATGATGATGATGATGAT 585  
Db 1135 GCAGCCGACCGAAGAGACACACAGATCCATTTGAGGGGATCTACTAATCAAAAGTAACTCT 1194  
QY 586 GTGATTTGAAAAGATTAACACCAATTTGAAGCTGTTGGGAAAGAAATTCGGTAACCTTAGAG 645  
Db 1195 GTTATTTGAAAAGATTAACACCAATTTGACAGCATGCGGTAAATTTCAACCAACCTGGA 1254  
QY 646 AAAAGACTGGAGACTTTGAACAAAGATGGAAGACGGGTTTCTAGATGTGTGACATAC 705  
Db 1255 AAAAGATGAGAAATTTAATAAAGGTTGATGATGATGATGATGATGATGATGATGATGAT 1314  
QY 706 AATGCTGAGCTTTTATGCTGATGAGAAATGAGAGGACACTGATCTTCAATGATTTCTAAT 765  
Db 1315 AATGCCGAATTTGTTGTTCTATTGGAATAAGAAAGAACTTTGATTTACCTGATCTCAAT 1374  
QY 766 GTCAAGAAATCTGTATAGTAAGTCAGAAATGACAGTGAAGACAACTCAAAAGAACTAGGA 825  
Db 1375 GTGAGAACCTATATGAGAAAGTAAGAACGCCACTTAAACAAATGCCAAGAAATTTGGA 1434  
QY 826 AATGATGTTTGAATTTTATCAAAATGTGATGATGATGATGATGATGATGATGATGATGAT 885  
Db 1435 AATGCTGCTTTGAATTTTACCAAAATGATGATGATGATGATGATGATGATGATGATGAT 1494  
QY 886 GGGACATATGATATATCCCAAGTGAAGAAAGACTGAACTAACTAAATGAAATGAAATCAAA 945  
Db 1495 GGGACTTATGATATACCCCAATATCTCAGAAAGATTAACAAATTAACAGAGGAGATAGAT 1554  
QY 946 GGGGTAAATTTGAGACAGATGGGGTTTATCAATCTTGGCCATTTATGCTTACAGTAGCA 1005  
Db 1555 GGAGTAAAGCTGAATCAACAAAGATTTTACCAATTTTGGCGATATATTTCAACTGTCGCC 1614  
QY 1006 GGTCTATATGAC-TGGCAATCATGATGGCTGGGATCTCTTCTGGGTGCTGCCAAGCGG 1064  
Db 1615 AGTTCAATTTGATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1674  
QY 1065 GTCTGCAAGTGCAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1099  
Db 1675 GTCTTTACAGTGCAGATATGATTTTAAATTTAGG 1709

RESULT 14  
US-08-229-781-27  
Sequence 27, Application US/08229781  
Patent No. 5589174  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/229,781  
FILING DATE: April 19, 1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1754 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: A/Sultia/1/89  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:

PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-229-781-27

Query Match 39.5%; Score 447.8; DB 1; Length 1754;  
Best Local Similarity 69.8%; Pred. No. 2.6e-118;  
Matches 605; Conservative 0; Mismatches 262; Indels 0; Gaps 0;

QY	226	GGATCCGGGATCATGAAAACAGAGAACCTTGGAAGCTGTGAGCCCAATGCCAACT	285
DB	855	GGGTGAGGAATCATCCCTCAACCAACATCATGATGATGAGCGCAATGTCAACA	914
QY	286	CCCTTGGGAGCAATAATCAACATTACCTTTTCACATGTCCACCCCTACATATGT	345
DB	915	CCCCAGGAGCTATTAACAGTGTCTCTCCCAAGATGACACCAGTCACATAGGA	974
QY	346	GAGTCCCCCAATATGTAATAATCGGAGAACTTGTAGCAACAGCACTAAGAACTT	405
DB	975	GAGTGTCCAAAGTATGTCTCAGGAGTACAAAATTAAAGATGTTACAGACTAAGACATC	1034
QY	406	CCCCAGATTGAATCAAGAGATTTGTTGGGCAATAGCTGTTTATAGAAAGAGATG	465
DB	1035	CCATCCATTCAATCCAGAGCTTTGTTGGAGCAATTCGCGGTTTCATTGAAGGGGGTGG	1094
QY	466	CAGGAATGTTGACGGTTGGTATGATACATCAACCAATGACAGGATCAGGATAT	525
DB	1095	ACTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1154
QY	526	GCAGCAGACAAAGATCCACTCAAAAGCAATTTGATGATGATGATGATGATGATGAT	585
DB	1155	GCTGGGATCAAAAAGACACCAAAATGCCATTAAAGCAATTAACAAAGCTAATTTCT	1214
QY	586	GTGATTTGAAAAGATTAACACCAATTTGAGCTGTTGGAAAAGATTTGGTAACTTAG	645
DB	1215	GTAAATCGAAGAAATGAAACCTCAATTCACAGCTGTGGCAAAAGATTCAACAAATTTGAA	1274
QY	646	AAAAGCTGGAGAACTTTGACAAAAGATGGAACGGGTTCTAGATGTGACATAC	705
DB	1275	AGAAGATGAAATTAATTAATAAAGTTGATGATGATGATGATGATGATGATGATGAT	1334
QY	706	AATGCTGAGCTTTGATCTGATGGAATGAGAGACATTTGATGATGATGATGATGAT	765
DB	1335	AATGCAAGATTTGTTGTTCTCTAGTGAATTAAGAGCTTTGATGATGATGATGATGAT	1394
QY	766	GTCAGAAATCTGTATATGTAAGTCAAGTGCAGCTGAGAGACAACTCAAGAACTAGA	825
DB	1395	GTGAAGAAATCTGTATGAGAAAGTAAGCAATTAAGCAATTAAGCAATTAAGCAATTA	1454
QY	826	AATGATGTTTGAATTTTATCACAATGTGATGATGATGATGATGATGATGATGATGAT	885
DB	1455	TACGGGTGTTTGAATTTTATCACAATGTGATGATGATGATGATGATGATGATGATGAT	1514
QY	886	GGGACATATGATTTCCCAAGATGAGAGAGCTTAACATTAATTAAGAAATGAATCAA	945
DB	1515	GGAATTTATGATTTCCCAAGATGAGAGAGCTTAACATTAATTAAGAAATGAATCAA	1574
QY	946	GGGTTAAATTTGAGCAGCATGAGGGGTTTATCAAAATCTTGGCAATTTATGCTACAGTA	1005
DB	1575	GGAGTGAATTTGAGCAGCATGAGGGGTTTATCAAAATCTTGGCAATTTATGCTACAGTA	1634
QY	1006	GGTTTATGTCACATGCAATATGATGCTGGGATCTCTTCTTGGGTGCTGCTCAACGGG	1065
DB	1635	AGTTTACATGCTGCTTGTGCTCCCTGGGGCAATGAGCTTGTGAGATGTTCTTAATGGG	1694
QY	1066	TCTTCAGATGAGGATCTGCATATGA	1092
DB	1695	TCTTTCAGATGAGGATCTGCATATGA	1721



RESULT 15  
US-08-630-918-27  
Sequence 27, Application US/08630918  
Patent No. 5631350  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKINO et al.  
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,918  
FILING DATE: April 5, 1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 38,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1754 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
ORIGINAL SOURCE:  
ORGANISM: A/Suila/1/89  
US-08-630-918-27

Query Match 39.5%; Score 447.8; DB 1; Length 1754;

Best Local Similarity 69.8%; Pred. No. 2,6e-118;

Matches 605; Conservative 0; Mismatches 262; Indels 0; Gaps 0;

QY 226 GGATCGGGGATCATGAAACAGAGGAAACACTTGAGAACTGAGACCAATGCCAAACT 285  
DB 855 GGGTCAGAGATCATGCTCAAAACGATCAATGATGATGAGCGGAAGTGTCAACA 914  
QY 286 CCTTGGGAGCATATAATACATTTACTTTTCCAAATGTCACCCACTGCATAGGT 345  
DB 915 CCCAGGGGAGCTATAACAGTAGTCTTCTTCCAGAAATGTACACCCAGTCACAAATAGA 974  
QY 346 GAGTCCCCCAATATGAAAAATCGGAGAGTTGCTTACCAACAGAGACTAGGAATGTT 405  
DB 975 GAGTGTCCAAATATGTCAGAGATCAAAAATTAAGATGTTCACAGACTAAGGAACTATC 1034  
QY 406 CCCAGATTGAATCAATAGATTTGTTGGGCAATAGCTGTTTATAGAGAGAGATG 465  
DB 1035 CCATCCATCAATCAATAGATTTGTTGGGCAATAGCTGTTTATAGAGAGAGATG 1094  
QY 466 CAAGGAATGCTGAGATTTGTTGATGATACCATCAGAGAAATGACAGGATCAGGAT 525  
DB 1095 ACTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1154

QY 526 GCAGCAGACAAGATCCACTCAAAAGCACTTGTGATGATCATCCAAAGTAATTC 585  
DB 1155 GCTGCGGATCAAAAAGCAGACAAAATGCCATTAAAGGAATTCAAACAAAGGATTC 1214  
QY 586 GTGATTGAAAGATTAACACCCCAATTTGAAGCTGTTGGGAAGAATTCGTTACTAGAG 645  
DB 1215 GTAAATGAGAAAATGAACTCAATTCACAGCTGTGGGCAAAAGATTCAAACAAATTAAGA 1274  
QY 646 AAAAGACTGGAACCTTGAACAAAAGATGGAAGACGGCTTTTCAATGTGTGACATAC 705  
DB 1275 AGAAGATGGAATCTTAATAATAAAGTTGATGATGATTTCTGACATTTGGACATAT 1334  
QY 706 AATGCTGACCTTTTACTCTGATGAAATAGAGAGACACTTTCATGATTCATAT 765  
DB 1335 AATGCAGAATTTGTTGTTTACTGGAATAAGCAATTTGATTTTCTATGACTCAAT 1394  
QY 766 GTCAAGAAATCTGTATAGTAAGTCAAGATGCAAGCTGAGAGACAACTCAAGACTAGGA 825  
DB 1395 GTCAAGAAATCTGTATGAGAAAGTAAGCAATTAAGAAATATGCAAGAAATAGGA 1454  
QY 826 AATGATGTTTGAATTTTATCAAAATGATGATGATGATGATGATGATGATGATGATGAT 885  
DB 1455 TACGGGTGTTGAATTTTCAACCAAGTGAACAAATGAATGCAATGGAAGTGTGAAAAT 1514  
QY 886 GGCACATATGATTTATCCCAAGTATGAAGAGCTTAACATAATGAATGAATCAAA 945  
DB 1515 GGAATCTTATGATTTATCCCAAGTATGAAGAGCTTAACATAATGAATGAATCAAA 1574  
QY 946 GGGGTAATAATGAGCAGATGGGGGTTTATCAAAATCTTGCCATTTATGCTACAGTAGGA 1005  
DB 1575 GGAGTAAATTTGAATTCATCAATGAGGAGTCTATCAGATTTGCGCATCTACCACTGTCGC 1634  
QY 1006 GGTCTATGTCTACTGCAATCATGATGCTGGATCTCTTTCTGGGTGCTCTCAACGG 1065  
DB 1635 AGTTCACTGTGTGTTGGTCTCCCTCGGGGGAATCAGCTTCGATGTGTTCTAATGG 1694  
QY 1066 TCTCTCAGTCAGAGATGTCATATGA 1092  
DB 1695 TCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1721

Search completed: August 10, 2003, 16:15:38  
Job time : 59.7644 secs

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BenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 19:11:43 ; Search time 1741.95 Seconds  
(without alignments)  
15836.045 Million cell updates/sec

Title: US-09-918-568-49

Perfect score: 1135  
Sequence: 1 CTAGCAAGAGCGGGGTAT.....AACACCCCTGTTCTGCTAG 1135

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_in:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vr1:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_ror:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vr1:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DE	ID	Description
C 1	67.2	5.9	1201	13	BX376097	BX376097 BX376097
C 2	62.2	5.5	1101	29	CNS00396	AL063921 Drosophila
C 3	55	4.8	639	29	CNS0170D	AL108367 Drosophila
C 4	54.2	4.8	994	18	BX414650	BX414650 BX414650

Result No.	Score	Match	Length	DE	ID	Description
C 5	52.8	4.7	1101	29	CNS0006J	AL062049 Drosophila
C 6	52.4	4.6	997	29	CNS005TE	AL060767 Drosophila
C 7	52.2	4.6	1167	13	BX463903	BX463903 BX463903
C 8	51.8	4.6	847	29	CNS023EX	AL200130 Tetradon
C 9	50.2	4.4	1101	29	CNS0182P	AL108811 Drosophila
C 10	49.6	4.4	468	29	CNS06XGD	AL149699 t7 end of
C 11	49.4	4.4	918	29	CNS006MW	AL065068 Drosophila
C 12	48.8	4.3	1201	13	BX406178	BX406178 BX406178
C 13	48.6	4.3	938	29	CNS006TJ	AL065906 Drosophila
C 14	48.4	4.3	1201	13	BX461128	BX461128 BX461128
C 15	47.8	4.2	300	9	A0087765	A0087765 A0087765
C 16	47.6	4.2	1200	29	CNS016CO	AL106578 Drosophila
C 17	47.4	4.2	1101	29	CNS0106X	AL098595 Drosophila
C 18	47	4.1	1101	29	CNS000D1	AL065414 Drosophila
C 19	46.8	4.1	1200	13	BX414560	BX414560 BX414560
C 20	46.2	4.1	1106	13	BX438107	BX438107 BX438107
C 21	46	4.1	1001	13	BX329654	BX329654 BX329654
C 22	46	4.1	1101	29	CNS008ES1	AL069797 Drosophila
C 23	46	4.1	1201	9	AL536104	AL536104 AL536104
C 24	46	4.1	1201	13	BX355654	BX355654 BX355654
C 25	45.8	4.0	1101	29	CNS016HF	AL106749 Drosophila
C 26	45.8	4.0	1101	29	CNS017KX	AL108171 Drosophila
C 27	45.6	4.0	516	28	A0879779	A0879779 HS_4821_A
C 28	45.2	4.0	781	29	AG171177	AG171177 Pan treg1
C 29	45.2	4.0	932	9	AL514901	AL514901 AL514901
C 30	45.2	4.0	941	28	AZ682404	AZ682404 ENT1016F
C 31	45.2	4.0	1044	13	BX415231	BX415231 BX415231
C 32	44.8	3.9	673	12	BM485652	BM485652 pmtc.pk0
C 33	44.6	3.9	963	29	CNS006X1	AL066049 Drosophila
C 34	44.6	3.9	984	9	AL525973	AL525973 AL525973
C 35	44.6	3.9	1001	29	CNS01400	AL103554 Drosophila
C 36	44.4	3.9	930	29	CNS01644	AL106270 Drosophila
C 37	44.4	3.9	1100	29	CC206010	CC206010 CH261-159
C 38	44.2	3.9	1101	29	CNS0039W	AL063937 Drosophila
C 39	44	3.9	630	14	CB271310	CB271310 taa21c05
C 40	44	3.9	644	14	CD567533	CD567533 lab78g10
C 41	44	3.9	917	28	BH166948	BH166948 ENT578TF
C 42	44	3.9	1201	13	BX461310	BX461310 BX461310
C 43	43.8	3.9	467	13	BU497794	BU497794 PFE50a08
C 44	43.8	3.9	859	29	CNS00KLL	AL077728 Drosophila
C 45	43.8	3.9	1125	13	BX436449	BX436449 BX436449

## ALIGNMENTS

RESULT 1  
LOCUS BX376097/c. 1201 bp mRNA linear EST 08-MAY-2003  
DEFINITION BX376097 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens  
CDNA clone CSDDC022YM12 5-PRIME, mRNA sequence.

ACCESSION BX376097  
VERSION BX376097  
KEYWORDS BX376097.1 GI:30434756  
SOURCE EST.  
ORGANISM Homo sapiens (human)

REFERENCE  
AUTHORS Li, W.-B., Gruber, C., Jesse, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
COMMENT Contact: Genoscope  
Genoscope Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 2866.f  
Contact: Feng Liang Email: fliang@lifetech.com URL:  
http://fulllength.invitrogen.com/invitrogen/Corporation 1600  
Faraday Avenue Genoscope sequence ID: CSDDC022B6060P1.  
Location/Qualifiers 1. 1201

FEATURES  
source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDC022M12"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_1lb="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pcnvsBSP6 vector. Library was normalized."
BASE COUNT
ORIGIN
79 a      152 c      66 g      270 t      634 others

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Query Match	Score 67.2;	DB 13;	Length 1201;
Best Local Similarity	14.6%;	Pred No. 0.00023;	
Matches 123;	Conservative 256;	Mismatches 464;	Indels 2;
			Gaps 1;

Ox . AACATGGCCATAATTTCACAGAGAAGTCTGCACACATTTCTAAGACGCGAACGTCACTGTGA 169  
Db 1010 MNNMNMNMMMNHNKKNHNNKMKKNHMKHTMTNTTKWMTKTLYIMDMRMHMNVAKMMNK 951

[illegible]

Db 890 GGGGMMVGMRGSGYMMMGTTGKKTIMGKNNMGKMMGMMGNTDMMKTTMTTKMMKHMTM 831

[illegible]

Ov	410	AGATTGAATCAAGAGGATCTTTTGGGGCAATAGCGGGTTTATACAAGAGGATTCGCAAC	469
Db	770	HMNMKGCTMGTMMAGTCKMKGKMTMTNTMKYMMMMMMMMMKGRKMMMKMGKMMNM	711

Db 710 AMMKMMMTMTMTGTMMTMTMGCKRTMTMTMKMNKMKMKRAGCKMNAVKKNNKNAMNN 651

Ddb 650 NGKNNNNKKTKKKNNKKKNMKNNNMMNNKKMKMGKMNMGAKANNMKM--KINN 593

Qy 530 CAGCAAAAGAATCCACTCAAAAGGCATTGTGTAATCACCMACAAGTAAATTCGTGA 589

Db 592 NKMMNNNNMKKKKKNNNNNNKKKKMMNNNNNNKKKKMMNNNNNNKKKKNNNNNNNAGC 533

Qy 590 TTGAAGAAGATAAACACCCCAATTTCGAGCTGTTGGGAAGAAGATTCCGTAACCTTAGAGAAA 649

Db	532	KMKKMMNNNNNNNNNNNNNNNNKKNNNNNNNNMMAMMGGNNNGKKNN	473
QY	650	GACTGCAGAACTTGACACAAGAATGGAGAAGCGGTTTCTAGATGTGTGCACATCACAATG	709

DB 412 MMMGNGMNNNNMMARNNAAAMNNAANAAGKKGKNNKAAANNAANNNAKKAKAANA 413

QY 710 CTGAGCTTTAGTCTGTGATGGAATGAGAGGACCTTGCTTCATGATTCATATGTA 769

412 ACNNCCMNAC MNNRKAANNNAKAKNNNNNNNNNNMANKAKAAACNCNANNNKKAAAAKA 353  
DU  
770 AGAATCTGTATAGTAAGTCGAGAATGCAGCTGAGACACAACGTCGAAGAAGTACGAAAATG 829  
QY

830 GATGTTTGAATTATCATCAAAATGTGATGATGCATGAAAGTGTAACCGGA 889

QY 890 CATATGATTATCCCAAGTATGAAGAGAGCTCTAAACTAATAGAAATGAATCAAAAGGGG 949

QY	950	TA AAA	954
Db	172	CAAGA	168

CNS00396/c			
LOCUS	1101 bp	DNA	linear
DEFINITION	Drosophila melanogaster genome survey sequence TEU3 end of BAC #.		
	BACR08k10 of RPcI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.		

ACCESSION	AL063921
VERSION	AL063921.1
KEYWORDS	GI:4941778
SOURCE	GSS.
ORGANISM	Drosophila melanogaster (fruit fly)
	Drosophila melanogaster

ORGANISM: Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 1101)

UNPUBLISHED  
 AUTHORS  
 TITLE  
 JOURNAL  
 Genoscope, Centre National de Sequencage :  
 Direct Submission  
 Submitted (02-JUN-1999)  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : [secret@genoscope.cns.fr](mailto:secret@genoscope.cns.fr))

**COMMENT**

- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BACP Drosophila melanogaster BAC library was prepared by Kazutoyo Oseegawa and Airon Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY.

The library is named PCl-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library

location/Qualifiers

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source
1. .1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
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BASE COUNT	201 a	64 c	131 g	202 t	503 others
clone="BACR08K10"					
/clone_lib="RPCT-98"					
/note="end : TET3"					

ORIGIN	Score	DB	Length
Query Match	5.58;	62.2;	1101
Best Local Similarity	15.5%;	Pred. No. 0.0029;	
Matches 87.	Conservative 763.	Mismatches 200.	Totals 3

Matches	677	Conservative	2027	Mismatches	2037	Indels	3	Gaps	1
420	AAGAGCAATTCTTTGGGCGCAATAGCTGGCTTTATAGAACGAGAGATCGCAGACGATCGTTGA	479							
1099	ARRGGDDTTWDDTTRKDDMDMTKKWTTMMKDRADDDRRMGDDDRBMMDDGAGTMTATATMMN	1040							

OY 480 CGGTGGTATGATACCATCAGCAATGACCAGGATGCAGTCACGACAAGA 539  
 : : : : | | | : : : : : : : : : :  
Db 1039 WWWATWDTWDKWWWATAKTDTATTWMTATARRADWAGGDRGRDRPRAATDAGAG 980

OY  
540 ATCCACTCMAAAGGCATTTGATGAATCACCACAACMGTAATTCTGTGATTGGAAAGT 599

: : : : : | | : : :  
979 RRDGGRRKDKDDKDSDDDKGCGKKKAALAAAAMWATTKWMDDMDWDKDWIDGAKDKRAD 920

[illegible]

660 CTTGACAAAAAGATGGAAGACGGCTTTCTAGATGTGTGACATACATGCTGACGCTTTT 719



Db	873	DTAMWTRRDKKATMKWADDDADDAKTTTTTTTTTMMKAAWTDMAWNTAKWMAADATWMAADAW	814
OY	789	CAGAAATCAGCTGAGAGACAACGTCAAAGAACTAGAAATGATGTTTGAATTTTATCA	848
Db	813	AARAAWMAARAWRAAAAMWMAADADMMWMMWMAADAAW--AAADTKDKRAMRAADWAR	756
OY	849	CAATGTGATGATGATCATGAATAGTGTGAAAAACGGGACATGTGATTTATCCCAAGTA	908
Db	755	AAAAAAAMWDMGWSGRADPAGKDKAAWAAWMDGSGGRDKPRDWAAWDDDAADAAARRAAAAA	696
OY	909	TGAAGAAGAGCTCTAACTAAATAGAAATGAATCAAGGGGTAATTCAGACACCATGGG	968
Db	695	ATAMWATWMMKMDKMAAAAAAMDATKGRKDDADMMAAWTTTTTTTTTAAMAAADAM	636
OY	969	GATTATCAAAATCCTGCCATTATTAGCTACAGTAGCAGGTTCTATGTACTGCGCAATCAT	1028
Db	635	KKMKATATTTTTTTTTTTTTTTTTTTTTKKTITAKWTTWMDADDWTTTTTTTTTTTTTWWAAAT	576
OY	1029	GATGCGTGGATCTCTTCGCGG	1053
Db	575	KTKTKTKTKTKTKTKTTTTTTTRDWD	551

RESULT 5			
CNS0006J			
LOCUS	CNS0006J	1101 bp	DNA linear GSS 03-JUN-1999
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC # BR01M22 of RPEC-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.		
ACCESSION	AL062049		
VERSION	AL062049..1 GI:4938511		
KEYWORDS	GSS.		
SOURCE	Drosophila melanogaster (fruit fly)		
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Epiphytoidae; Drosophilidae; Drosophila. 1 (bases 1 to 1101) Genoscope. Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage		
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			

**COMMENT**  
medRxiv preprint doi: <https://doi.org/10.1101/2019.05.21.19095117>; this version posted May 21, 2019. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted medRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY 4.0 International license.

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see [http://www.fruitfly.org/TheBDGP/Drosophila\\_melanogaster\\_BAC\\_library](http://www.fruitfly.org/TheBDGP/Drosophila_melanogaster_BAC_library) was prepared by Kazuhiro Oseegawa and Aaron Mammosier in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPc1-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES	Location/Qualifiers
Source	1..1101
	/organism="Drosophila melanogaster"
	/mol_type="genomic DNA"
	/db_xref="taxon:7227"
	/clone="BACR01M23"
	/clone_lib="RPC1-98"
	/note="end : TET3"
BASE COUNT	333 a 162 c 148 g 177 t 281 others
ORIGIN	

Query March	4.78;	Score 52.8;	DB 29;	Length 1101;
Best Local Similarity	25.78;	Pred. No. 0.35;		
Matches 151;	Conservative 165;	Mismatches 268;	Indels 4;	Gaps 2;

OY		453	AGAAAGGAGGTGGCAAGGAATGTTGACGGTGGTAATGCATCACAGCATGCCA	512
OY		496	RRATGGRRAATTBRRAAGTTATWTTGAAAAAAAAAAAAAWTTTAAGCAAAAAAAAAAMATA	555
OY		513	GCGATCAGGGTAGCGAGCAAAAAGATCCACTCAAAGAAGCTTGATGGAATCCAA	572
Db		556	TKAAATTTTTTTRRTFRAGTATTTDTDRAKMAAAAAAAAAAATNTTGAABAAABAAAAA	615
OY		573	CAAGTAATTCGTGATTTGAAAAGATTAACACCCTTTGAGTCTGTTGGAGAGATT	632
Db		616	AARAAAGTGTGTAAGAAAAAAAAAAAAAAAAADATTAARAAWKMAAAGGAAAAAAAAATMAA	675
OY		633	CGGTAACCTTGAACAAGACGTGACACCTTGACACAAAAGATGGAAGCGCTTCTGCA	692
Db		676	AAKAAMTKGTATAAAAAAAAAAAAAAAAAAGGAAAGGKRARGARARGRGGRAMPAAAA	735
OY		693	TGTTGGACATACACATGCTGAGCTTTTATGTTCTGATGAAAATGAGAGCACCTTGACT	752
Db		736	KTKRKKKTTRKRRBAAGRARRAMAAGAAAAAABAADAATKTGTWAKMAMPTAAWKKD	795
OY		753	TCATGATCTAATGTCAGAACTCTTATAGTAAAGTCAGATGCAGTCAGACACACT	812
Db		796	WKATDAAAKAAARTEDMTTAKAKDKTWGAAAGATGAMGAARGRWGKGKDGTRARR	855
OY		813	CAAGAAGACAGGAAATGATTTTATACAAATTTGATGATGATGATGATGATGATG	872
Db		856	ARAGAGGMDKMAAMMAAAATTAARKMDTATAADRRAKMDRRRAAAAADRDD - KGRA	914
OY		873	TACTGTGAAAAACGGACATGATTAATCCCACTATGAAGAAGACTTAACTAAATVG	932
Db		915	GMWTGRRRARARTRKAKRRGAAGAKAKARRAKGAMKMDGKKKMDMAAMAKAKGT	974
OY		933	AAATGAATCAAGGGGTAAATTTGAGCAGCAGTGGGGTTTATCAATCCTTGCCATTYA	992
Db		975	GDMKRRARR --- AKTGMRARADKDWRAAADDTFMTKAMMMTDMWATATDKDKTKDA	1031
OY		993	TGCTACAGTAGCAGGTTCTATGCTCCTGGCAATCATATAGCTGGGAT	1040
Db		1032	KKKAKMTTTRIDRAKAAKADDTAATATATAMWDADDKAKDAADK	1079

RESULT 6	
CNS005TE/c	
LOCUS	
DEFINITION	CNS005ITE 997 bp DNA linear GSS 03-JUN-1999
ACCESSION	Drosophila melanogaster genome survey sequence TEt3 and of BAC #
VERSION	BACR12KR2.2 of RPCI-98 library from Drosophila melanogaster (fruit
KEYWORDS	fly), genomic survey sequence.
SOURCE	AL060767
ORGANISM	AL060767.1 GI:4943573
TITLE	GSS
JOURNAL	Drosophila melanogaster (fruit fly)
AUTHORS	Drosophila melanogaster
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
	Ephydroidea; Drosophilidae; Drosophila-
	1 (bases 1 to 997)
	Genoscope.
	Direct Submission
	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
	BP 191 91006 EVRI cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
	- Web : www.genoscope.cns.fr)
COMMENT	Determination of this BAC-end sequence was carried out as part of a

**COMMENT**

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the *Drosophila* melanogaster genome using these BACs. For further information please see: <http://www.fruitfly.org> The BDGP *Drosophila* melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's Laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPc1-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's



FEATURES	source
BASE COUNT	164 a 133 c 130 g 342 t .78 others
ORIGIN	<pre> /oranism="Tetradon nigroviridis" /mo_type="genomic DNA" /db_xref="taxon:99883" /clone="143K10" /clone_11b="G" /note="Genoscope sequence ID : COAG143BF05SP1-end : PUC-Orl" </pre>
Query Match	4.6%; Score 51.8; DB 29; Length 847;
Best Local Similarity	44.3%; Pred. No. 0.57;
Matches	98; Conservative 23; Mismatches 100; Indels 0; Gaps 0;
QY	736 GAGAGGACACTGTCCTTCATGATTCCTAATGTCAGAAATCTGTATAGTAAGTCAGAAATG 795
DB	564 GTGTTGGCATATGACACCATTTTGAAGAAATTAAGATTAAGTAAGAAAGAAAGTA 505
QY	796 CAGCTGAGAGCAACGTCGAAGCACTGGAATGGAATGATGCTTTGATTTTATCACAAGT 855
DB	504 TAAATTTAAAAAAATWAAATTAATTTAAAAATATATTAAGAAATTAATWAAATWAAAG 445
QY	856 GATGATGATATCATGAAATAGTGTAAAAACGGCACTATGATTTATCCCAATGTAAGAA 915
DB	444 AAAAAATWAAAAAATTAATGCAAAAAAATATGAAAAAATAAATAAAAAAATAAAAAA 385
QY	916 GAGTCTAAACTAAATAGAAATGAATCAACGAGGTAAAT 956
DB	384 TAAAGCAAAAAAATAATTAATAAATAAATTAARABATWAAW 344
RESULT 9	
CNS0182P	
LOCUS	
DEFINITION	CNS0182P 1101 bp DNA linear GSS 26-JUL-1999
ACCESSION	
VERSION	
KEYWORDS	ALI08811.1 GI:5629115
SOURCE	GSS.
ORGANISM	Drosophila melanogaster (fruit fly)
	Drosophila melanogaster
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

REFERENCE	Ephydroidea: Drosophilidae; Drosophila.
AUTHORS	I. (bases 1 to 1101)
TITLE	Genoscope.
JOURNAL	Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) : <a href="http://www.edgp.ebi.ac.uk/">http://www.edgp.ebi.ac.uk/</a> . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and genevieve Payan. It has been constructed in the vector pelobac11.
COMMENT	
FEATURES	Location/Qualifiers
source	1..1101 /organism="Drosophila melanogaster" /mol_type="genomic DNA" /db_xref="taxon:7227" /clone="BACN37D10" /clone_lib="DrosBAC" /plasmid="pelobac11" /note="end : SP6"
BASE COUNT	274 a 268 c 128 g 73 t 358 others
ORIGIN	
Query Match	4.4%; Score 50.2; DB 29; Length 1101;
Best Local Similarity	21.0%; Pred. NO.1.3:
Matches 109;	Conservative 198; Mismatches 208; Indels 4; Gaps 2;
OY	563 GAATCACCAACAAGTAATTCTGTGATTGAAGAATAAACACCATTGAAGCTGTTG 622
Db	584 KDRWDAAGAAARAAAAAARAAKMTAAAAAARAAAAAATTTTAA 643
OY	623 GGAAGAATTCGGTACTTAGAGAAAACCTGGGAACCTTGAAACAAAAGATGGAAGCG 682
Db	644 AAAAAGGSGKTGKGKAADGDGGAADAAMWRGGRRRARAARAAAAADAKRAAAAAA 703
OY	683 GGTTTCTAGATGTGGACATACAAVCGTGAAGCTTTTATGTTGATGGAAGAAATGAGAGA 742
Db	704 AAAAAAAAAAADAGK---KKWKKGDKDGSKARKATTAAMAKGRKDWTATAMTTDATYA 760
OY	743 CACTGACTTCATGATTTCTAATGTCAAGAATCTGTATAGTAAGTCAGATGCAGCTGA 802
Db	761 DTWKATATPDIDAKRAAAGRRKRDPARTXADGSRARRRBRAMAAGKRARAGARRAARR 820
OY	803 GAGACAAGCTCAAAGACTAGGAATGATGTTTTGATTTTATCACAATATGATGATG 862
Db	821 AADDRDMDMAAAAAA--AAATTRDWMWDMDWDTIRWDDTTAAWMDARRAR 879
OY	863 AATGCATGATGTGTGAAAAAGGAGCATGTGTTAVCCAGTATGAAGAAGATCTA 922
Db	880 RRRRRRRRRARRARRAADTDITKDRADATTTTKTWTITDDDDMDKARDRWAAK 939
OY	923 AACCTAATAGAATGAATCAAAAGGGGTAAATTTAGACACATGGGGTTATCAATCC 982
Db	940 ADAGMKWRBARDDNAATAKDDDKDWGCRGKRGKDKRMDKGTGCKDDDDMDKTW 999
OY	983 TTGCCATTATCTCAGTACAGAGTTCTATGCTACTGCGAATCATGATGCGTGGATCT 1042
Db	1000 TRDMMWMTRTWDMWMDWGRRGWTRFKRWGAWRADAARDDTDGKDJTRADXDRKT 1059
OY	1043 CTTTCGGGTGCTCCAAGGGGTCTCGACGTCGACAGA 1081
Db	1060 DTTKRDGDDMRKDRDKRRKGDGDKTKDATTDDDDA 1098
RESULT 10	
CNS06XGD/c	CNS06XGD 468 bp DNA linear GSS 06-JUL-2001
LOCUS	TF end of clone XAX0A00207 of library XAX0XA from strain CBS 7064
DEFINITION	of Pichia farinosa, genomic survey sequence.



```

ACCESSION AL419699
VERSION AL419699.1
KEYWORDS GI:12402877
SOURCE GSS.
ORGANISM Pichia farinosa
Pichia farinosa
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
REFERENCE
AUTHORS Souciet,J., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,J., Bon,E., Brothier,P., Casarigola,S.,
de-Montigny,J., Dujon,B., Durieux,P., Lepingle,A., Llorente,B.,
Malpartuy,A., Neugejlisse,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876
REFERENCE
AUTHORS de Montigny,J., Stehner,C., Souciet,J., Tekala,F., Dujon,B.,
Wincker,P., Artiguenave,F. and Potier,S.
Genomic exploration of the hemiascomycetous yeasts: 15. Pichia
sorbitophila
JOURNAL FEBS Lett. 487 (1), 87-90 (2000)
MEDLINE 20584725
PUBMED 11152890
REFERENCE
AUTHORS 3 (bases 1 to 468)
Genoscope.
Direct Submission
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
FEATURES
source 1..468
/organism="Pichia farinosa"
/mol_type="genomic DNA"
/db_xref="EBI:7064"
/db_xref="taxon:4920"
/clone_lib="XAXOAO02F07"
/clone_lib="XAXOAA"
/notes="end : 77"
misc_feature <13..>159
/notes="similar to Saccharomyces cerevisiae ORF YLR127c |
APC2 ; component of the anaphase promoting complex ]"
/evidence="not experimental"
BASE COUNT 124 a 59 c 212 t 18 others
ORIGIN
Query Match 4.4%; Score 49.6; DB 29; Length 468;
Best Local Similarity 50.5%; Pred. No. 1.6;
Matches 104; Conservative 6; Mismatches 96; Indels 0; Gaps 0;

```

```

Db 137 TGATACCTAATCARGAAAACCTGMAAATTCAGACCATAGTATYCCAAATATAAAG 78
Qy 915 AGAGTCTAAACTAATAGAAATGAA 940
Db 77 ATGATATAGTACAGAAGATATCAAA 52
RESULT 11
LOCUS CNS006MW
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC #
BAC14F09 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL065768
VERSION AL065768.1
KEYWORDS GI:4944648
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
AUTHORS 1 (bases 1 to 918)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Hamamer in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
pl and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.
FEATURES
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/notes="end : 77"
BASE COUNT 251 a 169 c 125 g 130 t 243 others
ORIGIN
Query Match 4.4%; Score 49.4; DB 29; Length 918;
Best Local Similarity 21.3%; Pred. No. 2;
Matches 60; Conservative 114; Mismatches 108; Indels 0; Gaps 0;

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OY 923 AACTAATAGAAATGAATCA 943  
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Db 376 ACATTAAGAGAAAAATATTTA 396

Search completed: August 10, 2003, 10:57:45  
Job time : 1743.95 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search,  
using sw model

Run on: August 9, 2003, 18:20:24 ; Search time 182.31 Seconds  
(without alignments)  
12843.535 Million cell updates/sec

Title: US-09-918-568-49

Perfect score: 1135  
Sequence: 1 CTAGCAAAAGCGGGGTAT.....AACACCTTGTTCCTCTAG 1135

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications -NA.\*  
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2: /cgn2\_6/p/odata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/p/odata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/p/odata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/p/odata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/p/odata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DE	ID	Description
1	1135	100.0	1135	5	US-09-918-568-49	Sequence 49, Appl
2	908.8	80.1	1783	5	US-09-918-568-46	Sequence 46, Appl
3	838	73.8	1728	5	US-09-918-568-28	Sequence 28, Appl
4	447.8	39.5	1754	9	US-09-918-568-27	Sequence 27, Appl
5	400	35.2	400	9	US-09-918-568-33	Sequence 33, Appl
6	397	35.0	400	9	US-09-918-568-34	Sequence 34, Appl
7	382.4	33.7	410	9	US-09-918-568-35	Sequence 35, Appl
8	379.6	33.4	394	9	US-09-918-568-36	Sequence 36, Appl
9	263	23.2	1777	9	US-09-918-568-57	Sequence 57, Appl
10	252.6	22.3	1110	9	US-09-918-568-29	Sequence 29, Appl
11	251.6	22.2	442	9	US-09-918-568-32	Sequence 32, Appl
12	241.8	21.3	429	9	US-09-918-568-30	Sequence 30, Appl
13	233.6	20.6	424	9	US-09-918-568-31	Sequence 31, Appl
14	233.6	20.6	424	9	US-09-918-568-31	Sequence 31, Appl
15	233.6	20.6	1711	13	US-10-099-619-1	Sequence 1, Appl
16	125.2	11.0	334	9	US-09-918-568-38	Sequence 38, Appl

17	123.6	10.9	329	9	US-09-918-568-39	Sequence 39, Appl
18	123.6	10.9	334	9	US-09-918-568-40	Sequence 40, Appl
19	121	10.7	329	9	US-09-918-568-37	Sequence 37, Appl
20	118.8	10.5	329	9	US-09-918-568-41	Sequence 41, Appl
21	44.4	3.9	1115	14	US-10-184-644-440	Sequence 440, App
22	44.4	3.9	1115	14	US-10-184-634-440	Sequence 99638, A
23	42.4	3.7	719	13	US-10-027-632-99638	Sequence 99639, A
24	42.4	3.7	719	13	US-10-027-632-99639	Sequence 126, App
25	41.8	3.7	3423	14	US-10-037-270-126	Sequence 41, Appl
26	41.8	3.7	3441	9	US-09-880-192-411	Sequence 126, App
27	41.8	3.7	3444	13	US-10-114-893-126	Sequence 126, App
28	41.6	3.7	475	11	US-09-918-995-23463	Sequence 8307, A
29	41.4	3.6	25574	11	US-09-764-891-8307	Sequence 8306, App
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31	40.8	3.6	4239	10	US-09-070-927A-450	Sequence 22350, A
32	40	3.5	471	11	US-09-918-995-22350	Sequence 51, Appl
33	40	3.5	1777	13	US-10-042-417-51	Sequence 421, App
34	40	3.5	2843	11	US-09-822-846-421	Sequence 468, App
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36	39.8	3.5	1257	9	US-09-877-065-2	Sequence 71, Appl
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#### ALIGNMENTS

RESULT 1  
US-09-918-568-49  
Sequence 49, Application US/09918568  
Patent No. US2002005482A1  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/918,568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200  
 TELEFAX: 202-721-8250  
 TELEX: <unknown>  
 INFORMATION FOR SEQ ID NO: 49:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1135 base pairs  
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 STRANDEDNESS: double  
 TOPOLOGY: linear  
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 HYPOTHEetical: <unknown>  
 ANTI-SENSE: <unknown>  
 FRAGMENT TYPE: <unknown>  
 ORIGINAL SOURCE:  
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 DEVELOPMENTAL STAGE: <unknown>  
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 OTHER INFORMATION:  
 PUBLICATION INFORMATION:  
 AUTHORS:  
 TITLE:  
 JOURNAL:  
 VOLUME:  
 ISSUE:  
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 FILING DATE:  
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 RELEVANT RESIDUES IN SEQ ID NO:  
 SEQUENCE DESCRIPTION: SEQ ID NO: 49:  
 US-09-918-568-49  
 Query Match 100.0%; Score 1135; DB 9; Length 1135;  
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 Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ; Sequence 46, Application US/09918568  
 ; Patent No. US20020054882A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yoshinobu OKUNO et al.  
 ; TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
 ; NUMBER OF SEQUENCES: 58  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
 ; STREET: 2033 K Street, N.W., #800  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.

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1      ZIP: 20006
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3      COMPUTER READABLE FORM:
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5      MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
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7      COMPUTER: IBM Compatible
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16     FILING DATE: 02-Aug-2001
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18     CLASSIFICATION: <unknown>
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22     APPLICATION NUMBER: 09/004,422
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24     FILING DATE: January 8, 1998
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26     APPLICATION NUMBER: 08/443,862
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28     FILING DATE: May 22, 1995
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30     APPLICATION NUMBER: 08/229,781
31
32     FILING DATE: April 19, 1994
33
34     APPLICATION NUMBER: 08/054,016
35
36     FILING DATE: April 29, 1993
37
38     ATTORNEY/AGENT INFORMATION:
39
40     NAME: Warren M. Cheek, Jr.
41
42     REGISTRATION NUMBER: 33,367
43
44     REFERENCE/DOCKET NUMBER: <unknown>
45
46     TELECOMMUNICATION INFORMATION:
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48     TELEPHONE: 202-21-8200
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58     LENGTH: 1783 base pairs
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112    LOCATION:
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116    OTHER INFORMATION:
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118    PUBLICATION INFORMATION:
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120    AUTHORS:
121
122    TITLE:
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124    JOURNAL:
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126    VOLUME:
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128    ISSUE:
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130    PAGES:
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132    DATE:
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134    DOCUMENT NUMBER:
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136    FILING DATE:
137
138    PUBLICATION DATE:
139
140    RELEVANT RESIDUE: IN SEQ ID NO:
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144    US-09-918-568-46

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Best Local Similarity	98.7%	Pred. No. 5.4e-238		
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QY	328	CACCCACGCAAAATAGGTGAGTGGCCCCCAATATGTAAATGCGGAAGTGGTCTTTGCA	387	
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QY	448	TTTATTAGAGGAGATGGCAAGAAATGTTGACGGTTGGTATGCATACATCACACAAAT	507	
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QY	1108	TAAATTAATAAACACCCCTGTGTTCTGCTAG 1135		
DB	1753	TAAATTAATAAACACCCCTGTGTTCTGCTAG 1780		

Patent No. US2002005482A1  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/918,568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mairen M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8250  
TELEFAX: 202-721-8250  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1728 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL: <Unknown>  
ANTI-SENSE: <Unknown>  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: A/12um1/5/65  
STRAIN: <Unknown>  
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CLONE: <Unknown>  
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FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:

Query Match 73.8%; Score 838; DB 9; Length 1728;  
Best Local Similarity 95.6%; Pred No. 1.2e-218;  
Matches 862; Conservative 0; Mismatches 40; Indels 0; Gaps 0;  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 28;  
US-09-918-568-28  
QY 208 AAGTATGCAAACTAAACGATCCGGATCATGAAACAGAAAGAACCTTGAGAACTGT 267  
DB 827 AAAATATCGAAAAGAGGTAGTTCAGGATCATGAAAGAGAAACACTTGGGAACTGT 886  
QY 268 GAGACCAATGCCAACTCTTTGGAGCAATAATACACATTACCTTTTACAAATGTC 327  
DB 887 GAGACCAATGCCAACTCTTTGGAGCAATAATACACACTTTTACAAATGTC 946  
QY 328 CACCCACATGCAATGAGTGGAGTGGCCCAATATGTAATGGAAGTGGCTTAAACA 387  
DB 947 CACCCACATGCAATGAGTGGAGTGGCCCAATATGTAATGGAAGTGGCTTAAACA 1006  
QY 388 ACAGGACTAAGGAATGTTCCCGATGTAATCAAGAGATGTTGGGCAATAGCTGT 447  
DB 1007 ACAGGACTAAGGAATGTTCCCGATGTAATCAAGAGATGTTGGGCAATAGCTGT 1066  
QY 448 TTTATAGAAGAGGATGGCAAGATGTTGACGTTGTTATGATACCATCACAGCAAT 507  
DB 1067 TTTATAGAAGAGGATGGCAAGATGTTGACGTTGTTATGATACCATCACAGCAAT 1126  
QY 508 GACCAAGGATCGAGGTATGACAGCAAGCAAGATCCACTCAAAAGGCAATTTGATGATC 567  
DB 1127 GACCAAGGATCGAGGTATGACAGCAAGCAAGATCCACTCAAAAGGCAATTTGATGATC 1186  
QY 568 ACCAACAAGTAAATTTGTGTGATTAAGAAAGATAACACCCAAATTTGAAGCTGTGGGAAA 627  
DB 1187 ACCAACAAGTAAATTTGTGTGATTAAGAAAGATAACACCCAAATTTGAAGCTGTGGGAAA 1246  
QY 628 GAATTCGTAATTTAGAGAAAAGACTGAGAACTTGACAAAGATGGAAGAGAGGTTT 687  
DB 1247 GAATTCGTAATTTAGAGAAAAGACTGAGAACTTGACAAAGATGGAAGAGAGGTTT 1306  
QY 688 CTAGATGCTGACATACATGCTGAGCTTTAGTCTGATGGAAGATGAGAGACACTT 747  
DB 1307 CTAGATGCTGACATACATGCTGAGCTTTAGTCTGATGGAAGATGAGAGACACTT 1366  
QY 748 GACTTTCATGATTTCAATGTCAGAAATCTGTATAGTAAGTCAGAAATGCAAGCTGAGAGAC 807  
DB 1367 GACTTTCATGATTTCAATGTCAGAAATCTGTATAGTAAGTCAGAAATGCAAGCTGAGAGAC 1426  
QY 808 AACGTCAAGAACTAGGAAATGATGTTTAAATTTATCACAAAATGATGATGATGTC 867  
DB 1427 AACGTCAAGAACTAGGAAATGATGTTTAAATTTATCACAAAATGATGATGATGTC 1486  
QY 868 ATGATAGTGAAGAAACGGGACATATGATATCCCAAGTATGAAAGAGTCTAAACTA 927  
DB 1487 ATGATAGTGAAGAAACGGGACATATGATATCCCAAGTATGAAAGAGTCTAAACTA 1546  
QY 928 AATAGAAATGAATCAAAAGGGTAAATTTAGAGCAATGAGGGGTTTATCAAACTCTTGCC 987  
DB 1547 AATAGAAATGAATCAAAAGGGTAAATTTAGAGCAATGAGGGGTTTATCAAACTCTTGCC 1606  
QY 988 ATTATGCTACAGTACAGGTTTATATGCTACGCAATCATGATGCTGGAGATCTCTTC 1047  
DB 1607 ATTATGCTACAGTACAGGTTTATATGCTACGCAATCATGATGCTGGAGATCTCTTC 1666





QY 886 GGACATATGATATCCAGATGATAGAGAGATCTAACTAAATAGAAATCAAA 945  
1515 GGACTTATGACTATCCAAATATTCGAGATCAAAAGTTAAACAGGAAAAATGAT 1574  
QY 946 GGGTAAATGACAGCATGGGGGTTTATCAATCTTGCATTATGCTACAGTAGCA 1005  
1575 GGAGTGAATGATGATCAATGAGGAGTATCAGATTCTGGCATCTCAACTGTCCG 1634  
QY 1006 GGTTCTATGTCATGCGCAATGATGATGCTGGATCTTCTGTGGTGTGCTCCAGGG 1065  
1635 AGTTCAGTGTGCTTTTGTCTCCCTGGGGCAATCAGCTTCTGATGTCTAATGG 1694  
QY 1066 TCTCTGAGTGCAGAGATCTGATAGA 1092  
1695 TCTTGCAGTGTAGAAATGATGATCTGA 1721  
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RESULT 5  
US-09-918-568-33  
Sequence 33, Application US/09918568  
Patent No. US20020054882A1  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/918,568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 400 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL: <Unknown>  
ANTI-SENSE: <Unknown>  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: A/Okuda/57  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>

DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>  
CELL LINE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-918-568-33

Query Match 35.2%, Score 400; DB 9; Length 400;  
Best Local Similarity 100.0%; Pred. No. 3,3e-99;  
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 295 GCAATTAATACACATACCTTTTCACAAATGTCACCCAGCTGCAATAGGTGAGTCC 354  
Db 1 CCAATTAATACACATTAACCTTTTCACAAATGTCACCCAGCTGCAATAGGTGAGTCC 60  
QY 355 AAATATGTAATGCGAAGAGTGTGCTTAGCAACAGAGCTAAGATGTTCCCGAGATT 414  
Db 61 AAATATGTAATGCGAAGAGTGTGCTTAGCAACAGAGCTAAGATGTTCCCGAGATT 120  
QY 415 GAATCAGAGATTTGTTGGGCAATAGCTGTGTTTATAGAGAGAGATGCAAGAAATG 474  
Db 121 GAATCAGAGATTTGTTGGGCAATAGCTGTGTTTATAGAGAGAGATGCAAGAAATG 180  
QY 475 GTTACGGTTGATATGATACATCAGCAGCAATGACAGGATCAGGATGTCAGCAGAC 534  
Db 181 GTTACGGTTGATATGATACATCAGCAGCAATGACAGGATCAGGATGTCAGCAGAC 240  
QY 535 AAAGATTCACCTCAAAAGGCAATTTGATGATGATCACCACAAAGTAAATCTGTGATTGAA 594  
Db 241 AAAGATTCACCTCAAAAGGCAATTTGATGATGATCACCACAAAGTAAATCTGTGATTGAA 300  
QY 595 AAGATTAACACCCCAATTTGAAGCTGTGGGAAGAAATTCGCTAATTAGAGAAAAAGCTG 654  
Db 301 AAGATTAACACCCCAATTTGAAGCTGTGGGAAGAAATTCGCTAATTAGAGAAAAAGCTG 360  
QY 655 GAGAACTGGAACAAAGATGGAAGAGCGGGTTCTGATGAT 694  
Db 361 GAGAACTGGAACAAAGATGGAAGAGCGGGTTCTGATGAT 400

RESULT 6  
US-09-918-568-34  
Sequence 34, Application US/09918568  
Patent No. US20020054882A1  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING

NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wendt, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/918,568  
FILING DATE: 02 Aug--2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993

ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX: <Unknown>

INFORMATION FOR SEQ. ID NO. 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 409 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: cDNA no genomic RNA  
HYPOTHEetical: <Unknown>  
ANTI-SENSE: <Unknown>  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: A/adachi/2/57  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>  
CELL LINE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>

FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:

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1  PAGES:
2  DATE:
3  DOCUMENT NUMBER:
4  FILING DATE:
5  PUBLICATION DATE:
6  RELEVANT RESIDUES IN SEQ ID NO:
7  SEQUENCE DESCRIPTION: SEQ ID NO: 34:
8  US-09-918-568-34
9
10 Query Match      35.0%; Score 397; DB 9; Length 409;
11 Best Local Similarity 98.8%; Pred.No. 2,2e-98;
12 Matches 400; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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14 QY      290  TGGGAGCATATAATACACATTACCTTTTCACATGTCACCCACTGACATFAGGTAGT 349
15          |||||
16          5  TTGGGCAATATAATACACATTGCTTTTCACAAATGTCACCCACTGACATFAGGTAGT 64
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18 QY      350  GCCCCAATATGTAATAATCGGAGAAGTGGCTTAGCAACAGAGCTAGAGTAAGTAATGTTCCCC 409
19          |||||
20          65  GCCCCAATATGTAATAATCGGAGAAGTGGCTTAGCAACAGAGCTAGAGTAAGTAATGTTCCCC 124
21
22 QY      410  AGATTGAATCAAGAGATTGTTTGGGCAATAGCTGTTTATAGAAAGAGATGGCAAG 469
23          |||||
24          125  AGATTGAATCAAGAGATTGTTTGGGCAATAGCTGTTTATAGAAAGAGATGGCAAG 184
25
26 QY      470  GAATGCTTGACGCTTGGTATGATACCAATGACAGCAATGACAGGATCAGGTAATGCAG 529
27          |||||
28          185  GAATGCTTGATGTTGGTATGATACCAATGACAGCAATGACAGGATCAGGTAATGCAG 244
29
30 QY      530  CAGACAAAGATCCACATCAAAAGCATTTGATGTAATACCAACAGTAATTTCTGTGA 589
31          |||||
32          245  CAGACAAAGATCCACATCAAAAGCATTTGATGTAATACCAACAGTAATTTCTGTGA 304
33
34 QY      590  TTGAAAAGATTAACACCCATTTGAAAGCTGTTGGAAAGAAATTCGTAACCTTAGAGAAA 649
35          |||||
36          305  TTGAAAAGATTAACACCCATTTGAAAGCTGTTGGAAAGAAATTCGTAACCTTAGAGAAA 649
37
38 QY      650  GACTGGAGAACTTGAACAAAAAGATGGAAGACGGGTTCTAGATG 694
39          |||||
40          365  GACTGGAGAACTTGAACAAAAAGATGGAAGACGGGTTCTAGATG 409
41
42 Db
43
44 RESULT 7
45 US-09-918-568-35
46 ; Sequence 35, Application US/09918568
47 ; Patent No. US20020054882A1
48 ; GENERAL INFORMATION:
49 APPLICANT: Yoshinobu OKUNO,et al.
50 TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
51 ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
52 NUMBER OF SEQUENCES: 58
53 CORRESPONDENCE ADDRESS:
54 ADDRESS: Wenderoth, Lind & Ponack, L.L.P.
55 STREET: 2033 K Street, N.W., #800
56 CITY: Washington
57 STATE: D.C.
58 COUNTRY: U.S.A.
59 ZIP: 20006
60
61 COMPUTER READABLE FORM:
62 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
63 COMPUTER: IBM Compatible
64 OPERATING SYSTEM: MS-DOS
65 SOFTWARE: Wordperfect 5.1
66 CURRENT APPLICATION DATA:
67 APPLICATION NUMBER: US/09/918,568
68 FILING DATE: 02-Aug-2001
69 CLASSIFICATION: <Unknown>
70 PRIOR APPLICATION DATA:
71 APPLICATION NUMBER: 09/004,422
72 FILING DATE: January 8, 1998
73 APPLICATION NUMBER: 08/443,862
74 FILING DATE: May 22, 1995
75 APPLICATION NUMBER: 08/229,781

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QY 46 AACGATGGTTGCGGTTGGTATGGATGCATCAGCAATGACAGGAGTACGGGTATG 526  
 183 AAGGAATGATGATGGTTGGTATGGATACCATCAGCAAGATGATCAGGGATCAGGGTTGG 242  
 QY 527 CACGACAGCAAAAGATTCACACTCAAAGGCAATTTGATGGAATCACCACCAAGTAAATCTG 586  
 243 CACGACAGCAAAAGATTCACACTCAAAGGCAATTTGATGGAATCACCACCAAGTAAATCTG 302  
 QY 587 TGATTTAAAGATTAACACCCCAATTTGAAGCTGTTGGAAAGAAATTCGTAACCTAGAGA 646  
 303 TGATTTAAAGATTAACACCCCAATTTGAAGCTGTTGGGAAAGAAATTCATTAATTTAGAGA 362  
 QY 647 AAGAGCTGGAGAACTTGAACAAAAGATGAGAAAGCGGTTTCAGATG 694  
 Db 363 AAGAGCTGGAGAACTTGAACAAAAGATGAGAAAGCGGTTTCAGATG 410  
 RESULT 8  
 US-09-918-568-36  
 Sequence 36, Application US/09918568  
 Patent No. US20020034882A1  
 GENERAL INFORMATION:  
 TITLE OF INVENTION: Yoshinobu OKUNO et al.  
 APPLICANT: POLYPEPTIDES FOR USE IN GENERATING  
 ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
 NUMBER OF SEQUENCES: 58  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Wenderoth, Lind & Penack, L.L.P.  
 STREET: 2033 K Street, N.W., #800  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20006  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/918,568  
 FILING DATE: 02-Aug-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/004,422  
 FILING DATE: January 8, 1998  
 APPLICATION NUMBER: 08/443,862  
 FILING DATE: May 22, 1995  
 APPLICATION NUMBER: 08/229,781  
 FILING DATE: April 19, 1994  
 APPLICATION NUMBER: 08/054,016  
 FILING DATE: April 29, 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warren M. Cheek, Jr.  
 REGISTRATION NUMBER: 33,367  
 REFERENCE/DOCKET NUMBER: <Unknown>  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-721-8200  
 TELEFAX: 202-721-8250  
 TELEX: <Unknown>  
 INFORMATION FOR SEO ID NO: 36:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 394 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to genomic RNA  
 HYPOTHETICAL: <Unknown>  
 ANTI-SENSE: <Unknown>  
 FRAGMENT TYPE: <Unknown>  
 ORIGINAL SOURCE:  
 ORGANISM: A/kaiizuka/2/65  
 STRAIN: <Unknown>

INDIVIDUAL ISOLATE: <Unknown>  
 DEVELOPMENTAL STAGE: <Unknown>  
 HAPOTYPE: <Unknown>  
 TISSUE TYPE: <Unknown>  
 CELL TYPE: <Unknown>  
 CELL LINE: <Unknown>  
 ORGANELLE: <Unknown>  
 IMMEDIATE SOURCE:  
 LIBRARY: <Unknown>  
 CLONE: <Unknown>  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT: <Unknown>  
 MAP POSITION: <Unknown>  
 UNITS: <Unknown>  
 FEATURE:  
 NAME/KEY:  
 LOCATION:  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 PUBLICATION INFORMATION:  
 AUTHORS:  
 TITLE:  
 JOURNAL:  
 VOLUME:  
 ISSUE:  
 PAGES:  
 DATE:  
 DOCUMENT NUMBER:  
 FILING DATE:  
 PUBLICATION DATE:  
 RELEVANT RESIDUES IN SEQ ID NO:  
 SEQUENCE DESCRIPTION: SEQ ID NO: 36;  
 US-09-918-568-36

Query Match 33.4%; Score 379.6; DB 9; Length 394;  
 Best Local Similarity 97.7%; Pctd. No. 1.2e-93;  
 Matches 385; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 301 AATACAACTTACCTTTTCACATGTCACCCACATAGTGTGAGTCCCAATAT 360  
 Db 1 AATACAACTTACCTTTTCACATGTCACCCACATAGTGTGAGTCCCAATAT 60  
 QY 361 GTAATCGAGAGTTGGTCTTACGACAGAGCTAAGAGATGTTCCAGATTGATCA 420  
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 QY 421 AAGAGTTGTTGGCCATAGTGTGTTTATGAAGAGAGATGCGAAGATGTTGAC 480  
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 QY 661 TTGAACAAAAGATGGAAGCGGGTTCTAGATG 694  
 Db 361 TTGAACAAAAGATGGAAGCGGGTTCTAGATG 394

TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
 ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
 NUMBER OF SEQUENCES: 58  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
 STREET: 2033 K Street, N.W., #800  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20006  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/918,568  
 FILING DATE: 02-Aug-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/004,422  
 FILING DATE: January 8, 1998  
 APPLICATION NUMBER: 08/443,862  
 FILING DATE: May 22, 1995  
 APPLICATION NUMBER: 08/229,781  
 FILING DATE: April 19, 1994  
 APPLICATION NUMBER: 08/054,016  
 FILING DATE: April 29, 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warren M. Cheek, Jr.  
 REGISTRATION NUMBER: 33,367  
 REFERENCE/DOCKET NUMBER: <Unknown>  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-721-8200  
 TELEFAX: 202-721-8250  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 54:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1777 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to genomic RNA  
 HYPOTHETICAL: <Unknown>  
 ANTI-SENSE: <Unknown>  
 FRAGMENT TYPE: <Unknown>  
 ORIGINAL SOURCE:  
 ORGANISM: A2/Alch1/2/68  
 STRAIN: <Unknown>  
 INDIVIDUAL ISOLATE: <Unknown>  
 DEVELOPMENTAL STAGE: <Unknown>  
 HAPOTYPE: <Unknown>  
 TISSUE TYPE: <Unknown>  
 CELL TYPE: <Unknown>  
 CELL LINE: <Unknown>  
 ORGANELLE: <Unknown>  
 IMMEDIATE SOURCE:  
 LIBRARY: <Unknown>  
 CLONE: <Unknown>  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT: <Unknown>  
 MAP POSITION: <Unknown>  
 UNITS: <Unknown>  
 FEATURE:  
 NAME/KEY:  
 LOCATION:  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 PUBLICATION INFORMATION:  
 AUTHORS:  
 TITLE:  
 JOURNAL:  
 VOLUME:





INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>  
CELL LINE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
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LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
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AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 29;  
US-09-918-568-29

Query Match 22.2% Score 251.6; DB 9; Length 442;  
Best Local Similarity 73.1% Pred. No. 1,4e-58;

Matches 333; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 313 CTTTTCACAAATGCCACCACTGACAAATAGTGAGTGGCCCAAAATGTAAATCGAG 372  
DB 1 CTTTTCACAAATATACACCACTGACAAATAGTGAGTGGCCCAAAATCGAGATGCC 60  
QY 373 AAGTTGCTTTCACCAAGGACTAAGGAATGTTCCCAAGATTGATCAAGAGATTGTTT 432  
DB 61 AATTTGAGGATGTTACAGGACTAAGGAATGTTCCCAAGATTGATCAAGAGATTGTTT 120  
QY 433 GGGGCAATAGTGGTTTATAGAGGAGATGGCAAGAAATGTTGAGGTTGATGGA 492  
DB 121 GAGGCATTTGCCGTTTATTAAGGGGATGACTGAAATGATGATGATGATGAT 180  
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DB 181 TATCATCATCAGAAATGAACAGGATCAGGATGATGACAGGATCAAAAGAACAAAT 240  
QY 553 GCATTGATGAAATCAACCAAGGTAATTTCTGATGTAAGAAAGATTAACACCAATTT 612  
DB 241 GCCATTAAAGGATTAACAAGGAACTGTTATCGAGAAATGAACACTCAATTC 300  
QY 613 GAAGCTGTTGGGAAGAAATTCGTAACCTAGAGAAAGAACTGGAGAACTGAACAAAG 672  
DB 301 ACAGCTGTGGTTAAAGAAATTAACAAGAAAGAAAGATGAAATTAATTAATAAAG 360  
QY 673 ATGAAGAAGGTTCTAGATGTGAGACATACAAATGCTGAGCTTTTACTGATGGA 732  
DB 361 GTTGATGATGATTTCTGACATTTTGACATATATATGCAATTTGTTACTGGA 420  
QY 733 AATGAGAGACACTGACTTTC 754  
DB 421 AATGAAGAGACTCTGATTTCC 442

RESULT 12  
US-09-918-568-32

Sequence 32, Application US/09918568  
Patent No. US20020054882A1  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/918,568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/228,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 429 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL: <Unknown>  
ANTI-SENSE: <Unknown>  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: A/Osaka/930/88  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>  
CELL LINE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:





Db 1 CCTTCCAGATGTCACCCAGTCACATAGAGAGTCCCAAGTACGTCAAGAGTACA 60  
QY 373 AAGTTGCTTTAGCAACAGAGTAAAGATGTTCCCAAGATTGAATCAAGAGATTGTT 432  
Db 61 AAATTAGAGATGTTACAGAGTAAAGATGTTCCCAAGATTGAATCAAGAGATTGTT 120  
QY 433 GGGGCAATAGCTGTTTATAGAGAGAGATGCGCAAGAAATGGTTGACGGTTGTATGA 492  
Db 121 GGAGCATATGCGGTTTCATTAAGAGGGGATGAGTGAATGATAGATGATGTTATCGT 180  
QY 493 TACCATCAGACAGATGACAGGATGAGTATGCGACAGACAAATCCACTCAAAAG 552  
Db 181 TATCATCTCAGATGACAGAGATCTGGCTATGCTGCGATCAAAAAAGCACAAAT 240  
QY 553 GCATTGTGATGATACCAACAGATTAATCTGTGATGAAAGATTAACACACCAATTT 612  
Db 241 GCCATTAAAGGATTAACAACAGAGTACTCTGTATGAGAAATGAACACTCAATTC 300  
QY 613 GAAGCTGTTGGAAAGATTCGGTAACTTAGAGAAAAAGCTGAGAACTTGAACAAAAG 672  
Db 301 ACAGCTGTGGTAAAGAAATTCACAAATTAAGAAAAAGATGAAATTAATAAAAA 360  
QY 673 ATGGAAGAGGGTCTCTAGATGATGACATACAAATGCTGAGCTTTTACTTCTGATGAA 732  
Db 361 GTTGATGATGATTTCTTGACATTTGACATATAATGCAGAATGTTGGTTCTACTGAA 420  
QY 733 AATG 736  
Db 421 AATG 424

## RESULT 14

US-09-918-568-31  
Sequence 31, Application US/09918568  
Patent No. US20020054882A1  
GENERAL INFORMATION:  
APPLICANT: TOSHINOBU OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/918, 568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX: <unknown>

INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 424 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL: <unknown>  
ANTI-SENSE: <unknown>  
FRAGMENT TYPE: <unknown>  
ORIGINAL SOURCE:  
ORGANISM: A/Yamagata/120/86  
STRAIN: <unknown>  
INDIVIDUAL ISOLATE: <unknown>  
DEVELOPMENTAL STAGE: <unknown>  
HAPLOTYPE: <unknown>  
TISSUE TYPE: <unknown>  
CELL TYPE: <unknown>  
CELL LINE: <unknown>  
ORGANELLE: <unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <unknown>  
CLONE: <unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <unknown>  
MAP POSITION: <unknown>  
UNITS: <unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-918-568-31  
Query Match 20.6%; Score 233.6; DB 9; Length 424;  
Best Local Similarity 71.9%; Pred. No. 1.1e-53;  
Matches 305; Conservative 0; Mismatches 119; Indels 0; Gaps 0;  
QY 313 CCTTTACAGATGTCACCCAGTCACATAGAGAGTCCCAAGTACGTAAATGAGAG 372  
Db 1 CCTTCCAGATGTCACCCAGTCACATAGAGAGTCCCAAGTACGTAAATGAGAGTACA 60  
QY 373 AAGTTGCTTTAGCAACAGAGTAAAGATGTTCCCAAGATTGAATCAAGAGATTGTT 432  
Db 61 AAATTAGAGATGTTACAGAGTAAAGATGTTCCCAAGATTGAATCAAGAGATTGTT 120  
QY 433 GGGGCAATAGCTGTTTATAGAGAGAGATGCGCAAGAAATGGTTGACGGTTGTATGA 492  
Db 121 GGAGCATATGCGGTTTCATTAAGAGGGGATGAGTGAATGATAGATGATGTTATCGT 180  
QY 493 TACCATCAGACAGATGACAGGATGAGTATGCGACAGACAAATCCACTCAAAAG 552  
Db 181 TATCATCTCAGATGACAGAGATCTGGCTATGCTGCGATCAAAAAAGCACAAAT 240  
QY 553 GCATTGTGATGATACCAACAGATTAATCTGTGATGAAAGATTAACACACCAATTT 612  
Db 241 GCCATTAAAGGATTAACAACAGAGTACTCTGTATGAGAAATGAACACTCAATTC 300  
QY 613 GAAGCTGTTGGAAAGATTCGGTAACTTAGAGAAAAAGCTGAGAACTTGAACAAAAG 672

Db 301 ACAGCTGTGGCAAAATTCACAAATTAGAAAAGATGAGAAACTTAAATAAAAA 360  
QY 673 ATGGAACAGCGGTTTATAGATGTGGACATACAAATCGAGCTTTAGTTGATGAGAA 732  
Db 361 GTTGATGATGATTTTGGCAATTTGGACATTTATATGCAAAATGTTGGTCTACTGGA 420  
QY 733 AATG 736  
Db 421 AATG 424

RESULT 15  
US-10-099-619-1  
: Sequence 1, Application US/10099619  
: Publication No. US2002016834A1  
: GENERAL INFORMATION:  
: APPLICANT: CLAESSENS, JOHANNES AJ  
: APPLICANT: WALTER, FUCHS  
: TITLE OF INVENTION: RECOMB  
: FILE REFERENCE: 20010010US  
: CURRENT APPLICATION NUMBER: US/10/099,619  
: PRIOR APPLICATION DATE: 2002-03-15  
: PRIOR FILING DATE: 2001-03-15  
: NUMBER OF SEQ ID NOS: 2  
: SOFTWARE: PatentIn version 3.1  
: SEQ ID NO 1  
: LENGTH: 1711  
: TYPE: DNA  
: ORGANISM: AVIAN INFLUENZA VIRUS  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: (11)..(1705)  
: OTHER INFORMATION: ISOLATE A/ITALY/445/99 (H7/N1)  
US-10-099-619-1

Query Match 20.4%; Score 233.6; DB 13; Length 1711;  
Best Local Similarity 56.4%; Pred. No. 2,5e-53;  
Matches 493; Conservative 0; Mismatches 369; Indels 18; Gaps 2;

QY 232 GGGATCATGAAACAAAGAGACACTGTAGACCAAAATGCCAAACTCTTGG 291  
Db 833 GGGATTCAGAGTGAATACAGTTGAMGCCAATTTGMAAGAGATTGCTATCACAGTGA 892  
QY 292 GGAGCATATAATCAATATTACTTTTCACAAATGTCACCCACTGACAAATAGTGATGC 351  
Db 893 GGGACATATAATAGTATTGGCCCTTCAGAACATAATATAGCAGGGCAGTAGGGAATGT 952  
QY 352 CCCAAATATGTAAATCGGAGAGTTGGTCTTAGCAACAGAGACTAAGGAATGTCCCGAG 411  
Db 953 CCGAGATATGTTAAGTAAGAGACTGTGCTGCTGCAACAGGAGTGAAGATGTTCCCGAA 1012  
QY 412 ATTGAATCA-----AGAGATTGTTGGGCAATAGCTGCTTTTATAGAA 456  
Db 1013 ATTCAAAAAGATCGAGTGTGAGAGAGAGGCTATTGTTGCTCTATAGCGGTTTCATTGAA 1072  
QY 457 GGAGATGGCAAGGATGGTTGACGTTGTATGATACCATCAAGCAATGACAGGGA 516  
Db 1073 AATGATGGGAAGGTGTGATGTGGTGTATGCTTCAGGGCATCAAAATGCAAGGA 1132  
QY 517 TCAGGATATGACAGCAACAAAGATCCACTTATGATGGAATCACCACAAG 576  
Db 1133 GAGGAACTGCTGCAATTTCAAAAGACCCCAATTCAGCAATTTATCAAGTAAAGAGAAA 1192  
QY 577 GTAAATTCGTGTATTTAAAGATTAACACCCCAATTTGAAGCTGTGGAAAAGATTCGGT 636  
Db 1193 TTGAACCGGCTTATTAATAAAACTAACCAACAAATTTGAGTTATATAGCAATGATTCAC 1252  
QY 637 AACTTAGAGAAAGATTTGGAGAACTTGACAAAAAGATGAGACGGGTTTCTAGATGTG 696  
Db 1253 GAGGTTGAAAAGCAATTTGGCAATGTGATTAATTTGAGACCAAGATTCACAGCAAGTG 1312  
QY 697 TGACATACAAATGCTAGCTTTAGTTCGATGAGAAATGAGAGACACTTGACTTCAT 756

Db 1313 TGGTCTATATAAGCTGAACCTCTGTGTAGCAATGAGAGAACCGACATACATTTGATCTGACC 1372  
QY 757 GATTCTATATGTCAGAAATCTGTATAGTAAGTCAAGATGCAAGTGAAGACACAGTAAA 816  
Db 1373 GACTCAGAAATGAAACAAACTATACGAAACGAGTGAAGACTACTAGACAGAAATGCTGAA 1432  
QY 817 GAAGTGAAGATGATGTTTGAATTTATACAAATGTATGATGATGATGATGATGATGATGAT 876  
Db 1433 GAAGATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1492  
QY 877 GTGAAAAACGAGACATATGATTTATCCCAAGTATGAAAGAGTCTAAACTAAATAGAAAT 936  
Db 1493 ATTAGAAACAAACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1552  
QY 937 GAATCAAGAGGGTAAATTTGAGCAGCAGTGGGGTTATCAAAATCCTTGCATTATAGCT 996  
Db 1553 CAGATTGACCCAGTCAAACTAAGCAGCGGCTACAAAGATGATGATGATGATGATGATGATG 1612  
QY 997 ACAGTACAGGTTCTATGCTACGCTGCAATGATGATGATGATGATGATGATGATGATGATG 1056  
Db 1613 GGGGCATCATGTTTCATATCTTGGCCATTGCAATGGGCTTGTCTTCATATATGTAG- 1671  
QY 1057 TCCAACGGTCTCTGCAAGTGCAGAGATCTGCATATGATTAAT 1096  
Db 1672 -AAATGAAACAAATGCGGCTGACATTTGATATTAATTT 1709

Search completed: August 9, 2003, 19:22:41  
Job time: 185.31 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 18:45:33 ; Search time 2795.67 Seconds

(without alignments)  
16242.876 Million cell updates/sec

Title: US-09-918-568-57

Perfect score: 1110

Sequence: 1 CTAGACGCAACACAGGAT.....TAAACACCCCTGTTCTG 1110

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Genem1:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_ph:\*  
7: gb\_pl:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sy:\*  
11: gb\_un:\*  
12: gb\_vl:\*  
13: gb\_vl:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_ph:\*  
24: em\_pi:\*  
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40: em\_pi:\*  
41: em\_pi:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1110	100.0	1110	6	AR181971	AR181971 Sequence
2	1110	100.0	1110	6	E08894	E08894 DNA encodin
3	1110	100.0	1110	6	I32536	I32536 Sequence 57
4	1110	100.0	1110	6	I43481	I43481 Sequence 57
5	868	78.2	1777	6	AR181968	AR181968 Sequence
6	868	78.2	1777	6	I32533	I32533 Sequence 54
7	868	78.2	1777	6	I43478	I43478 Sequence 54
8	867	78.1	1765	14	OR1N11	V01085 Hemagglutin
9	862.2	77.7	1736	14	AF348176	AF348176 Influenza
10	862.2	77.7	1736	14	AF348177	AF348177 Influenza
11	862.2	77.7	1765	14	OR1N16	V01103 Influenza
12	860.6	77.5	1736	14	AF348178	AF348178 Influenza
13	860.6	77.5	1736	14	AF348179	AF348179 Influenza
14	860.6	77.5	1765	14	FLAHMA	J02135 Influenza A
15	860.6	77.5	1765	14	INA289703	AJ289703 Influenza
16	851	76.7	1765	14	FLAHM2	M55059 Influenza
17	851	76.7	1765	14	FLAHM2	J02132 Influenza
18	843	75.9	1738	14	FLAHM1	J02090 Influenza
19	833.4	75.1	1765	6	AX350190	AX350190 Sequence
20	832	75.0	1764	6	AX350204	AX350204 Sequence
21	831.8	74.9	1768	14	OR1N12	V01086 Hemagglutin
22	830.2	74.8	1765	14	FLAN2HAC	M73774 Influenza
23	830.2	74.8	1765	14	OR1N1	V01098 Influenza
24	827.6	74.6	1765	14	FLADORNHA	M54895 Influenza
25	814.8	73.4	1744	14	IA007146	U07146 Influenza
26	814.2	73.4	1653	14	FLAHM3DKC	M16739 Influenza
27	811.6	73.1	1762	6	ORA77HA	X05907 Influenza
28	808.4	72.8	1653	14	FLAHM3DKG	E01133 CDNA encodl
29	807.8	72.8	1653	14	FLAHM3DKF	M16743 Influenza
30	806.2	72.6	1653	14	FLAHM3DKA	M16737 Influenza
31	803	72.3	1653	14	OR1N15	V01089 Influenza
32	803	72.3	1653	14	OR1N15	V01089 Influenza
33	801.4	72.2	1685	14	IYU08858	U08858 Influenza
34	801.4	72.2	1685	14	IYU08859	U08859 Influenza
35	801.4	72.2	1685	14	IYU08905	U08905 Influenza
36	795	71.6	1765	14	FLAN2HAD	M73775 Influenza
37	791.8	71.3	1653	14	FLAHM3DKB	M16738 Influenza
38	791.2	71.3	1647	14	FLAHM3	M19057 Influenza
39	788	71.0	1647	14	FLAHM3	M19056 Influenza
40	787	70.9	1653	14	FLAHM3	J02092 Influenza
41	785.4	70.8	1653	14	FLAHM3	D00929 Influenza
42	783.8	70.6	1653	14	FLAHM3DKD	M16740 Influenza
43	782.2	70.5	1759	14	IY1252129	AJ5252129 Influenza
44	782.2	70.5	1759	14	IY1252131	AJ5252131 Influenza
45	780.6	70.3	1653	14	FLA1076HA	D00930 Influenza

#### ALIGNMENTS

RESULT 1  
AR181971  
LOCUS AR181971 1110 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 57 from patent US 6337070.  
ACCESSION AR181971  
VERSION AR181971.1 GI:20224887  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1110)  
AUTHORS Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.  
TITLE Polypeptides for use in generating anti-human influenza virus  
antibodies  
JOURNAL Patent: US 6337070-A 57 08-JAN-2002;

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FEATURES
  source
    1..1110
    /organism="unknown"
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Query Match      100.0%; Score 1110; DB 6; Length 1110;
Best Local Similarity 100.0%; Pred. No. 4.2e-295;
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ATTTTCTGTGCTCTCGGCCAAGACCTTCCAGGAAATGACAAGCAGCAGCAGCTG 120
    |||
DB 61 ATTTTCTGTGCTCTCGGCCAAGACCTTCCAGGAAATGACAAGCAGCAGCAGCTG 120

QY 121 TGCCCTGGGACATCATGCGGTGCCAAGCGAACACTAGTGAANAACATCAGATGATCAG 180
    |||
DB 121 TGCCCTGGGACATCATGCGGTGCCAAGCGAACACTAGTGAANAACATCAGATGATCAG 180

QY 181 ATTGAAGTGAATAGCTACTAGTACTGAGTCTCCTCAACGGGGAAATATGCAAC 240
    |||
DB 181 ATTGAAGTGAATAGCTACTAGTACTGAGTCTCCTCAACGGGGAAATATGCAAC 240

QY 241 AATATGTATACCTGTATTTCTGAATGATCATCTCCAAATGGAAGCATTTCCCAATGACAAG 300
    |||
DB 241 AATATGTATACCTGTATTTCTGAATGATCATCTCCAAATGGAAGCATTTCCCAATGACAAG 300

QY 301 CCCTTTCAAAAGCTAACAAGATCATATGAGAGCATGCCCAAGTATGTTAAGCAAAAC 360
    |||
DB 301 CCCTTTCAAAAGCTAACAAGATCATATGAGAGCATGCCCAAGTATGTTAAGCAAAAC 360

QY 361 ACCCTGAAGTGGCAACAGGATGGGCAATGACCAAGAAACAACATAGAGCCTATTC 420
    |||
DB 361 ACCCTGAAGTGGCAACAGGATGGGCAATGACCAAGAAACAACATAGAGCCTATTC 420

QY 421 GGGCAATAGCAGGTTTCTATAGAAATGTTGGGAGGAAATGATAGAGGTGTGACGCT 480
    |||
DB 421 GGGCAATAGCAGGTTTCTATAGAAATGTTGGGAGGAAATGATAGAGGTGTGACGCT 480

QY 481 TTTCAGCATCAAAATTTCTGAGGGCACAGACAGCAGCAGATCTTAAAGCACTCAAGCA 540
    |||
DB 481 TTTCAGCATCAAAATTTCTGAGGGCACAGACAGCAGCAGATCTTAAAGCACTCAAGCA 540

QY 541 GCCATCGCAAAATCAATGGAATTTGAACAGGTTAATCGAAGACAGACAGCAAAATTC 600
    |||
DB 541 GCCATCGCAAAATCAATGGAATTTGAACAGGTTAATCGAAGACAGACAGCAAAATTC 600

QY 601 CATCAAAATCGAAAGAAATTTCTCAGAAATAGAGGAGAAATTCAGAGCCTCGAGAAATAC 660
    |||
DB 601 CATCAAAATCGAAAGAAATTTCTCAGAAATAGAGGAGAAATTCAGAGCCTCGAGAAATAC 660

QY 661 GTTGAAGACATTAATATGATCTGCTGCTTACAAATGCGGAGCTTCTGTGCTGTGAG 720
    |||
DB 661 GTTGAAGACATTAATATGATCTGCTGCTTACAAATGCGGAGCTTCTGTGCTGTGAG 720

QY 721 AATCAACATACAAATTTGACCTGACTGACTCGGAATGAAACAGCTTTGAAAAAACAAG 780
    |||
DB 721 AATCAACATACAAATTTGACCTGACTGACTCGGAATGAAACAGCTTTGAAAAAACAAG 780

QY 781 AGGCACTGAGGAGAAATGCTGAAGAGATGGCAATGCTTCAAAATATACACAAA 840
    |||
DB 781 AGGCACTGAGGAGAAATGCTGAAGAGATGGCAATGCTTCAAAATATACACAAA 840

QY 841 TTGACAAACGCTTGCATAGAGTCAATCAGAAATGTTACTTATGACCATGATGATACAGA 900
    |||
DB 841 TTGACAAACGCTTGCATAGAGTCAATCAGAAATGTTACTTATGACCATGATGATACAGA 900

QY 901 GAGCAACATTAACAACACCGCTTTCAGATCAAAAGTGTGAAGTGAAGTGTGATACAAA 960
    |||
DB 901 GAGCAACATTAACAACACCGCTTTCAGATCAAAAGTGTGAAGTGAAGTGTGATACAAA 960

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QY 961 GACTGATCCCTGGATTTCCCTTGGCATATCATGCTTTTGGTGTGTTGCTG 1020
    |||
DB 961 GACTGATCCCTGGATTTCCCTTGGCATATCATGCTTTTGGTGTGTTGCTG 1020

QY 1021 GGGTTCATCATATGCGCCTGCGAGAGGCAACATTAAGTCAACATTTGCATTGAGTG 1080
    |||
DB 1021 GGGTTCATCATATGCGCCTGCGAGAGGCAACATTAAGTCAACATTTGCATTGAGTG 1080

QY 1081 TATTAGTATTAATAAACACCCCTGTGTTCTG 1110
    |||
DB 1081 TATTAGTATTAATAAACACCCCTGTGTTCTG 1110

RESULT 2
E08994
LOCUS      E08994      1110 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION DNA encoding an immunogenic peptide derived from human influenza A
            virus haemagglutinin that doesn't have globular region.
ACCESSION  E08994
VERSION    E08994.1 GI:22024632
KEYWORDS   JP 1995089992-A/4.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 1110)
AUTHORS    Okuno,Y., Isekawa,Y., Sasao,F. and Ueda,S.
TITLE      IMMUNOGENIC ARTIFICIAL POLYPEPTIDE
JOURNAL    Patent: JP 1995089992-A 4 04-APR-1995;
            TAKARA SHUZO CO LTD
COMMENT
  OS       None
  NC       Artificial sequences.
  PN       JP 1995089992-A/4
  PD       04-APR-1995
  PE       16-MAR-1994 JP 1994070194
  PF       20-APR-1993 JP 93P 115216
  PI       OKUNO YOSHINOBU, ISEKAWA YUJI, SASAO FUYOKO, UEDA SHIGEHARU PC
  C07K7/08,A61K39/145,C12N15/44,C12P21/02,C12N15/06,C12P21/08, PC
  (C12P21/02,
  PC       C12R1:91),(C12P21/08,C12R1:91),C07K9:00;
  CC       Strandedness: Double;
  FH       Key
  FE       Location/Qualifiers
  FT       source      1..1110
            /organism="artificial sequences" FT      CDS
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FEATURES
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    /mol_type="genomic DNA"
    /db_xref="taxon:32644"
BASE COUNT      374 a      216 c      258 g      262 t
ORIGIN
Query Match      100.0%; Score 1110; DB 6; Length 1110;
Best Local Similarity 100.0%; Pred. No. 4.2e-295;
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTAGAGCAAGCAGGGGATATTTCTATTAATCATGAGACCATCTGCTTGAAGTAC 60

QY 61 ATTTTCTGTGCTCTCGGCCAAGACCTTCCAGGAAATGACAAGCAGCAGCAGCTG 120
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QY 121 TGCCCTGGGACATCATGCGGTGCCAAGCGAACACTAGTGAANAACATCAGATGATCAG 180
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 Db 241 AATATTGATGACTGTCTTTCTGAATGCATCACTCCAAATGGAAGCATTTCCCAATGACAG 300  
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 Db 301 CCCCTTCAAAACGCTAACAGATCACATATGAGAGATGCCCAAGATATGTTTAAGCAAAAC 360  
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 Db 361 ACCCTGAAGTTGGCAACAGAGATGCGGAATGTACAGAGAAACAAACTAGAGGCTATTC 420  
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 Db 421 GCGCGAATAGCAGGTTTCATAGAAAATGTTGGAGGGAATGATAGACGTTGTACGGT 480  
 QY 481 TTCAGGATCAAAATTTCTGAGGCAAGAGCAAGCATCTTAAAGCACTCAAGCA 540  
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 QY 541 GCCATCGACCAAAATCAATGGGAAATTTGAACAGGTAATCGAGAGACGAAACGAGAAATTC 600  
 Db 541 GCCATCGACCAAAATCAATGGGAAATTTGAACAGGTAATCGAGAGACGAAACGAGAAATTC 600  
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 Db 661 GTTGAAGACACTAAATAATGATCTGTGTACAAATGCGAGACTTCTTGCTCTGAG 720  
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 Db 721 AATCAACATACAAATTTGACCTGACTCTGGAATGAACAAAGCTGTTGAAAAAACAAG 780  
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 Db 1021 GGGTTCATCATGTGGGCTGCGCAGAGAGGCAACATTAGGTGCAACATTTGCAATTTGAGTG 1080  
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RESULT 3  
 LOCUS 132536 1110 bp DNA linear PAT 06-FEB-1997  
 DEFINITION Sequence 57 from patent US 5589174.  
 ACCESSION 132536  
 VERSION 132536.1 GI:1823327  
 KEYWORDS  
 SOURCE Unknown.

ORGANISM Unknown.  
 REFERENCE Unclassified.  
 1 (bases 1 to 1110)  
 AUTHORS Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.  
 TITLE Anti-human Influenza virus antibody  
 JOURNAL Patent: US 5589174-A 57 31-DEC-1996;  
 FEATURES Location/Qualifiers  
 source 1..1110  
 BASE COUNT 374 a 216 c 258 g 262 t.  
 ORIGIN  
 Query Match 100.0%; Score 1110; DB 6; Length 1110;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-295;  
 Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGAAGCAAGCAGGGGATTAATTTCTATTATCATGAGACCATCTTCTTGAGCTAC 60  
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 Db 241 AATATTGATGACTGTATTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 300  
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 Db 301 CCCCTTCAAAACGTAACAGATCAATATGAGAGATGCCCAAGTATGTTAAGCAAAAC 360  
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 Db 361 ACCCTGAAGTTGGCAACAGAGATGCGGAATGTACAGAGAAACAAACTAGAGGCTATTC 420  
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 Db 421 GCGGAATAGCAGGTTTCTATAGAAAATGTTGGAGGGAATGATGAGGCTGTACGGT 480  
 QY 481 TTCAGGATCAAAATTTCTGAGGCAAGAGCAAGCATCTTAAAGCACTCAAGCA 540  
 Db 481 TTCAGGATCAAAATTTCTGAGGCAAGAGCAAGCATCTTAAAGCACTCAAGCA 540  
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Db 1081 TATTAGTAATTAATAAACACCCCTGTTCTG 1110

RESULT 4  
143481  
LOCUS 143481 1110 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 57 from patent US 5631350.  
ACCESSION 143481  
VERSION 143481.1 GI:2468725  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1110)  
AUTHORS Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.  
TITLE Anti-human influenza virus antibody  
JOURNAL Patent: US 5631350-A 57 20-May-1997;  
FEATURES  
Source 1..1110  
Location/Qualifiers  
/organism="unknown"  
BASE COUNT 374 a 216 c 258 g 262 t  
ORIGIN

Query Match 100.0%; Score 1110; DB 6; Length 1110;  
Best Local Similarity 100.0%; Pred. No. 4.2e-25;  
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 421 GCGGCAATAGCAGGTTTCATAGAAATGTTGGAGGGAATGATGAGCGTTGATACGCT 480

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RESULT 5  
AR181968  
LOCUS AR181968 1777 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 54 from patent US 6337070.  
ACCESSION AR181968  
VERSION AR181968.1 GI:20224864  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1777)  
AUTHORS Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.  
TITLE Polypeptides for use in generating anti-human influenza virus  
JOURNAL Patent: US 6337070-A 54 08-JUN-2002;  
FEATURES  
Source 1..1777  
Location/Qualifiers  
/organism="unknown"  
BASE COUNT 565 a 363 c 421 g 428 t  
ORIGIN

Query Match 78.2%; Score 868; DB 6; Length 1777;  
Best Local Similarity 100.0%; Pred. No. 2.7e-228;  
Matches 868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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QY 303 CTTTCAAAACGTAAATTAAGATCAATATGAGAGCATCCCAAGATATGTTAAGCAAAACAC 362  
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Db 963 CTTTCAAAACGTAAATTAAGATCAATATGAGAGCATCCCAAGATATGTTAAGCAAAACAC 1022  
QY 363 CCGAAGTTGGCAACGCGGATGGGAATGACCAGAAACAACATAGAGGCTATTCGG 422  
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Db 1023 CCGAAGTTGGCAACGCGGATGGGAATGACCAGAAACAACATAGAGGCTATTCGG 1082  
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Db 1083 CCGAATAGCAGGTTTATAGAAAATGTTGGGAGGAATGATAGCGTTGGTACGGTT 1142  
QY 483 CAGGCATCAAAATTCGAGGGCACAGACAGCAGATCTTAAAGCATTCAACAGC 542  
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Db 1443 GCAACTGAGGAGAAATGCTGAAGAGATGGGCAATGGTCTTCAAAATATACCAAAAG 1502  
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QY 1083 TTAGTAATTAATAAACACCCCTGTTTCTG 1110  
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Db 1743 TTAGTAATTAATAAACACCCCTGTTTCTG 1770

RESULT 6  
LOCUS I32533 1777 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 54 from Patent US 5589174.  
ACCESSION I32533  
VERSION I32533.1 GI:1823324  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1777)  
AUTHORS Okuno,Y., Isegawa,K., Sasao,F. and Ueda,S.

TITLE Anti-human Influenza virus antibody  
JOURNAL Patent: US 5589174-A 54 31-DEC-1996;  
FEATURES Location/Qualifiers  
source 1..1777  
BASE COUNT 565 a 363 c 421 g 428 t  
ORIGIN

Query Match 78.2%; Score 868; DB 6; Length 1777;  
Best Local Similarity 100.0%; Pred. No. 2.7e+228;  
Matches 868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 TATTGATACCTGATTTCTGAATGCATCACTCCAAATGGAAGCATTTCCCAATGACAAAGCC 302  
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Db 1743 TTAGTAATTAATAAACACCCCTGTTTCTG 1770



QY	423	CGCAATAGCAGGTTTATAGAAAATGTTGGAGGAGATGATGACGGTGTGACGGTTT	482
Db	1076	CGCAATAGCAGGTTTATAGAAAATGTTGGAGGAGATGATGACGGTGTGACGGTTT	1135
QY	483	CAGGATCAAAATTCGAGGGCAGACAGACAGATCTTAAAAAGCCTCAGACAGC	542
Db	1136	CAGGATCAAAATTCGAGGGCAGACAGACAGATCTTAAAAAGCCTCAGACAGC	1195
QY	543	CATCGACCAATCAATGGGAAATGTAACGGGTATCGAAGACAGACAGAAATTCGA	602
Db	1196	CATCGACCAATCAATGGGAAATGTAACGGGTATCGAAGACAGACAGAAATTCGA	1255
QY	603	TCAAAATCGAAAAAGATTTCTCAGAGATAGAGGAGATTTTCAGAGACCTCGAAGATACGT	662
Db	1256	TCAAAATCGAAAAAGATTTCTCAGAGATAGAGGAGATTTTCAGAGACCTCGAAGATACGT	1315
QY	663	TGAAGACACTAAATTCATCTCTGGTCTTCAATGCGGAGCTTCTTGCTCGAGAA	722
Db	1316	TGAAGACACTAAATTCATCTCTGGTCTTCAATGCGGAGCTTCTTGCTCGAGAA	1375
QY	723	TCAACATACATATGATCTGACTCGGAAATGAACAAGCTGTTGAAAAACAAGGAG	782
Db	1376	TCAACATACATATGATCTGACTCGGAAATGAACAAGCTGTTGAAAAACAAGGAG	1435
QY	783	GCAACTGAGGAGAAAACTGTAAGAGATGGGCAATGGTCTTCAAAATATACCAACAATG	842
Db	1436	GCAACTGAGGAGAAAACTGTAAGAGATGGGCAATGGTCTTCAAAATATACCAACAATG	1495
QY	843	TGCAACGCTTGATGATGATCAATCGAAATGCTACTTATGACCATGATGATACAGAGA	902
Db	1496	TGCAACGCTTGATGATGATCAATCGAAATGCTACTTATGACCATGATGATACAGAGA	1555
QY	903	CGAAGCATTAACCAACGGTTTCAGATCAAGGTGTGAAGTGAAGTCTGGATACCAAGA	962
Db	1556	CGAAGCATTAACCAACGGTTTCAGATCAAGGTGTGAAGTGAAGTCTGGATACCAAGA	1615
QY	963	CTGGATCTGTGGATTCCTTTGGCATATCATGCTTTTGTGTTGTGTTGCTGGG	1022
Db	1616	CTGGATCTGTGGATTCCTTTGGCATATCATGCTTTTGTGTTGTGTTGCTGGG	1675
QY	1023	GTTTCATCATGTGGGCTTGGCAGAGAGGCAACATTTAGTGCAACATTTGACTGTGA	1082
Db	1676	GTTTCATCATGTGGGCTTGGCAGAGAGGCAACATTTAGTGCAACATTTGACTGTGA	1735
QY	1083	TTAGTAATTAATAAACACCCCTGTTTCT	1109
Db	1736	TTAGTAATTAATAAACACCCCTGTTTCT	1762
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LOCUS	AF348176	Influenza A virus (A/Hong Kong/1/68(H3N2))	
DEFINITION	complete cds.	hemagglutinin gene.	
ACCESSION	AF348176		
VERSION	AF348176.1	GI:14009691	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
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TITLE			
JOURNAL			

FEATURES	University of Ottawa, 451 Smyth Rd, Ottawa, Ont K1H 8M5, Canada				
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BASE COUNT	551 a	357 c	410 g	418 t	
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Query Match	77.7%; Score 862.2; DB 14; Length 1736;				
Best Local Similarity	99.7%; Pred. No. 1.1e-226;				
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QY	303 CTTTCAAAAGCTTAACAGATCAGATATGAGAGATGAGAGATGATGATTAAGCAAAACAC	362			
Db	927 CTTTCAAAAGCTTAACAGATCAGATATGAGAGATGAGAGATGATGATTAAGCAAAACAC	986			
QY	363 CCTGAAGTTGGCAACAGGATGCGGATGATACCAAGAAACAATAGAGGCTATTGGG	422			
Db	987 CCTGAAGTTGGCAACAGGATGCGGATGATACCAAGAAACAATAGAGGCTATTGGG	1046			
QY	423 CGCAATAGCAGGTTTCTAGAAAATGTTGGAGAGATGATGAGAGGTTGATGAGGTTT	482			
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Db	1167 CATCGACCAATCAATGGGAAATTTGAAACAGGTTATCGAAGAGACAGACAGAAATTCGA	1226			
QY	603 TCAAAATCGAAAAAGATTTCTCAGAGATAGAGGAGATTTTCAGAGACCTCGAAGATACGT	662			
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QY	723 TCAACATACATATGATCTGACTCGGAAATGAACAAGCTGTTGAAAAACAAGGAG	782			
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QY	843 TGACACGCTTGATGATGATCAATCGAAATGCTACTTATGACCATGATGATACAGAGA	902			

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QY 903 CGAAGCATTTAAACACCGGTTTCAGATCAAAAGGTGTTGAACGAGAGTGTGATPACAAAGA 962

Db 1527 CGAAGCATTTAAACACCGGTTTCAGATCAAAAGGTGTTGAACGAGAGTGTGATPACAAAGA 1586

QY 963 CTGATCCTGTGATGATTTCTGTTGACATATCATGCTTTTGTGTTGTTGTTGCTGGG 1022

Db 1587 CTGATCCTGTGATGATTTCTGTTGACATATCATGCTTTTGTGTTGTTGTTGCTGGG 1646

QY 1023 GTTCATCATGTGGGCTGCGACAGAGCAGACATTGGTGCAACATTGTCATTGAGCTGA 1082

Db 1647 GTTCATCATGTGGGCTGCGACAGAGCAGACATTGGTGCAACATTGTCATTGAGCTGA 1706

QY 1083 TTAGTAATTTAAACACCGCTTGTCT 1109

Db 1707 TTAGTAATTTAAACACCGCTTGTCT 1733

RESULT 10  
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LOCUS Influenza A virus (A/Hong Kong/1/68(H3N2)) isolate MA12  
DEFINITION hemagglutinin gene, complete cds.  
ACCESSION AF348177  
VERSION AF348177.1 GI:14009693  
KEYWORDS  
SOURCE  
ORGANISM  
Influenza A virus (A/Hong Kong/1/68(H3N2))  
Influenza A virus (A/Hong Kong/1/68(H3N2))  
viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza  
A viruses; Influenzavirus A; Influenza A virus; H3N2 subtype.  
REFERENCE  
AUTHORS Brown, E.G., Liu, H., Kit, L.C., Baird, S. and Nesraliah, M.  
TITLE Pattern of mutation in the genome of Influenza A virus on  
adaptation to increased virulence in the mouse lung: identification  
of functional themes  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (12), 6883-6888 (2001)  
MEDLINE 21287244  
PUBMED 11371620  
REFERENCE 2 (bases 1 to 1736)  
AUTHORS Brown, E.G., M. Liu, H., Chang Kit, L., Baird, S. and Nesraliah, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-FEB-2001) Biochemistry, Microbiology, and Immunology,  
University of Ottawa, 451 Smyth Rd, Ottawa, Ont K1H 8M5, Canada  
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Db 927 CTTTCAAAACGTAACAGATCATATGAGAGATGCCCAAGTATGTAAAGCAAAAC 986

QY 363 CCTGAAGTTGGCAGAGGATGCGAATGTACAGAGAAACAACTAGAGCCATTGCG 422

Db 987 CCTGAAGTTGGCAGAGGATGCGAATGTACAGAGAAACAACTAGAGCCATTGCG 1046

QY 423 CGCATATGAGGTTTATGAGAAATGCTGGGAGAGGAGATGTATAGAGGTTGACGGTT 482

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QY 483 CAGGATCAAAATTTCTGAGGACAGAGCAAGACAGAGATCTTAAAGCACTCAAGCAGC 542

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QY 603 TCAATTCGAAAAAGGATCTCAGAGATGAGAGGAGAAATTCAGAGCTCGAGAAATCGT 662

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QY 1083 TTAGTAATTTAAACACCGCTTGTCT 1109

Db 1707 TTAGTAATTTAAACACCGCTTGTCT 1733

RESULT 11

LOCUS ORINF6 1765 bp RNA linear VRL 15-FEB-1999

DEFINITION Influenza virus genes for the two haemagglutinins.

ACCESSION V01103.1 GI:60800

VERSION V01103.1 GI:60800

KEYWORDS haemagglutinin.

SOURCE Influenza A virus

ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza



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Best Local Similarity 99.5%: Pred. No. 3e-226;
Matches 863; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 13
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LOCUS
DEFINITION
AF348179 1736 bp. RNA linear. VRL 07-JUN-2001
hemagglutinin gene, complete cds.
AF348179
AF348179.1 GI:14009697
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Influenza A virus (A/Hong Kong/1/68(H3N2))
Influenza A virus (A/Hong Kong/1/68(H3N2))
Viruses; sRNA negative-strand viruses; Orthomyxoviridae; Influenza
A viruses; Influenzavirus A; Influenza A virus; H3N2 subtype.
REFERENCE
1 (bases 1 to 1736)
Brown, E.G., Liu, H., Kit, L.C., Baird, S. and Nesrallah, M.
Pattern of mutation in the genome of Influenza A virus on
adaptation to increased virulence in the mouse lung: identification
of functional themes
Proc. Natl. Acad. Sci. U.S.A. 98 (12), 6883-6888 (2001)
2 (bases 1 to 1736)
Brown, E.G., M. Liu, H., Chang Kit, L., Baird, S. and Nesrallah, M.
Direct Submission
Submitted (12-FEB-2001) Biochemistry, Microbiology, and Immunology,
University of Ottawa, 451 Smyth Rd, Ottawa, Ont K1H 8M5, Canada
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BASE COUNT      553 a      356 c      408 g      419 t
ORIGIN
Query Match      77.5%: Score 860.6; DB 14; Length 1736;
Best Local Similarity 99.5%: Pred. No. 3e-226;
Matches 863; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 243 TATTGATACCTGTAATTTCTGAATGCATCTCCAAATGAGACATTCCTCCATGACAAAGCC 302
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RESULT 14  
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LOCUS FLAHAMA  
DEFINITION Influenza A virus (A/NT/60/68/29c(H3N2)) hemagglutinin  
PREPROPEPTIDE gene complete cds.  
ACCESSION J02135  
VERSION J02135.1 GI:324156  
KEYWORDS glycoprotein; haemagglutinin.  
SOURCE Influenza A virus (A/NT/60/68/29c(H3N2))  
ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenza A virus; Influenza A virus; H3N2 subtype.  
REFERENCE 1 (bases 1 to 1765)  
AUTHORS Both, G.W. and Sleight, M.J.  
TITLE Complete nucleotide sequence of the haemagglutinin gene from a human influenza virus of the Hong Kong subtype  
JOURNAL Nucleic Acids Res. 8 (12), 2561-2575 (1980)  
MEDLINE 81053698  
PUBMED 6253883  
REFERENCE 2 (bases 79 to 1061)  
AUTHORS Sleight, M.J., Both, G.W., Underwood, P.A. and Bender, V.J.  
TITLE Antigenic drift in the hemagglutinin of the Hong Kong influenza subtype: correlation of amino acid changes with alterations in

Journal  
J. Virol. 37 (3), 845-853 (1981)  
MEDLINE 81194918  
PUBMED 6164798  
REFERENCE 3 (bases 78 to 1730)  
AUTHORS Sleight, M.J., Both, G.W., Underwood, P.A. and Bender, V.J.  
TITLE Antigenic drift in the hemagglutinin of the Hong Kong influenza subtype: correlation of amino acid changes with alterations in viral antigenicity  
J. Virol. 37 (3), 845-853 (1981)  
MEDLINE 81194918  
PUBMED 6164798  
COMMENT A/NT/60/68/29c is a laboratory-isolated variant of A/NT/60/68. Hemagglutinin is cleaved after translation to yield HA1 & HA2. The putative assignments for signal, HA1 & HA2 are suggested by comparison to the protein sequence for A/mem/102/72 Ward, C.W. & Doppeide, T.A. (1980) Virology 103, 37-53). Sequence compared with NBRF data.

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30..77  
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1065..1727  
mat\_peptide /product="hemagglutinin HA2 chain"  
BASE COUNT 565 a 361 c 415 g 424 t  
ORIGIN

Query Match 77.5%; Score 860.6; DB 14; Length 1765;  
Best Local Similarity 99.5%; Pred. No. 3e-226;  
Matches 863; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

243 TATGTACTCTGATTTTCGATGCTACCTCCAAATGAGAGATTTCCCAATGACAGCC 302  
896 TATGTACTCTGATTTTCGATGCTACCTCCAAATGAGAGATTTCCCAATGACAGCC 955  
303 CTTTCAAAAGCTTAACAGATCAGATGAGAGATCCCAAGTATGTAAGCAAAAC 362  
956 CTTTCAAAAGCTTAACAGATCAGATGAGAGATCCCAAGTATGTAAGCAAAAC 1015  
363 CCTGAAGTTGGCAACAGGATGGGAATGTACCGAGAAACAACATAGAGGCTATTGCG 422  
1016 CCTGAAGTTGGCAACAGGATGGGAATGTACCGAGAAACAACATAGAGGCTATTGCG 1075  
423 CGCAATAGCAGCTTTATAGAAATGGTTGGAGGAGATGATAGCGTTGTCAGCGTTT 482  
1076 CGCAATAGCAGCTTTATAGAAATGGTTGGAGGAGATGATAGCGTTGTCAGCGTTT 1135  
483 CAGGCATCAAAATTCGAGGGCAGACAGACAGCAGATCTTTAAAGCACTCAACGAG 542  
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Db      1196  CATGACCAAAATCAATGGGAAATTAAGACAGGTAATCGAGAGACGAACGAGAAATTCGA 1255
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QY      843  TGACACGCTTCATAGATGATCAGAAATGATGATGATGATGATGATGATGATGATG 902
Db      1496  TGACACGCTTCATAGATGATCAGAAATGATGATGATGATGATGATGATGATGATG 1555
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Db      1556  CGAAGCATTAACAACCGGTTTCAGATCAAAAGCTGTGTAAGCTGATGATGATGATG 1615
QY      963  CTGATCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1022
Db      1616  CTGATCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1675
QY      1023  GTTCATCATGTGGGCTCCAGAGAGGACATTAAGTGCAACATTTGATTTGATGATG 1082
Db      1676  GTTCATCATGTGGGCTCCAGAGAGGACATTAAGTGCAACATTTGATTTGATGATG 1735
QY      1083  TTAGTAATTAACAACCGCTTGTCT 1109
Db      1736  TTAGTAATTAACAACCGCTTGTCT 1762

RESULT 15
LOCUS   INA289703
DEFINITION Influenza A virus segment 4 gene for haemagglutinin, genomic RNA, strain clone 7a (H3N2).
ACCESSION AJ289703.1 GI:11595851
VERSION 1
KEYWORDS haemagglutinin; segment 4 gene.
SOURCE  Influenza A virus (A/PR/8/34 (H1N1) x A/England/939/69 (H3N2))
ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A; Influenza A virus.

REFERENCE
AUTHORS 1. Molsin, M.A., Morris, S.J., Smith, H. and Sweet, C.
TITLE    Influenza virus-induced apoptosis: a dual role for viral neuraminidase
JOURNAL  2 (bases 1 to 1765)
REFERENCE
AUTHORS  Sweet, C.
TITLE    Direct Submission
JOURNAL  Submitted (05-JUN-2000) Sweet C., School of Biosciences, University of Birmingham, Edgbaston, Birmingham, West Midlands, B15 2TT, UNITED KINGDOM

FEATURES
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/function="haemagglutination, receptor binding and fusion

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BASE COUNT 564 a 367 c 415 g 419 t
sig_peptide 30..78
ORIGIN
Query Match 77.5%; Score 860.6; DB 14; Length 1765;
Best Local Similarity 97.9%; Pred. No. 3e-226;
Matches 872; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

219 CTCACGGGAGAAATATGCAACATATGATACCTGATTTCTGATGATCACTCCAA 278
Db      872  CTCATTAATGAGGTACATGATGCCCTATTGATCTGATTTCTGAATGATCACTCCAA 931
QY      279  TGAAGCATTTCCCAATGACAAGCCCTTTCAAACGTAACAAGATCAATATGAGAGATG 338
Db      932  TGAAGCATTTCCCAATGACAAGCCCTTTCAAACGTAACAAGATCAATATGAGAGATG 991
QY      339  CCCCAGATATGTAAAGCAAAACACCTGTAAGTGGCAACAGGATGGGAATGATACAGA 398
Db      992  CCCCAGATATGTAAAGCAAAACACCTGTAAGTGGCAACAGGATGGGAATGATACAGA 1051
QY      399  GAAACAACTAGAGGCTTATTCGGGCAATAGAGTTCATAGAAAATGTTGGGAGG 458
Db      1052  GAAACAACTAGAGGCTTATTCGGGCAATAGAGTTCATAGAAAATGTTGGGAGG 1111
QY      459  AATGATAGACGCTGTGATACGCTTCAGGATCAAAATTTGAGGCGACAGAGACAGC 518
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QY      639  AATTCAGACCTGAGAAATATGTTGAAGACACTAAATAGATCTGTCTTACAATGC 698
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QY      699  GGAGCTTCTTTCGCTGCGAGATCAACATACATTTGACTGACAGTACCTGGAATGAA 758
Db      1352  GGAGCTTCTTTCGCTGCGAGATCAACATACATTTGACTGACAGTACCTGGAATGAA 1411
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Db      1412  CAAGCTGTTGAAAAACAGAGGAGCAATGAGGAGAAATGCTGAAGAGATGGGCAATG 1471
QY      819  TTGCTTCAAAATATACCAAAATGTCAGACGCTTGATAGATCAATCAAGATGATGAT 878
Db      1472  TTGCTTCAAAATATACCAAAATGTCAGACGCTTGATAGATCAATCAAGATGATGAT 1531
QY      879  TTATGACCATGATATATACAGAGAGCAAGATTAACACCGGTTTCAGATCAAGCTGT 938
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OY 939 TGAAGTGAAGTGGATACAAAGACTGATCCTGTGATTTGCTTGGCATATCATGCTT 998  
|||||  
Db 1592 TGAAGTGAAGTGGATACAAAGACTGATCCTGTGATTTGCTTGGCATATCATGCTT 1651  
|||||  
OY 999 TTTGCTTTGTGTTTGTGCTGGGGTTCATCATGTGGGCTGCAGAGAGGCAACATTAG 1058  
|||||  
Db 1652 TTTGCTTTGTGTTTGTGCTGGGGTTCATCATGTGGGCTGCAGAGAGGCAACATTAG 1711  
|||||  
OY 1059 GTGCACATTTGCATTTGAGTGTATTAGTAATTAATAAACACCCCTGTTCT 1109  
|||||  
Db 1712 GTGCACATTTGCATTTGAGTGTATTAGTAATTAATAAACACCCCTGTTCT 1762  
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(GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 18:20:24 ; Search time 213.016 Seconds  
(without alignments)  
14066.412 Million cell updates/sec

Title: US-09-918-568-57  
Perfect score: 1110  
Sequence: 1 CTAGACGCAAGCAGCGGAT.....TAAACACACCTGTTCTG 1110

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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N.Geneseq\_19jun03:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	866.4	78.1	1777	15	AAO72855
3	833.4	75.1	1765	24	ABA93937
4	832	75.0	1764	24	ABA93944
5	808.4	72.8	1762	8	AAV70642
6	787	70.9	1653	24	ABO82723
7	774.8	69.8	1793	18	AAV55212
8	774.8	69.8	1793	20	AAV00773

9	774.8	69.8	1793	22	AAO09586
10	768.8	69.3	6477	11	AAO02030
11	756.6	68.2	1757	18	AAV59216
12	756.6	68.2	1757	20	AAV00777
13	756.6	68.2	1757	22	AAO09590
14	751.8	67.7	1757	18	AAV59219
15	751.8	67.7	1757	20	AAV00780
16	751.8	67.7	1757	22	AAO09593
17	745.4	67.2	1701	19	AAV49298
18	645.2	58.1	666	14	AAO47358
19	645.2	58.1	666	15	AAO70204
20	642	57.8	666	14	AAO47359
21	642	57.8	666	15	AAO70205
22	641.4	57.8	918	14	AAO47361
23	641.4	57.8	918	15	AAO70190
24	631.8	56.9	918	15	AAO70208
25	630.2	56.8	670	15	AAO70207
26	603.6	54.5	1762	21	AAZ50976
27	603.6	54.4	1762	13	AAO29111
28	603.6	54.4	1762	13	AAO29112
29	602	54.2	1762	21	AAZ50975
30	587.8	53.0	1797	11	AAO04597
31	586	52.8	1788	8	AAV71067
32	582.8	52.5	1698	20	AAZ30211
33	582.8	52.5	1698	21	AAZ47007
34	581.2	52.4	1698	20	AAV49391
35	578	52.1	1698	19	AAZ30213
36	418.4	37.7	690	14	AAO47362
37	418.4	37.7	690	15	AAO70209
38	418.4	37.7	690	15	AAO70191
39	333.6	30.1	2005	21	AAZ75002
40	333.6	30.1	4930	21	AAV75002
41	332.8	30.0	4610	21	AAV75005
42	329	29.6	329	15	AAO64461
43	329	29.6	329	15	AAO72840
44	321	28.9	1711	24	AAV50113
45	320.2	28.8	6802	22	AAV62468

#### ALIGNMENTS

RESULT 1				
ID	AAO72807	standard.	CDNA:	1110 BP.
AC	AAO72807			
DT	25-MAR-2003	(updated)		
DT	22-JUN-1995	(first entry)		
DE	DNA encoding stem region of A2/Aichi/2/68 influenza virus.			
XX	Conserved peptide; stem region; haemagglutinin; HA; H1N1; H2N2;			
KW	subtype; human; Influenza A virus; immunogenic artificial peptide;			
KW	antigen; vaccine; infection; ss.			
OS	Human influenza A virus.			
FT	Key	Location/Qualifiers		
FT	CDS	34..1077		
XX		/*tag= a		
XX	PN	EP621339-A2.		
XX	PD	26-OCT-1994.		
XX	PF	20-APR-1994; 94EP-0302819.		
XX	PR	20-APR-1993; 93JP-0115216.		
XX	PR	16-MAR-1994; 94JP-0070194.		
XX	PA	(TAKI ) TAKARA SHUZO CO LTD.		

Influenza virus A/  
Plasmid pinf 4-49.  
Influenza A/Shando  
Influenza virus A/  
Influenza virus A/  
Influenza A/Johann  
Influenza virus A/  
Influenza virus A/  
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Sequence encoding  
Influenza haemagl  
Sequence encoding  
Influenza haemagl  
Sequence encoding  
Sequence encoding  
Sequence encoding  
POT5208NS1H3m158  
Cold-adapted equin  
EIV HA (A1/Fontain  
EIV HA (A2/Suffolk  
Wild type equine i  
Equine haemagglut  
Sequence encoding  
Sequence of the ha  
Equine influenza v  
EIV Fontainebleau  
Sequence of the ha  
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Sequence encoding  
Sequence encoding  
Nucleotide sequenc  
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Nucleotide sequenc  
A/Aichi/2/68 human  
HA gene fragment o  
Recombinant infect  
Modified influenza

XX Isegawa Y, Okuno Y, Sasao F, Ueda S;  
 XX MPI: 1994-325949/41.  
 DR P-PSDB: AAR63591.  
 XX  
 PT Human influenza-A virus haemagglutinin polypeptide(s) - useful in  
 XX Influenza-A vaccine composition  
 PS  
 XX Claim 17, Page 59, 68pp: English.  
 CC This sequence encodes the stem region of the hemagglutinin (HA) molecule  
 CC of the A2/Aichi/2/68 strain of human influenza A virus. This antigenic  
 CC molecule contains the conserved peptides derived from the stem region  
 CC of the H1N1 and H2N2 subtypes of human influenza A virus. Immunogenic  
 CC polypeptides such as this are antigenically equivalent to the stem region  
 CC of the HA molecule of influenza A virus. This artificial peptide may be  
 CC used as a vaccine for prophylaxis of influenza A virus infection.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 XX  
 SQ Sequence 1110 BP; 374 A; 216 C; 258 G; 262 T; 0 other;  
 Query Match 100.0%; Score 1110; DB 15; Length 1110;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-310; Indels 0; Gaps 0;  
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 DB 1 CTAGAGCAAAACGAGGAGTAATCTATTAATCATGAACCATCTTGTGAGCTAC 60  
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 DB 301 CCCCTTCAAAACGCTAAACAGATCAATATGAGATGCCCAAGATGTTAAGCAAAAC 360  
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 DB 361 ACCCTGAAGTGGCAACAGGATGCGAATGTACCAAGAGAAACAACTAGAGGCTATTC 420  
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 DB 541 GCCATCGACCAATATGAGGAAATTTGAACAGAGGTAAATCGAGAGAGCAAGAAATTC 600  
 QY 601 CATCAAAATCGAAAAGGAATTTCTCAGAGTAGAAGGAGAGAAATTCAGAGCTCGAGAAATAC 660  
 DB 601 CATCAAAATCGAAAAGGAATTTCTCAGAGTAGAAGGAGAGAAATTCAGAGCTCGAGAAATAC 660  
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 DB 721 AATCAACATCAATTTGACCTGACGTGCGGAAATGAACAGTGTGTAACAAACAGG 780  
 QY 781 AGGCAACATGAGGAAATGCTGTAAGAGATGGGCAATGGTCTTCAAAATATACACAA 840  
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 DB 1081 TATTAGTAATTAACACACCTTGTGTTCTG 1110  
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 AA072855  
 ID AA072855 standard; cDNA; 1777 BP.  
 XX  
 AC AA072855;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 23-JUN-1995 (first entry)  
 XX  
 DE Full length H3N2 influenza A virus, strain A2/Aichi/2/68 HA gene.  
 XX  
 KW Conserved peptide; stem region; hemagglutinin; HA; H1N1; H2N2; PCR;  
 KW subtype; human; influenza A virus; immunogenic artificial peptide;  
 KW antibody; vaccine; infection; polymerase chain reaction; primer;  
 KW amplify; C179; region A; region B; ds.  
 XX  
 OS Influenza A virus.  
 XX  
 FH Key  
 FT CDS  
 FT Location/Qualifiers  
 FT 36..1737  
 FT /\*tag= a  
 FT /product= Full length HA from H3N2 subtype  
 FT sig\_peptide  
 FT 37..84  
 FT /\*tag= b  
 FT /tag= C  
 FT /product= Stem region of N-terminal domain  
 FT misc\_feature  
 FT 247..903  
 FT /\*tag= d  
 FT /product= Globular head domain  
 FT FT  
 FT 904..1734  
 FT /\*tag= e  
 FT /product= Stem region of C-terminal domain  
 PN EP621339-A2.  
 XX  
 PD 26-OCT-1994.  
 XX  
 PF 20-APR-1994; 94EP-0302819.  
 XX  
 PR 20-APR-1993; 93JP-0115216.  
 PR 16-MAR-1994; 94JP-0070194.  
 XX

PA (TAKI ) TAKARA SHUZO CO LTD.  
 XX Isegawa Y, Okuno Y, Saito F, Ueda S;  
 XX WPI; 1994-325949/41.  
 DR P-PSDB; AAR63590.  
 XX  
 PT Human Influenza-A virus haemagglutinin polypeptide(s) - useful in  
 PT Influenza-A vaccine composition  
 XX  
 XX Example 2; Page 54-58; 6fpp; English.  
 CC This sequence was amplified using the primer sequences given in  
 CC AA07852-54 and represents a cDNA which encodes the full length  
 CC hemagglutinin (HA) gene of the H3N2 subtype of human influenza A  
 CC virus, strain A2/Alchi/2/68. The full length protein encoded by this  
 CC amplified cDNA contains two conserved regions, the A' region, TGMKN  
 CC and the B region, QINGLR(L/V)IEK. These regions are close to  
 CC each other in the stem of the HA molecule and they represent epitopes  
 CC which are recognised by the antibody C179. C179 binds to the stem  
 CC of the HA molecule and thus inhibits the membrane fusion action  
 CC of the HA molecule and neutralises the virus. Polypeptide molecules  
 CC which contain the conserved peptide regions, A and B, esp. HA molecules  
 CC lacking the globular head region (see also AA072807), are antigenically  
 CC equivalent to the stem region of the HA molecule of influenza A virus.  
 CC These artificial peptides may be used as vaccines for prophylaxis of  
 CC influenza A virus infection.  
 CC (updated on 25-MAR-2003 to correct PN field.)  
 CC  
 XX  
 XX Sequence 1777 BP; 565 A; 363 C; 420 G; 429 T; 0 other;  
 SQ  
 Query Match 78.1%; Score 866.4; DB 15; Length 1777;  
 Best Local Similarity 99.5%; Pred. No. 1.8e-239;  
 Matches 867; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 243 TATGTACCTGATTTCTGATGATCATCTCCAAATGGAAGCATTCCCAATGACAAGCC 302  
 DB 903 TATGTACCTGATTTCTGATGATCATCTCCAAATGGAAGCATTCCCAATGACAAGCC 962  
 QY 303 CTTTCAAAACGTAAACAAATCATATGAGATGATCCCAATGATGTTAAAGCAAAAC 362  
 DB 963 CTTTCAAAACGTAAACAAATCATATGAGATGATCCCAATGATGTTAAAGCAAAAC 1022  
 QY 363 CCTGAAGTTGGCAACATGGATGCGAATGTACAGAGAAACAACATAGAGGCTATTGCG 422  
 DB 1023 CCTGAAGTTGGCAACATGGATGCGAATGTACAGAGAAACAACATAGAGGCTATTGCG 1082  
 QY 423 CGCAATAGCAGGTTTCATGAAAATGTTGGAGGGAATGATAGACGTTGTACGTTT 482  
 DB 1083 CGCAATAGCAGGTTTCATGAAAATGTTGGAGGGAATGATAGACGTTGTACGTTT 1142  
 QY 483 CAGGCATCAAAATTCCTAGAGGCAACAGCAAGCAAGATCTTAAAGCACTCAACAGC 542  
 DB 1143 CAGGCATCAAAATTCCTAGAGGCAACAGCAAGCAAGATCTTAAAGCACTCAACAGC 1202  
 QY 543 CATGACCAAAATCAATGGAAAATTTGAACAGGTAATCGAAGACAGACAGAAATTCGA 602  
 DB 1203 CATGACCAAAATCAATGGAAAATTTGAACAGGTAATCGAAGACAGACAGAAATTCGA 1262  
 QY 603 TCAATTCGAAAAGAAATTCAGAAATAGAGGAGAAATTCAGAGCCTCGAGAAATACGT 662  
 DB 1263 TCAATTCGAAAAGAAATTCAGAAATAGAGGAGAAATTCAGAGCCTCGAGAAATACGT 1322  
 QY 663 TGAGACACTAAATATATCTCTGCTTACAAATGGGAGGCTTCTGTGCTCTGGAGAA 722  
 DB 1323 TGAGACACTAAATATATCTCTGCTTACAAATGGGAGGCTTCTGTGCTCTGGAGAA 1382  
 QY 723 TCAACATACAAATGACCTGACTGCTCGGAAATGAACAAGCTGTTGAAAAACAAGAG 782  
 DB 1383 TCAACATACAAATGACCTGACTGCTCGGAAATGAACAAGCTGTTGAAAAACAAGAG 1442  
 QY 783 GCAACTGAGGAGAAATCTGGAAGAGATGGCAATGGTCTCTCAAAATATACCAAAATG 842  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 1443 GCAACTGAGGAGAAATCTGGAAGAGATGGCAATGGTCTCTCAAAATATACCAAAATG 1502  
 QY 843 TGACAAAGCTGCTGATGATGATCAATGCAATGCTACTTATGCAATGATGATGATGATG 902  
 DB 1503 TGACAAAGCTGCTGATGATGATCAATGCAATGCTACTTATGCAATGATGATGATGATG 1562  
 QY 903 CGAAGCATTAACCAACCGGTTTCAGATCAAGGTGTTGAACATGAACTGATACAAAGA 962  
 DB 1563 CGAAGCATTAACCAACCGGTTTCAGATCAAGGTGTTGAACATGAACTGATACAAAGA 1622  
 QY 963 CTGGATCTGTGGATTTCTTTGCCATATGATGCTTTTGTGTTGTTGCTGGG 1022  
 DB 1623 CTGGATCTGTGGATTTCTTTGCCATATGATGCTTTTGTGTTGTTGCTGGG 1682  
 QY 1023 GTTCATCATGTGGCGCTGCGACAGAGCAACATAGTGCACATTTGATTTGATGATGAT 1082  
 DB 1683 GTTCATCATGTGGCGCTGCGACAGAGCAACATAGTGCACATTTGATTTGATGATGAT 1742  
 QY 1083 TTAGTAATTAACCAACCGCTTGTGTTCTG 1110  
 DB 1743 TTAGTAATTAACCAACCGCTTGTGTTCTG 1770  
 RESULT 3  
 ABA93937  
 ID ABA93937 standard; DNA; 1765 BP.  
 AC ABA93937;  
 XX  
 XX 07-MAY-2002 (first entry)  
 XX  
 DE Influenza A/Udorn/72 (H3N2) Strain HA encoding DNA SEQ ID NO:7.  
 XX  
 XX  
 KM Influenza A/Udorn/72 (H3N2) Strain; Influenzavirus A; diagnosis;  
 KW Influenza A virus; genome; gene; ds.  
 XX  
 XX Influenzavirus A.  
 FH  
 FT Key Location/Qualifiers  
 FT CDS 30..1730  
 FT FT /tag= a  
 FT FT /product= "HA protein"  
 XX  
 XX MO200200884-A2.  
 PD  
 PD 03-JAN-2002.  
 PF  
 PF 21-JUN-2001; 2001MO-US19826.  
 XX  
 XX 23-JUN-2000; 2000US-213650P.  
 XX  
 PA (AMCY ) AMERICAN CYANAMID CO.  
 XX  
 PI Galarza JM, Latham TE;  
 XX  
 DR WPI; 2002-139923/18.  
 DR P-PSDB; ABB05767.  
 PT  
 PT Polynucleotide encoding complete sequence of Influenza A/Udorn/72 and  
 PT polypeptide, useful in diagnosis and for generating new Influenza A  
 PT variant strains -  
 XX  
 PS Claim 1; Page 61-64; 103pp; English.  
 XX  
 CC The present invention describes an isolated polynucleotide (i) having  
 CC the complete sequence of the Influenza A/Udorn/72 (H3N2) strain in  
 CC positive strand, antigenomic message sense. ABA93934 to ABA93944 encode  
 CC the Influenza A/Udorn/72 (H3N2) strain proteins given in ABB05764 to  
 CC ABB05774 from the present invention. (i) is useful for designing  
 CC polymerase chain reaction (PCR) primers for use in a PCR assay to detect  
 CC the presence of the corresponding virus segment in a sample or for  
 CC designing and selecting peptides for use in an enzyme linked  
 CC immunosorbant assay to detect the presence of the corresponding protein



QY 423 CGCAATAGCAGTTTATAGAAAATGTTGGAGGGAATGATAGACGGTGTACGTTT 482  
DB 1076 CGCAATAGCAGTTTATAGAAAATGTTGGAGGGAATGATAGACGGTGTACGTTT 1135  
QY 483 CAGGCATCAAAATTCGAGGCAACAGACAGACAGATCTTTAAAGCACTCAAGCAC 542  
DB 1136 CAGGCATCAAAATTCGAGGCAACAGACAGACAGATCTTTAAAGCACTCAAGCAC 1195  
QY 543 CATCGACCAATCAATGGGAAATTTGAACGGGTATCGAAGACAGACAGAAATTCGA 602  
DB 1196 CATCGACCAATCAATGGGAAATTTGAACGGGTATCGAAGACAGACAGAAATTCGA 1255  
QY 603 TCAAAATCGAAAAGATTTCTCAGAACTAGAAAGGAGAAATTCAGACCTCGAGAAATACGT 662  
DB 1256 TCAAAATCGAAAAGATTTCTCAGAACTAGAAAGGAGAAATTCAGACCTCGAGAAATACGT 1315  
QY 663 TGAAGACATTAATATGATCTCTGGCTTACAAATGCGAGGCTTCTTGTGCTCTGAGAA 722  
DB 1316 TGAAGACATTAATATGATCTCTGGCTTACAAATGCGAGGCTTCTTGTGCTCTGAGAA 1375  
QY 723 TCAACATACAAATTTGACTGACTCGGAAATGAAACAGCTGTTGAAAAACAAGAG 782  
DB 1376 CCAACATACAAATTTGACTGACTCGGAAATGAAACAGCTGTTGAAAAACAAGAG 1435  
QY 783 GCAACTGAGGAAATTTCTGAAGAGATGGCAATGGTCTTCAAAATATACACAAATG 842  
DB 1436 GCAACTGAGGAAATTTCTGAAGAGATGGCAATGGTCTTCAAAATATACACAAATG 1495  
QY 843 TGACACAGCTTCATATGATCAATCAAGAAATGATCTTATGACATGATGTATACAGAGA 902  
DB 1496 TGACACAGCTTCATATGATCAATCAAGAAATGATCTTATGACATGATGTATACAGAGA 1555  
QY 903 CGAAGCATTAACAACATGGTTTCAGATCAAGATGTTGAATGAAGTGTGATACAAAGA 962  
DB 1556 CGAAGCATTAACAACATGGTTTCAGATCAAGATGTTGAATGAAGTGTGATACAAAGA 1615  
QY 963 CTGAGTCTGTGATTTCTTTGCCATATCATGCTTTTGTGTGTGTTTGTCTGGG 1022  
DB 1616 CTGAGTCTGTGATTTCTTTGCCATATCATGCTTTTGTGTGTGTTTGTCTGGG 1675  
QY 1023 GTTCATCATGTGGGCTTCCAGAGAGGCAACATTAAGTGCACATTTGATTTGAGTGA 1082  
DB 1676 GTTCATCATGTGGGCTTCCAGAGAGGCAACATTAAGTGCACATTTGATTTGAGTGA 1735  
QY 1083 TTGATATTAATAACAATCCTGTT 1106  
DB 1736 TTGATATTAATAACAATCCTGTT 1759

RESULT 5  
AAN70642  
ID AAN70642 standard: cDNA: 1762 BP.  
XX  
AC AAN70642;  
XX  
DT 25-MAR-2003 (updated)  
DT 29-APR-1991 (first entry)  
XX  
DE Sequence encoding influenza HA protein.  
XX  
KW HA; vaccine: ds.  
XX  
OS Influenza/A/Nilgata 10218.  
XX  
PN JP62051992-A.  
XX  
PD 06-MAR-1987.  
XX  
PF 30-AUG-1985; 85JP-0192915.  
XX  
PR 30-AUG-1985; 85JP-0192915.  
XX

PA (KAGA ) KAGAKU KASEI RYOHO KENKYUSHO.  
XX  
XX WPI: 1987-104909/15.  
XX  
PT Recombinant plasmid - combines influenza virus gene and  
PT transformation enzyme and can be used for prepn. of influenza  
PT virus protein  
XX  
XX  
PS Disclosure: Fig 3; 14pp; Japanese.  
CC Sequence may be inserted into a plasmid under the control of a  
CC phosphatase promoter, and used to transfer an E.coli expression  
CC system. The HA protein product may be used as vaccine against  
CC influenza viral infection.  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 1762 BP; 579 A; 359 C; 404 G; 420 T; 0 other:  
  
Query Match 72.8%; Score 808.4; DB 8; Length 1762;  
Best Local Similarity 96.7%; Pred. No. 9,9e-223;  
Matches 837; Conservative 0; Mismatches 26; Indels 3; Gaps 1;  
  
QY 244 ATTGATACCTGATTTCTAATGATCATCTCCAAATGAGAGATTTCCCATGACAGCCC 303  
DB 897 ATTGGCACCCTGCAGTTCGAATGCATCACTCCAAATGAGAGATTTCCCATGACAGCCC 956  
QY 304 TTTCAAAACGTAAACAGATCAATATGAGAGATGCCCCCAAGATGTTAAGCAAAACACC 363  
DB 957 TTTCAAAACGTAAACAGATCAATATGAGAGATGCCCCCAAGATGTTAAGCAAAACACT 1016  
QY 364 CTGAAGTTGGCAACAGGATGGGGAATGTACAGAGAAACAACTAGAGGCTTATTCGCC 423  
DB 1017 CTGAAGTTGGCAACAGGATGGGGAATGTACAGAGAAACAACTAGAGGCTTATTCGCC 1076  
QY 424 GCAATAGCAGTTTCTATATAAAATGTTGGAGGAAATATAGAGCGTTGATCGTTTC 483  
DB 1077 GCAATAGCAGTTTCTATATAAAATGTTGGAGGAAATATAGAGCGTTGATCGTTTC 1136  
QY 484 AGGCATCAAAATTTGAGGGGACAGAGACAGAGCATCTTAAAGCACTCAAGCAGCC 543  
DB 1137 AGGCATCAAAATTTGAGGGGACAGAGACAGAGCATCTTAAAGCACTCAAGCAGCC 1196  
QY 544 ATCGACCAAAATCAATGGGAAATTTGAACAGGATTAATCGAGAGAGCAAGCAAAATTCAT 603  
DB 1197 ATCGACCAAAATCAATGGGAAATTTGAACAGGATTAATCGAGAGAGCAAGCAAAATTCAT 1256  
QY 604 CAAATCGAAAAGATTTCTCAGAACTAGAGAGGAGAAATTCAGAGCTCGAGAAATTCGT 663  
DB 1257 CAAATCGAAAAGATTTCTCAGAACTAGAGAGGAGAAATTCAGAGCTCGAGAAATTCGT 1316  
QY 664 GAAAGACATTAATATGATCTGTGCTTTCATATGAGGAGGAGCTTGTGCTGTGGAGAT 723  
DB 1317 GAAAGACATTAATATGATCTGTGCTTTCATATGAGGAGGAGCTTGTGCTGTGGAGAT 1376  
QY 724 CAACATACAAATTTGACCTGACTGCTCGAAATGAACAAAGCTTTGAAAAACAAGAGAG 783  
DB 1377 CAACATACAAATTTGACCTGACTGCTCGAAATGAACAAAGCTTTGAAAAACAAGAGAG 1436  
QY 784 CAACTGAGGAGAAATTCGAGAGATGGGCAATGTTGCTTAAATATATACCAAAATGT 843  
DB 1437 CAACTGAGGAGAAATTCGAGAGATGGGCAATGTTGCTTAAATATATACCAAAATGT 1496  
QY 844 GACAAGCGTGTGATGAGTCAATCGAAATGATGATGATGATGATGATGATGATGATGAT 903  
DB 1497 GACAAGCGTGTGATGAGTCAATCGAAATGATGATGATGATGATGATGATGATGATGAT 1556  
QY 904 GAAGCATTAACAACCGGTTTTCAGATCAAAAGCTTTGAACAGTCAAGCTGATACAAAGAC 963  
DB 1557 GAAGCATTAACAACCGGTTTTCAGATCAAAAGCTTTGAACAGTCAAGCTGATACAAAGAC 1616  
QY 964 TGGATCCTGTGATTTCTTCCATATACATGCTTTTGTGCTTGTGCTGCTGGG 1023  
DB 1617 TGGATCCTGTGATTTCTTCCATATACATGCTTTTGTGCTTGTGCTGCTGGG 1676

OY 1024 TTCAATCATGTGGCCCTGCCAGAGCAACATTAGTGCATTTGAGTGTAT 1083  
 |||||||  
 Db 1677 TTCAATCATGTGGCCCTGCCAAAAAGCAACATTAGTGCATTTGAGTGTAT 1736  
 |||||||  
 OY 1084 TAGTAATTAATAAACACCCCTTGTTCCT 1109  
 |||||||  
 Db 1737 --TAATTAATAAACACCCCTGTTTCT 1759  
 |||||||  
 RESULT 6  
 ABQ82723  
 ID ABQ82723 standard; cDNA; 1653 BP.  
 XX  
 AC ABQ82723;  
 XX  
 DT 07-JAN-2003 (first entry)  
 XX  
 DE Influenza A/Bangkok/1/79(H3N2), haemagglutinin encoding cDNA.  
 XX  
 KW Influenza: Influenza A virus; pathogenicity; RNA viral disease;  
 KW viral infection; selenium; vaccine; virucide; anti-HIV; gene; ss.  
 XX  
 OS Influenza A virus.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 1..1653  
 FT /tag= a  
 FT /partial  
 FT /product= "haemagglutinin protein"  
 FT 1..984  
 FT /tag= b  
 FT /product= "ha1 chain"  
 FT mat\_peptide 988..1650  
 FT /tag= C  
 FT /product= "ha2 chain"  
 FT  
 XX WO200278717-A2.  
 XX  
 PN 10-OCT-2002.  
 XX  
 PD 26-MAR-2002; 2002WO-EP03025.  
 XX  
 PF 28-MAR-2001; 2001US-0819387.  
 XX  
 PR  
 XX (NEST ) SOC PROD NESTLE SA.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 XX  
 PI Beck M, German B, Levander O, Van Dael P;  
 XX  
 DR WPI: 2002-759948/82.  
 DR P-PSDB; ABP53894.  
 XX  
 PT Treatment of influenza or reducing the risk of contracting influenza  
 PT involves administering selenium to an individual  
 XX  
 PS Example 1; Page -: 31pp; English.  
 XX  
 CC The present invention describes a method for treating influenza or  
 CC reducing the risk of contracting influenza, which involves administering  
 CC selenium to an individual. Also described is a method for enhancing the  
 CC efficiency of a viral vaccine by administering an antioxidant, preferably  
 CC selenium, to an individual receiving the viral vaccine. The method can  
 CC be used for treating influenza, for reducing the risk of contracting  
 CC influenza, and for enhancing the efficacy of viral vaccine (preferably  
 CC influenza vaccine) in an infant, elderly, a patient or a pet. It can  
 CC also be used for treating virus such as coxsackie and HIV virus. The  
 CC method provides an improved treatment for viral infection, by reducing  
 CC in vivo mutations of the RNA virus. The method also improves a vaccine  
 CC used to prevent transmission of an RNA viral disease. The present  
 CC sequence encodes the haemagglutinin protein from influenza A/Bangkok/1/79  
 CC (H3N2).  
 CC N.B. The present sequence is not given in the specification, but is taken

CC from the Genbank accession number J02092, as specified on page 7.  
 XX  
 SQ Sequence 1653 BP; 540 A; 330 C; 389 G; 386 T; 8 other:  
 Query Match 70.9%; Score 787; DB 24; Length 1653;  
 Best Local Similarity 96.0%; Pred. No. 1.4e-216;  
 Matches 802; Conservative 0; Mismatches 33; Indels 0; Gaps 0;  
 OY 243 TATGATACCTGCTATTCTGTAATGATCATCTCCAAATGAGAGCAATTCATGACAGCC 302  
 |||||  
 Db 819 TATGACACCTGCACTGATGATGATCATCTCCAAATGAGAGCAATTCATGACAGCC 878  
 OY 303 CTTTCAAAAACGTAACAGATCATCATATGAGCATGCCCAAGATGTATTAAGCAAAACAC 362  
 |||||  
 Db 879 CTNTCAAAAACGTAACAGATCATCATATGAGGCGATGTCCTCAAGTATGTTAAGCAAAACAC 938  
 OY 363 CCTGAAGTTGGCAGACAGGATCGGAATGTACAGAGAAACAACTAGAGCCCTATTCCG 422  
 |||||  
 Db 939 TCTGAAGTTGGCAGACAGGATCGGAATGTACAGAGAAACAACTAGAGCATATTCCG 998  
 OY 423 CGCAATAGCAGGTTTCATAGAAATGCTGGGAGGGAATGATAGACGGTTGTAAGGTTT 482  
 |||||  
 Db 999 CGCAATAGCAGGTTTCATAGAAATGCTGGGAGGGAATGATAGACGGTTGTAAGGTTT 1058  
 OY 483 CAGCATCAAAAATTCCTGAGGCGACAGCAAGCAGCATCTTAAAGCAGCTCAAGCAGC 542  
 |||||  
 Db 1059 CAGGCATCAAAAATTCCTGAGGCGACAGCAAGCAGCATCTTAAAGCAGCTCAAGCAGC 1118  
 OY 543 CATCGACCAAAATCAATGGGAAATTTGAACAGGGTAAATCGAGAAAGCAAGAGAAATTCGA 602  
 |||||  
 Db 1119 AATCGACCAAAATCAATGGGAAATTTGAATAGGTTAATCGAGAAAGCAAGAGAAATTCGA 1178  
 OY 603 TCAATCGAAAAGAAATCTCAGAAAGTGAAGGAGAAATTCAGACCTCGAGAAATACGT 662  
 |||||  
 Db 1179 TCAATCGAAAAGAAATCTCAGAAAGTGAAGGAGAAATTCAGACCTCGAGAAATACGT 1238  
 OY 663 TGAAGACACTAAATAGATCTCTGCTCTTACAAATGCGAGCTTCTGCTCTGAGAA 722  
 |||||  
 Db 1239 TGAAGACACTAAATAGATCTCTGCTCTTACAAAGCGGAGCTTCTGCTCTGAGAA 1298  
 OY 723 TCAATATCAATTTGACTGACTGACTCGGAATTAACAAGCTGTTTAAAAAACAGAGAG 782  
 |||||  
 Db 1299 CCACATCAATTTGACTGACTGACTCGGAATTAACAAGCTGTTTAAAAAACAGAGAG 1358  
 OY 783 GCAACTGAGGGAATGCTGGAAGATGGGCAATGTTGCTCAAAATATACCACAAAATG 842  
 |||||  
 Db 1359 GCAACTGAGGGAATGCTGGAAGATGGGCAATGTTGCTCAAAATATACCACAAAATG 1418  
 OY 843 TGACAACGCTTGCAATAGATCAATCAGAAATGTTACTTATGACCATGATATATACAGAGA 902  
 |||||  
 Db 1419 TGACAATGCTTGCAATAGAGGTCATATCAGAAATGGAACCTTATGACCATGATATATACAGAGA 1478  
 OY 903 CGAAGCATTAATAACACCGGTTTCAGATCAAAAGTGTGAACCTGAGTCTGATACAAAGA 962  
 |||||  
 Db 1479 CGAAGCATTAATAACACCGGTTTCAGATCAAAAGTGTGAACCTGAGTCTGATACAAAGA 1538  
 OY 963 CTGATCTCTGAGATTCCTTGGCATATCATGCTTTTCTGTTGCTGTTTCTGCTGGG 1022  
 |||||  
 Db 1539 CTGATCTCTGAGATTCCTTGGCATATCATGCTTTTCTGTTGCTGTTTCTGCTGGG 1598  
 OY 1023 GTTCATCATGTGGGCGCTCGAGACAGCAACATTAGTGCATTTGATTTGA 1077  
 |||||  
 Db 1599 GTTCATCATGTNNNCCTGCGCAAAAGGCAACATTAGTGCATTTGATTTGA 1653  
 |||||  
 RESULT 7  
 AAT59212  
 ID AAT59212 standard; DNA; 1793 BP.  
 XX  
 AC AAT59212;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 19-AUG-1997 (first entry)







```
FT mat.peptide 73..1728 /tag=
FT /product= "Influenza virus A/Beijing/32/92 mature
FT HA protein"
FT misc_signal /tag=
FT /note= "Universal translation termination signal"
PN US6245532-B1.
XX
XX 12-JUN-2001.
XX
XX 09-OCT-1998; 9805-0169427.
XX
XX 30-MAY-1995; 9505-045348.
XX 13-SEP-1993; 9305-0120607.
XX (PROT-) PROTEIN SCI CORP.
XX Smith GE, Volovitz F, Wilkinson BE, Voznesensky AI, Hackett CS;
XX WPI: 2001-407272/43.
XX P-PSDB: AAE04951.
XX
XX Expressing a protein e.g. recombinant influenza virus haemagglutinin
XX PT comprising using a vector encoding a polypeptide comprising a
XX baculovirus signal peptide and a baculovirus expression system is
XX PT useful as a multivalent influenza vaccine -
XX
XX Claim 5; Column 35-38; 51bp; English.
XX
XX The present invention relates to a method for expressing an exogenous
XX protein in a baculovirus expression system which comprises using a vector
XX encoding a polypeptide comprising a baculovirus signal peptide operably
XX linked to a heterologous amino acid sequence. The method is especially
XX useful for preparing a protein which may be used to make a multivalent
XX influenza vaccine based on a mixture of recombinant haemagglutinin
XX (HA) antigens cloned from influenza viruses having epidemic potential.
XX The recombinant haemagglutinin proteins are full length,
XX uncleaved (HA0) glycoproteins including both the HA1 and HA2 subunits
XX (HA0) purified under non-denaturing conditions. The use of recombinant
XX DNA (rDNA) technology to produce influenza vaccine offers several
XX advantages, e.g., a recombinant DNA influenza vaccine can be produced
XX under safer and more stringently controlled conditions; propagation with
XX infectious influenza in eggs is not required; recombinant haemagglutinin
XX (rHA) protein can be more highly purified; purification procedures for
XX rHA do not have to include virus inactivation or organic extraction of
XX viral membrane components; production of HA via rDNA technology provides
XX an opportunity to avoid the genetic heterogeneity which occurs during
XX the adaptation and passage through eggs, which should make it possible to
XX better match vaccine strains with influenza epidemic strains, resulting in
XX improved efficacy. The present sequence is recombinant haemagglutinin
XX (rHA) DNA comprising Autocripha californica Nuclear Polyhedrosis Virus
XX (AcNPV) 61k gene partial polyhedrin promoter and signal sequence linked
XX to Influenza virus A/Beijing/32/92 mature HA coding region.
XX
XX SO Sequence 1793 BP; 593 A; 359 C; 408 G; 433 T; 0 other:
XX
XX Query Match 69.8%; Score 774.8; DB 22; Length 1793;
XX Best Local Similarity 94.2%; Pred. No. 5e-213;
XX Matches 816; Conservative 0; Mismatches 47; Indels 3; Gaps 1;
XX
XX 244 ATTGAACCTGTTTGTGAATGATCACTCCAAATGGAAGCTTCCCAATGCAAGGCC 303
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 898 ATTGGACCTGCGAGTTTGTATGATCACTCCAAATGGAAGCTTCCCAATGCAAGCC 957
XX
XX 304 TTTCAAAACGTAAACATGATCAATATGAGATGCCCAAGATGTTAAAGCAAAACACC 363
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 958 TTTCAAAATGTAAACAGGATCAATATGAGATGCCCAAGATGTTAAAGCAAAACACC 1017
XX
XX 364 CTGAATTTGGCAACAGGATGCGGATGTACCAAGAAACAACTAGAGGCATATTTCGC 423
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 1018 CTGAATTTGGCAACAGGATGCGGATGTACCAAGAAACAACTAGAGGCATATTTCGC 1077
```

```
QY 424 GCATATGACAGTTTCATAGAAAATGGTTGGAGGGAATGATAGCGTTGTACGGTTTC 483
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1078 GCATTCGACAGTTTCATAGAAAATGGTTGGAGGGAATGATAGCGTTGTACGGTTTC 1137
QY 484 AGGCATCAAAATTTCTGAGGGCAGAGCAACAGCAGATCTTAAAGCAGCTCAAGCAGCC 543
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1138 AGGCATCAAAATTTCTGAGGGCAGAGCAACAGCAGATCTTAAAGCAGCTCAAGCAGCA 1197
QY 544 ATGACCAAAATTCATATGGGAATTTGAACAGGCTAATGAGAGCAAGCAAGCAAAATTCAT 603
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1198 ATGACCAAAATTCATATGGGAATTTGAACAGGCTAATGAGAGCAAGCAAGCAAAATTCAT 1257
QY 604 CAATCGAAAAGCAATTTCTGAGAGTGAAGGAGGAGATTCAGAGCCTCGAAGATACGTT 663
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1258 CAATCGAAAAGCAATTTCTGAGAGTGAAGGAGGAGATTCAGAGCCTCGAAGATACGTT 1317
QY 664 GAAGACATTAATAATAGATCTCTGCTTACCAATCGGAGCCTTCTGCTCGAGAAAT 723
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1318 GAAGACATTAATAATAGATCTCTGCTTACCAATCGGAGCCTTCTGCTCGAGAAAT 1377
QY 724 CAACATACAAATTTACCTGACTGACTCGGAATTAACAGCTGTTGAAAAACAGAGAG 783
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1378 CAACATACAAATTTACCTGACTGACTCGGAATTAACAGCTGTTGAAAAACAGAGAG 1437
QY 784 CAACATAGGGAAGAAATGCTGAGAGATGGGCAATGGTTGCTTCAAAATATCCCAAAATGT 843
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1438 CAACATAGGGAAGAAATGCTGAGAGATGGGCAATGGTTGCTTCAAAATATCCCAAAATGT 1497
QY 844 GACAAAGCTTTCATAGATCAATCAGAAATGCTTATGACCATGATATACAGAGAC 903
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1498 GACAAATGCTTTCATAGATCAATCAGAAATGCTTATGACCATGATATACAGAGAC 1557
QY 904 GAAGCATTAACAAACCGGTTTCATCAAAAGTGTGACTGATGATCAAAAGAC 963
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1558 GAAGCATTAACAAACCGGTTTCATCAAAAGTGTGACTGATGATCAAAAGAC 1617
QY 964 TGATCTGCTGATGATGCTTTCATCAATGCTTTCATGCTTTCATGCTTTCATGCTG 1023
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1618 TGATCTGCTGATGATGCTTTCATCAATGCTTTCATGCTTTCATGCTTTCATGCTG 1677
QY 1024 TTGATCATGTGGGCTGCCAGAGAGCAACATTAGTGAACATTTGATGATGATAT 1083
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1678 TTGATCATGTGGGCTGCCAGAGAGCAACATTAGTGAACATTTGATGATGATAT 1737
QY 1084 TAGTATTTAAACACCCCTTGTTC 1109
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1738 --TAATTTAAACACCCCTTGTTC 1760
RESULT 10
AA002030
ID AA002030 standard; DNA: 6477 BP.
XX
XX AC AA002030;
XX
XX 09-JAN-2003 (updated)
XX DT 18-JUL-1989 (first entry)
XX
XX DE Plasmid pinf 4-49.
XX
XX XX Fusion proteins: gram negative outer membrane protein A; vaccines;
XX KM Influenza; foot and mouth disease; ss.
XX
XX OS Synthetic.
XX
XX XX Key Location/Qualifiers
XX FH 392..2314
XX FT /tag= a
XX FT /label=gram -ve outer membrane protein A
XX FT -10-signal 42..48
XX FT /tag= b
XX FT /label=tac promoter
```

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FT -35_signal 20..25
FT /*tag= c
FT /*label=lac promoter
FT misc_feature 945..962
FT /*tag= d
FT /*label=polylinker
XX EP35737-A.
XX 28-FEB-1990.
XX
XX 18-AUG-1989; 89EP-0115263.
XX
XX 24-AUG-1988; 88DE-3828666.
XX
XX (BEHW ) BEHRINGWERKE AG.
XX
XX Hobom G, Pistor S, Arnold N;
XX
XX WPI; 1990-060498/09.
XX
XX
XX Fusion proteins contg. Gram negative outer membrane protein A and immuno-
XX genetic component, useful as vaccines, and cells expressing them, useful as
XX live vaccines.
XX
XX Disclosure; page 11-15; 21pp; German.
XX
XX This plasmid is constructed by inserting a hybrid gram -ve outer membrane
XX protein A (omp A) gene into plasmid pBK236 forming pHS 56. This has a
XX fragment replaced by an 18kb polylinker resulting in plasmids pHS 64 and
XX pHS 164, the only difference being the presence of an improved promoter/
XX operator region from pBK 509 in latter. A cDNA sequence encoding human
XX Influenza H3 haemagglutinin (IHA) can be inserted in polylinker region
XX forming plasmids pInf 4-6 or pInf 4-39 respectively. The replacement of
XX IHA region of pInf 4-39 with an oligonucleotide linker results in this
XX expression plasmid (pInf 4-49) into which eg the alpha toxin gene from S.
XX aureus can be inserted and eg E.coli cells transformed.
XX
XX The resulting expressed alpha toxin is produced as a fusion protein.
XX Such fusion proteins are useful as vaccines and the transformed bacteria
XX are useful as live (oral) vaccines eg against Influenza and foot and
XX mouth disease
XX
XX (Updated on 09-JAN-2003 to add missing OS field.)
XX
XX Sequence 6477 BP; 1668 A; 1617 C; 1696 G; 1496 T; 0 other:
XX
XX Query Match 69.3%; Score 768.8; DB 11; Length 6477;
XX Best Local Similarity 90.8%; Pred. No. 4.8e-211;
XX Matches 843; Conservative 0; Mismatches 52; Indels 33; Gaps 1;
XX
XX 42 CATCATTCCTTTGAGCTACATTTCTGCTGCTCGGCCAAGACCTTCAGAAATGA 101
XX || || || || || || || || || || || || || || || || || || || ||
XX 769 CACCAAGCTCCACACATGTGACAGTGAATCGATAGGCGCAAGACCTTCAGAAATGA 828
XX
XX 102 CAACAGCAGACCAAGCGTGTGCGGACATCATCGGTGGCAAGCAAGCACTGAGAA 161
XX || || || || || || || || || || || || || || || || || || || ||
XX 829 CAACAGCAGACCAAGCGTGTGCGGACATCATCGGTGGCAAGCAAGCACTGAGAA 888
XX
XX 162 AACATCAGACATGATGATGAGTGAAGTGAATGCTACTAGTACTGAGAGCTCTC 221
XX || || || || || || || || || || || || || || || || || || || ||
XX 889 AACATCAGACATGATGATGAGTGAAGTGAATGCTACTAGTACTGAGAGCTCTC 944
XX
XX 222 AACGGGAAAAATGCAACAATATTGATACCTGTAATTTCTGAATGCACTCAATGG 281
XX || || || || || || || || || || || || || || || || || || || ||
XX 945 -----CTAGAGTACTCAATATGCACTCACTCAATGG 975
XX
XX 282 AAGCATCCCAATGACAAGCCCTTTCAAAAGTAAACAAGATGACATGTGAGCATGCC 341
XX || || || || || || || || || || || || || || || || || || || ||
XX 976 AAGCATCCCAATGACAAGCCCTTTCAAAAGTAAACAAGATGACATGTGAGCATGCC 1035
XX
XX 342 CAAGTATGTTAAGAAAAACCCCTGAAGTTGGCAACAGGATGGGGAATGACAGAGAA 401
XX || || || || || || || || || || || || || || || || || || || ||
XX 1036 CAAGTATGTTAAGAAAAACCCCTGAAGTTGGCAACAGGATGGGGAATGACAGAGAA 1095

```

```

QY 402 ACAACTAGAGCCCTATTTCGGGCAATAGCAGGTTTCATAGAAAATGGTTGGAGGAAT 461
DB || || || || || || || || || || || || || || || || || || || ||
DB 1096 ACAAACTAGAGCCCTATTTCGGGCAATAGCAGGTTTCATAGAAAATGGTTGGAGGAAT 1155
QY 462 GATAGACGTTGTCACGTTTCAGGCATCAAAATTTGAGGGCACAGACAGACAGAGA 521
DB || || || || || || || || || || || || || || || || || || || ||
DB 1156 GATAGACGTTGTCACGTTTCAGGCATCAAAATTTGAGGGCACAGACAGACAGAGA 1215
QY 522 TCTTAAAGCACTCAAGCAGCATGACCAATCAATGGAATTTGAACAGGGTAAATCA 581
DB || || || || || || || || || || || || || || || || || || || ||
DB 1216 TCTTAAAGCACTCAAGCAGCATGACCAATCAATGGAATTTGAACAGGGTAAATCA 1275
QY 582 GAAGACGAACGAGAAATTCATCAAAATGGAAGGAATTCAGAGTGAAGAGGAGAAAT 641
DB || || || || || || || || || || || || || || || || || || || ||
DB 1276 GAAGACGAACGAGAAATTCATCAAAATGGAAGGAATTCAGAGTGAAGAGGAGAAAT 1335
QY 642 TCAGACCTCGAAGAAATTCGTTGAAGACACTTAAATATGATCTGCTGCTTAAATGCGGA 701
DB || || || || || || || || || || || || || || || || || || || ||
DB 1336 CCAGATCTCGAAGAAATTCGTTGAAGACACTTAAATATGATCTGCTGCTTAAATGCGGA 1395
QY 702 GCTTCTGCGCTCGAAGAAATTCATCAAAATGACCTGACCTGACCGGAAATGACAA 761
DB || || || || || || || || || || || || || || || || || || || ||
DB 1396 GCTTCTGCGCTCGAAGAAATTCATCAAAATGACCTGACCTGACCGGAAATGACAA 1455
QY 762 GCTGTTGAAAAACAGAGGCAACTGAGGAAAAATGCTGAGAGATGGGCAATGGTTG 821
DB || || || || || || || || || || || || || || || || || || || ||
DB 1456 GCTGTTGAAAAACAGAGGCAACTGAGGAAAAATGCTGAGAGATGGGCAATGGTTG 1515
QY 822 CTTCAAAATATACCAAAATGTCACACGCTGATGAGCATGCAATGATGATGATGATGAT 881
DB || || || || || || || || || || || || || || || || || || || ||
DB 1516 CTTCAAAATATACCAAAATGTCACACGCTGATGAGCATGCAATGATGATGATGATGAT 1575
QY 882 TGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 941
DB || || || || || || || || || || || || || || || || || || || ||
DB 1576 TGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1635
QY 942 ACTGAAGTCTGGATACAAAGACTGATC 969
DB || || || || || || || || || || || || || || || || || || || ||
DB 1636 ACTGAAGTCTGGATACAAAGACTGATC 1663

```

RESULT 11  
AAT59216  
ID AAT59216 standard; DNA; 1757 BP.  
XX  
XX AAT59216;  
AC XX  
AC XX  
DT 25-MAR-2003 (updated)  
DT 19-AUG-1997 (first entry)  
XX  
XX  
DE Influenza A/Shandong/9/93 recombinant haemagglutinin gene.  
XX  
XX  
KW primer: PCR: polymerase chain reaction; universal; amplify: HA;  
KW haemagglutinin; recombinant production; baculovirus expression system;  
KW vaccine; insect cell culture; ss.  
XX  
XX  
OS Synthetic.  
XX  
XX  
FH  
FH  
FT key location/qualifiers  
FT misc\_signal 1..18  
FT /\*tag= a  
FT /\*note= "polyhedrin mRNA leader (partial)"  
FT CDS 19..1734  
FT /\*tag= b  
FT sig\_peptide 19..72  
FT /\*tag= c  
FT /\*note= "AcNPV 61k protein signal peptide"  
FT mat\_peptide 73..1728  
FT /\*tag= d  
FT /\*note= "coding region for mature rHA"  
FT misc\_signal 1747..1757  
FT /\*tag= e  
FT /\*note= "universal translation termination signal"

XX MO9637624-A1.  
 XX 28-NOV-1996.  
 PD 26-MAY-1995; 95WO-US06750.  
 PF 26-MAY-1995; 95WO-US06750.  
 PR 26-MAY-1995; 95WO-US06750.  
 XX (MICR-) MICROGENESYS INC.  
 PA (MGPM-) MG-PMC LLC.  
 PI Smith GE, Voliovitz F, Wilkinson BE, Voznesensky AI, Hackett CS;  
 DR MPI: 1997-021228/02.  
 DR P-PSDB; AAM01673.  
 PT Recombinant influenza haemagglutinin produced in baculovirus system  
 PT - avoids problems of growing virus in eggs and produces stable,  
 PT un-cleaved protein useful in vaccines  
 XX  
 PS Example 12; Page 80-81; 107pp; English.  
 XX Recombinant influenza haemagglutinin (HA) expressed in a  
 CC baculovirus expression system in cultured insect cells, allows vaccine  
 CC production without the need to grow virus in eggs. A purer, less  
 CC allergenic product is obtained and antigen drift caused by passages  
 CC through eggs is avoided. There is no need for viral inactivation or  
 CC organic solvent extn. of viral membrane components and vaccines can be  
 CC prepared, rapidly and cost effectively from primary sources of infection.  
 CC Recombinant HA is more stable (esp. for B strains) than HA1/HA2 complexes  
 CC and maintain correct folding during purification and storage. The present  
 CC sequence encodes the 5' end sequence of the HA gene for influenza  
 CC A/Shandong/9/93. The 61k signal peptide for baculovirus expression  
 CC and the polyhedrin promoter are included in the vector. It was used  
 CC in a study to compare the 1994-1995 formulation of the trivalent rHA  
 CC influenza vaccine with a licensed purified virus surface antigen  
 CC vaccine, Fluvirin (an attenuated influenza viral vaccine produced by  
 CC culturing in eggs).  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 XX Sequence 1757 BP; 582 A; 352 C; 403 G; 420 T; 0 other;  
 SQ  
 Query Match 68.2%; Score 756.6; DB 18; Length 1757;  
 Best local similarity 94.1%; Pred. No. 8.8e-208;  
 Matches 786; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

DB 1261 CAAATCGAANAAGAAATTCAGAGTAGAAGGAGAGAAATTCAGACCTCGAANAATATCTT 1320  
 QY 664 GAAGACACTAAATATGATCTGTGCTTCAATAGGAGACCTGTGCTCTGGAGAT 723  
 DB 1321 GAAGACACTAAATATGATCTGTGCTTCAATAGGAGACCTGTGCTCTGGAGAT 1380  
 QY 724 CAACATACAAATGACCTGACCTGACCTGCAATATGACCAACAGCTGTGAAACAAAGAGAG 783  
 DB 1381 CAACATACAAATGACCTGACCTGACCTGCAATATGACCAACAGCTGTGAAACAAAGAGAG 1440  
 QY 784 CAACATGAGGAAATGCTGAGAGAGATGGGCAATGTTGCTTCAAAATATACCAAAATCT 843  
 DB 1441 CAACATGAGGAAATGCTGAGAGAGATGGGCAATGTTGCTTCAAAATATACCAAAATCT 1500  
 QY 844 GACACGCTTGATAGATGATCAATGCAATATGCTACTATGACCATGATATACAGAGC 903  
 DB 1501 GACACGCTTGATAGATGATCAATGCAATATGCTACTATGACCATGATATACAGAGC 1560  
 QY 904 GACACGCTTGATAGATGATCAATGCAATATGCTACTATGACCATGATATACAGAGC 963  
 DB 1561 GACACGCTTGATAGATGATCAATGCAATATGCTACTATGACCATGATATACAGAGC 1620  
 QY 964 TCGATCCTGTGATTTCTTTCATATCATGCTTTTTCCTTTGCTTGTGCTGGG 1023  
 DB 1621 TCGATCCTGTGATTTCTTTCATATCATGCTTTTTCCTTTGCTTGTGCTGGG 1680  
 QY 1024 TTCATCATGTGGGCTGCCAGAGAGCAACATTAGTGAACATTGGCATTTGAG 1078  
 DB 1681 TTCATCATGTGGGCTGCCAGAGAGCAACATTAGTGAACATTGGCATTTGAG 1735

RESULT 12  
 AAX00777  
 ID AAX00777 standard; DNA; 1757 BP.  
 XX AAX00777;  
 AC AAX00777;  
 XX  
 DT 13-APR-1999 (first entry)  
 XX  
 DE Influenza virus A/Shandong/9/93 recombinant HA gene.  
 XX  
 KW Recombinant; glycosylation; influenza virus; haemagglutinin; baculovirus;  
 KW fusion protein; expression system; insect cell; immunogen; vaccine;  
 KW human; bird; ss.  
 XX  
 OS Synthetic.  
 OS Influenza virus.  
 OS  
 FH Key Location/Qualifiers  
 FT 5'UTR 1..18  
 FT /\*tag= a  
 FT /note= "polyhedrin mRNA leader sequence"  
 FT CDS 19..1731  
 FT /\*tag= b  
 FT sig\_peptide 19..72  
 FT /\*tag= c  
 FT mat\_peptide 73..1728  
 FT /note= "AcNPV 61k signal peptide"  
 FT /\*tag= d  
 FT terminator 1747..1757  
 FT /\*tag= e  
 XX  
 PN US5858368-A.  
 PD 12-JAN-1999.  
 XX  
 PD 30-MAY-1995; 95US-0453848.  
 PR 30-MAY-1995; 95US-0453848.  
 PR 13-SEP-1993; 93US-0120607.  
 XX





Recombinant influenza haemagglutinin (HA) expressed in a baculovirus expression system in cultured insect cells, allows vaccine production without the need to grow virus in eggs. A pret, less allergenic product is obtained and antigen drift caused by passages through eggs is avoided. There is no need for viral inactivation or organic solvent extr. of viral membrane components and vaccines can be prepd. rapidly and cost effectively from primary sources of infection. Recombinant HA is more stable (esp. for B strains) than HA1/HA2 complexes and maintain correct folding during purification and storage. The present sequence encodes the 5' end sequence of the HA gene for influenza A/Johannesburg/33/94. The 61k signal peptide for baculovirus expression and the polyhedrin promoter are included in the vector. This sequence is used to produce recombinant HA protein used in a trivalent influenza virus vaccine.

(updated on 25-MAR-2003 to correct PI field.)

Sequence 1757 BP; 580 A; 350 C; 405 G; 422 T; 0 other;

Query Match	Score	DB	Length
67.78;	751.8;	18;	1757;

Matches 783; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY	244	ATTGATACCTGATATTTCTGATGCGATCACTCCAAATGGAAACCATTTCCCAATGACAAGCC	303
Db	901	ATTGGCACTGCGACTTCTGTAATGCATCACTCCAAATGGAAACCATTTCCCAATGACAACCT	960
QY	304	TTTCAAAACGTTAAACAAGATCACATATATGAGCATGCCCAAGTATGTTAAAGCAAAACACC	363
Db	961	TTTCAAAATGTTAAACAGGATCACATATATGAGGCGCTGCCCAAGTATGTTAAAGCAAAACACT	1020
QY	424	GCAATAGCAGGTTTTCATAGAAAATGTTGGGAGGAAATGATAGACGGTTGGTACGGTTTC	483
Db	1081	GCAATGCCAGTTTTCATAGAAAATGTTGGGAGGAAATGATAGACGGTTGGTACGGTTTC	1140
QY	484	AGGCATCAAAATTCAGAGGCGACAGGACAAAGCAGACAGATCTTTAAAGCACTCAAGCACCC	543
Db	1141	AGGCATCAAAATTCAGAGGCGACAGGACAAAGCAGACAGATCTTTAAAGCACTCAAGCACGA	1200
QY	544	ATGACCAAAATTCATGGGAAATTTGAACAAGGTATTCGAGAAGACGAACGAGAAATTCAT	603
Db	1201	ATGACCAAAATTCATGGGAAATTTGAACAAGGTATTCGAGAAGACGAACGAGAAATTCAT	1260
QY	604	CAATCGAAAAGGAATTCCTCAGAGTAAAGGAGGAATTCAGACCTCGAGAAATTCAGTT	663
Db	1261	CAATCGAAAAGGAATTCCTCAGAGTAAAGGAGGAATTCAGACCTCGAGAAATTCAGTT	1320
QY	664	GAAAGACCTAAATATAGATCTCTGGCTTTACAAATGCGAGCTTCTTGTCGCTCGAGAAAT	723
Db	1321	GAAAGACCTAAATATAGATCTCTGGCTTTACAAATGCGAGCTTCTTGTCGCTCGAGAAC	1380
QY	724	CAACATTCATTTGACCTGACTGACTCGGAAATGAACAAGCTGTTTGAAGAAAACAAGAGG	783
Db	1381	CAACATTCATTTGATCTTAACTGACTCGAAGATGAACAACAGCTTTTGAAGAACAAAGGAG	1440
QY	784	CAACTGAGGAAAAATGCTGAAGAGATGGGCAATGCTTCCTCAAAATATATCCACAAATGT	843
Db	1441	CAACTGAGGAAAAATGCTGAAGAGATGGGCAATGCTTCCTCAAAATATATCCACAAATGT	1500
QY	844	GACAAAGCTTCATAGATCAATCAGAAATGTAATATGACATCGATATGATACAGAGAC	903
Db	1501	GACAAATGCTTCATAGAGGTCAATCAGAAATGGAATCTATGACCATGATGATACAGAGAC	1560
QY	904	GAAACATTAAACAACGGTTTCAGATCAAAAGTGTGAACCTGAAGTGTGATCAAAAGAC	963
Db	1561	GAAACATTAAACAACGGTTTCAGATCAAAAGTGTGAACCTGAAGTGTGATCAAAAGAT	1620
QY	964	TGGATCTGTGGAATTCCTTGCCATATCATAGCTTTTGGCTTGTGTGTTTGTGCTGGG	1023
Db	1621	TGGATCTGTGGAATTCCTTGCCATATCATAGCTTTTGGCTTGTGTGTTTGTGCTGGG	1680

Dy 1024 TTCAATCATGTGGGCTGCCAGAGAGGCACATTAGTGGCACATTTCATTGAG 1078  
|||||  
Db 1681 TTCAATCATGTGGGCTGCCAAAAAGGCACATTAGTGGCACATTTCATTGAG 1735

RESULT 15

.ID AAX00780 standard; DNA; 1757 BP.

AC AAX00780;

DT 13-APR-1999 (first entry)  
 XX

Influenza virus A/johannesburg/33/94 recombinant HA gene

KW Recombinant; glycosylation; influenza virus; haemagglutinin; baculovirus;  
KW fusion protein; expression system; Insect cell; Immunogen; vaccine;  
KW immune response; primer; PCR; amplification; reverse transcription;  
KW human; bird; ss.

OS	Synthetic.
OS	Influenza virus.

FH	key	Location/Qualifiers
FH	key	Location/Qualifiers

```
/*tag= a
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FT	CDS	19..1734
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FT	sig_peptide	19..72
----	-------------	--------

FT /note= "Ac

ET

FT terminator

XX  
DN 115E050350-1

XX 13-TAN-1000

XX 30-MAY-1995 0511C-0153940  
DE

XX 30-MAY-1995, 0511C-04530  
DB

PR 13-SEP-1993; 93US-0120607.  
XY

PA (PROT-) PROTH  
XY

PI Hackett CS, Smith C  
PI Wilkinson PE.

XX WDT: 1000-110703  
DB

DR P-PSDB; AAW75448.  
XY

PT Recombinant influenza virus h

[illegible][illegible]

CC influenza virus haemagglutinin fusion protein by a baculovirus expression system in cultured insect cells. The results are discussed in the context of a

CC is immunogenic, induces a protective immune response when used as a

CC This sequence represents the recombinant haemagglutinin gene from the

CC baculovirus Autographa californica nuclear polyhedrosis virus (AcNPV)

CC animals (including humans) or birds against influenza.

Sequence 1757 BP; 580 A; 350 C; 405 G; 422 T; 0 other;





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```
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8840
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 1110 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
ORIGINAL SOURCE:
ORGANISM: A2/Aichi/2/48
US-08-630-918-57

Query Match      100.0%; Score 1110; DB 1; Length 1110;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGAAGCAAGCAGCGGATTAATTCATATCATGAAGACCATTCCTTGAAGCTAC 60
DB 1 CTAGAAGCAAGCAGCGGATTAATTCATATCATGAAGACCATTCCTTGAAGCTAC 60
QY 61 ATTTCTGTCTGGCTCTGGGCCAAGACCTCCAGGAATGACACAGCAACGCTG 120
DB 61 ATTTCTGTCTGGCTCTGGGCCAAGACCTCCAGGAATGACACAGCAACGCTG 120
QY 121 TGCCTGGGACATCATGCGGTGCCAAGGAACTAGTGAAGAAACATCATCATGATG 180
DB 121 TGCCTGGGACATCATGCGGTGCCAAGGAACTAGTGAAGAAACATCATCATGATG 180
QY 181 ATTGAAGTACTAATGTTACTAGAGTCTCTCAACGGGGGAAATATGCAAC 240
DB 181 ATTGAAGTACTAATGTTACTAGAGTCTCTCAACGGGGGAAATATGCAAC 240
QY 241 AATATTGATCTGTATTTTCTGAATGCATCTCCAAATGGAAGCATTCCTCAATGACAAG 300
DB 241 AATATTGATCTGTATTTTCTGAATGCATCTCCAAATGGAAGCATTCCTCAATGACAAG 300
QY 301 CCCCTTCAAAACGTTAAACAGATCATATGAGGACATGCCCCAAGTATGTTAAGCAAAAC 360
DB 301 CCCCTTCAAAACGTTAAACAGATCATATGAGGACATGCCCCAAGTATGTTAAGCAAAAC 360
QY 361 ACCCTGAAGTTGGCAATAGGGATGGGGAATGTACCAAGAAACAACTAGAGCGCTATTTC 420
DB 361 ACCCTGAAGTTGGCAATAGGGATGGGGAATGTACCAAGAAACAACTAGAGCGCTATTTC 420
QY 421 GCGCGAATAGCAGGTTTCATAGAAAATGGTTGGAGGGAATGATAGCGTTGTACGGT 480
DB 421 GCGCGAATAGCAGGTTTCATAGAAAATGGTTGGAGGGAATGATAGCGTTGTACGGT 480
QY 481 TTCAGGCAATCAAAATTTGAGGGGACAGGACAGCAAGCATCTTAAAAAGCCTCAAGCA 540
DB 481 TTCAGGCAATCAAAATTTGAGGGGACAGGACAGCAAGCATCTTAAAAAGCCTCAAGCA 540
QY 541 GCCATCGAACCAATCAATGGGAAATTTGAACAGGGTAATCGAAGACGACAGCAAGAAATTC 600
DB 541 GCCATCGAACCAATCAATGGGAAATTTGAACAGGGTAATCGAAGACGACAGCAAGAAATTC 600
QY 601 CATCAAAATCGAAAAGGATTTCTCAGAAATGAGAGGAGAAATTCAGAGCTCGAGAAATTC 660
DB 601 CATCAAAATCGAAAAGGATTTCTCAGAAATGAGAGGAGAAATTCAGAGCTCGAGAAATTC 660
QY 661 GTTGAAGACACTAAATAGATCTGTGCTTTCATATGCGGAGCTCTTGTGCTGTGGAG 720
DB 661 GTTGAAGACACTAAATAGATCTGTGCTTTCATATGCGGAGCTCTTGTGCTGTGGAG 720
QY 721 AATCAACATACATTAATGATCTGACTGACTCGGAATGAACAAGCTTTTGAACAAACAGG 780
DB 721 AATCAACATACATTAATGATCTGACTGACTCGGAATGAACAAGCTTTTGAACAAACAGG 780
QY 781 AGGCAACGTGAGGGAATTCCTGAAGAGATGGGCATGTGTTGTTAAATATACACAAA 840
DB 781 AGGCAACGTGAGGGAATTCCTGAAGAGATGGGCATGTGTTGTTAAATATACACAAA 840
```

```
DB 781 AGGCAACGTGAGGGAATTCCTGAAGAGATGGGCATGTGTTGTTCAAAATATACACAAA 840
QY 841 TGTGCAACAGCTTGCATAGAGTCAATCAGAAATGATTAATGACCATGATGATACAGA 900
DB 841 TGTGCAACAGCTTGCATAGAGTCAATCAGAAATGATTAATGACCATGATGATACAGA 900
QY 901 GACGAAGCATTAACACACCGGTTTCAGATCAAAAGGTGTGAACCTGATGATACAAA 960
DB 901 GACGAAGCATTAACACACCGGTTTCAGATCAAAAGGTGTGAACCTGATGATACAAA 960
QY 961 GACTGATCTCTGATTTCTTTGCGCATATCATGCTTTTGTGTTGTTGCTG 1020
DB 961 GACTGATCTCTGATTTCTTTGCGCATATCATGCTTTTGTGTTGTTGCTG 1020
QY 1021 GGGTTCATCATGTTGGGCGTCCAGAGAGGCAACATAGTGCACATTTGCAATTTGAGTG 1080
DB 1021 GGGTTCATCATGTTGGGCGTCCAGAGAGGCAACATAGTGCACATTTGCAATTTGAGTG 1080
QY 1081 TATTAGTAATTAACACACCTTGTGTTCTG 1110
DB 1081 TATTAGTAATTAACACACCTTGTGTTCTG 1110

RESULT 3
US-09-004-422-57
Sequence 57, Application US/09004422
Patent No. 6337070
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,422
FILING DATE: January 8, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 1110 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL:
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ANTI-SENSE:  
 FRAGMENT TYPE:  
 ORIGINAL SOURCE:  
 ORGANISM: AZ/Alchl/2/68  
 STRAIN:  
 INDIVIDUAL ISOLATE:  
 DEVELOPMENTAL STAGE:  
 HAPLOTYPE:  
 TISSUE TYPE:  
 CELL LINE:  
 ORGANELLE:  
 IMMEDIATE SOURCE:  
 LIBRARY:  
 CLONE:  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT:  
 MAP POSITION:  
 UNITS:  
 FEATURE:  
 NAME/KEY:  
 LOCATION:  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 PUBLICATION INFORMATION:  
 AUTHORS:  
 TITLE:  
 JOURNAL:  
 VOLUME:  
 ISSUE:  
 PAGES:  
 DATE:  
 DOCUMENT NUMBER:  
 FILING DATE:  
 PUBLICATION DATE:  
 RELEVANT RESIDUES IN SEQ ID NO:  
 US-09-004-422-57

Query Match 100.0%; Score 1110; DB 4; Length 1110;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGAGCAAGCAGGGGATATCTTATTAATCATGAAGACCATTGCTTTGAGCTAC 60  
 DB 1 CTAGAGCAAGCAGGGGATATCTTATTAATCATGAAGACCATTGCTTTGAGCTAC 60  
 QY 61 ATTTTCTGTCTGGCTCTCGGCCAAGACCTTCCAGGAATGACACAGCAGCAACGCTG 120  
 DB 61 ATTTTCTGTCTGGCTCTCGGCCAAGACCTTCCAGGAATGACACAGCAGCAACGCTG 120  
 QY 121 TGCTGGACATCATGCGGTGCCAAAGGGAACACTAGTGAAGCAATCAGATGATCAG 180  
 DB 121 TGCTGGACATCATGCGGTGCCAAAGGGAACACTAGTGAAGCAATCAGATGATCAG 180  
 QY 181 ATTGAAGTGAATGCTACTAGCTAGCTAGCTCCTCAACGGGGAAAAATATGCAAC 240  
 DB 181 ATTGAAGTGAATGCTACTAGCTAGCTAGCTCCTCAACGGGGAAAAATATGCAAC 240  
 QY 241 AATATTGATACCTGATTTTCTGATGCTACCTCCAAATGGAAGATCCCAATGCAAG 300  
 DB 241 AATATTGATACCTGATTTTCTGATGCTACCTCCAAATGGAAGATCCCAATGCAAG 300  
 QY 301 CCCCTTCAAAACGTAACAGATCATATGAGAGATCCCAAGTATGTTAAGCAAAAC 360  
 DB 301 CCCCTTCAAAACGTAACAGATCATATGAGAGATCCCAAGTATGTTAAGCAAAAC 360  
 QY 361 ACCCTGAAGTTGGCAACAGGATCGGAATGTACAGAGAAACAACCTAGAGGCTATTTC 420  
 DB 361 ACCCTGAAGTTGGCAACAGGATCGGAATGTACAGAGAAACAACCTAGAGGCTATTTC 420  
 QY 421 GGGCAGATAGAGTTTTCATAGAAAATGTTGGGAGGAATGATAGAGGTTGATCGGT 480  
 DB 421 GGGCAGATAGAGTTTTCATAGAAAATGTTGGGAGGAATGATAGAGGTTGATCGGT 480

QY 481 TTCAGGCATCAAAATTTCTGAGGGCACAGACAGCAGATCTTAAAGCACTCAAGCA 540  
 DB 481 TTCAGGCATCAAAATTTCTGAGGGCACAGACAGCAGATCTTAAAGCACTCAAGCA 540  
 QY 541 GCCATCGACCAATCAATGGAATTTGAACAGGGATATCGAAGACGAACGAGAAATTC 600  
 DB 541 GCCATCGACCAATCAATGGAATTTGAACAGGGATATCGAAGACGAACGAGAAATTC 600  
 QY 601 CATCAATTCGAAAAGGAATTTCTCAGAGTACAGAGGAGAAATTCAGACCTCGAGAAATAC 660  
 DB 601 CATCAATTCGAAAAGGAATTTCTCAGAGTACAGAGGAGAAATTCAGACCTCGAGAAATAC 660  
 QY 661 GTTGAAGACACTAAATATGATCTCTGCTTACAAATGCGAGCTCTTTCGCGCTCGAG 720  
 DB 661 GTTGAAGACACTAAATATGATCTCTGCTTACAAATGCGAGCTCTTTCGCGCTCGAG 720  
 QY 721 AATCAACATACAAATTTGACCTGACCTCGAATGGAACAAAGCTTTGAAAAACAAG 780  
 DB 721 AATCAACATACAAATTTGACCTGACCTCGAATGGAACAAAGCTTTGAAAAACAAG 780  
 QY 781 AGGCACTGAGGGAATGCTGAAGAGATGGGCAATGCTTCAAAATATACACAAA 840  
 DB 781 AGGCACTGAGGGAATGCTGAAGAGATGGGCAATGCTTCAAAATATACACAAA 840  
 QY 841 TGTGACACGGCTTGATAGATGATCAATCGAATAGTGTACTATGACATGATATACAGA 900  
 DB 841 TGTGACACGGCTTGATAGATGATCAATCGAATAGTGTACTATGACATGATATACAGA 900  
 QY 901 GACGAGCATTAACAAACCGGTTTCAGATCAAAAGTGTGAAGTCAAGTGTGATACAAA 960  
 DB 901 GACGAGCATTAACAAACCGGTTTCAGATCAAAAGTGTGAAGTGTGATACAAA 960  
 QY 961 GACTGATCTGTGATTTCTTTGCCATATCATGCTTTTGTCTTGTGTTTCTG 1020  
 DB 961 GACTGATCTGTGATTTCTTTGCCATATCATGCTTTTGTCTTGTGTTTCTG 1020  
 QY 1021 GGGTTCATCATGTGGCGCTGCGCAGAGGCAACATTAAGTGCACATTTGCAATTTGAGTG 1080  
 DB 1021 GGGTTCATCATGTGGCGCTGCGCAGAGGCAACATTAAGTGCACATTTGCAATTTGAGTG 1080  
 QY 1081 TATTAGTAATTAACACCCCTGTGTTCTG 1110  
 DB 1081 TATTAGTAATTAACACCCCTGTGTTCTG 1110

RESULT 4  
 US-08-229-781-54  
 ; Sequence 54, Application US/08229781  
 ; Patent No. 5589174  
 ; GENERAL INFORMATION:  
 APPLICANT: Yoshinobu OKUNO et al.  
 TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY  
 NUMBER OF SEQUENCES: 58  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Menderoth, Lind & Ponack  
 STREET: 805 Fifteenth Street, N.W., #700  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/229,781  
 FILING DATE: April 19, 1994  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/054,016  
 FILING DATE: April 29, 1993

DB	Query Match	Best Local Similarity	Matches	868: Conservative	78.2%: Score 868; DB 1; Length 1777; 100.0%: Prid. No. 2,1e-277; 0: Mismatches 0; Indels 0; Gaps 0;
Db	1083	CGCAATAGCAGAGTTT	ATAGAAAATGGTTGGAGGGAATGATAGACGGTTGTACGGTTT	1142	
Db	1023	CCTAAGTTGGCAAC	AGGGATGCGGAATGTACCAAGAGAAACAAACTAGAGGCTATTGCG	1082	
Qy	363	CCTAAGTTGGCAAC	AGGGATGCGGAATGTACCAAGAGAAACAAACTAGAGGCTATTGCG	422	
Db	963	CTTCAAAAGCTAATA	TAAGTACATATATGAGAGATGCCCAAGATGTTTAAGCAAAAACAC	362	
Qy	303	CTTCAAAAGCTAATA	TAAGTACATATATGAGAGATGCCCAAGATGTTTAAGCAAAAACAC	362	
Db	903	TATGATACCTGTAT	TTCTGAATGATCATCTCCAAATGGAGCATTTCCCAATGACAAAGCC	962	
Qy	243	TATGATACCTGTAT	TTCTGAATGATCATCTCCAAATGGAGCATTTCCCAATGACAAAGCC	302	
Qy	423	CGCAATAGCAGAGTTT	ATAGAAAATGGTTGGAGGGAATGATAGACGGTTGTACGGTTT	482	
Db	1083	CGCAATAGCAGAGTTT	ATAGAAAATGGTTGGAGGGAATGATAGACGGTTGTACGGTTT	1142	

```

QY      483 CAGCATTCAAATTTCTGAGGCGACAGCAGCAGCATCTTTAAACACTCAAGCAGC 542
Db      1143 CAGCATCAAATTTCTGAGGCGACAGCAGCAGCATCTTTAAACACTCAAGCAGC 1202
QY      543 CATGACCAAAATCAATGGGAAATTTGAACAGGGTATGAGAAAGACGAACGAAATTTCCA 602
Db      1203 CATGACCAAAATCAATGGGAAATTTGAACAGGGTATGAGAAAGACGAACGAAATTTCCA 1262
QY      603 TCAATATGAAAGGAATTTCTGAGAAGTGAAGGAGAAATTTAGAGACTCGAAGAAATACCT 662
Db      1263 TCAATATGAAAGGAATTTCTGAGAAGTGAAGGAGAAATTTAGAGACTCGAAGAAATACCT 1322
QY      663 TGAAGACACTAAATATGATCTCTGCTCTTACAAATGCGAGAGCTTGTGCGCTCGAGAA 722
Db      1323 TGAAGACACTAAATATGATCTCTGCTCTTACAAATGCGAGAGCTTGTGCGCTCGAGAA 1382
QY      723 TCAACATACAAATTTGACCTGACTGACTCGGAATGAAACAAAGCTGTTGAAAAACAGAGAG 782
Db      1383 TCAACATACAAATTTGACCTGACTGACTCGGAATGAAACAAAGCTGTTGAAAAACAGAGAG 1442
QY      783 GCACCTGAGGGAATATGCTGTAAGAGATGGGCAATGGTTGCTTCAAATATACCAAAATG 842
Db      1443 GCAACTGAGGGAATATGCTGTAAGAGATGGGCAATGGTTGCTTCAAATATACCAAAATG 1502
QY      843 TGACAAACGCTTGCATAGATCAATCAGAAATGTAATGATGACCATGATATCAGAGA 902
Db      1503 TGACAAACGCTTGCATAGATCAATCAGAAATGTAATGATGACCATGATATCAGAGA 1562
QY      903 CGAAGCATTAAACACCGGTTTCAGATCAAAAGTGTTGAACGTGAGTCAAGAAGA 962
Db      1563 CGAAGCATTAAACACCGGTTTCAGATCAAAAGTGTTGAACGTGAGTCAAGAAGA 1622
QY      963 CTGATCTCTGGGATTCCTTGGCCATATCATGCTTTTGGCTTGTTGTTGGCTGGCG 1022
Db      1623 CTGATCTCTGGGATTCCTTGGCCATATCATGCTTTTGGCTTGTTGTTGGCTGGCG 1082
QY      1023 GTTTCATCATGCGGCGCTCGCCAGAGAGGCAACATTAGGTGCAACATTTGCATTGAGTGA 1082
Db      1683 GTTTCATCATGCGGCGCTCGCCAGAGAGGCAACATTAGGTGCAACATTTGCATTGAGTGA 1142
QY      1083 TTAGTAATTTAAAAACACCCCTTGTGTTG 1110
Db      1143 TTAGTAATTTAAAAACACCCCTTGTGTTG 1170

RESULT 5
US-08-630-918-54
: Sequence 54, Application US/08630918
: Patent No. 5631350
: GENERAL INFORMATION:
: APPLICANT: yoshinobu OKUNO et al.
: TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
: NUMBER OF SEQUENCES: 58
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Wenderoth, Lind & Ponack
: STREET: 805 Fifteenth Street, N.W., #700
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: Wordperfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/630.918
: FILING DATE: April 5, 1996
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/229,781
: FILING DATE: April 19, 1994

```

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ. ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1777 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
ORIGINAL SOURCE:  
ORGANISM: A2/Aichi/2/68  
US-08-630-918-54

Query Match 78.2% Score 868: DB 1: Length 1777:

Best Local Similarity 100.0%: Pred. No. 2,1e-277;

Matches 868: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

243 TATTGATACCTGATTTCTGATGATCATCTCAATGGAAGCATTCCTCAATGACAGCC 302  
1023 CTTGAGTTGGGCAACGAGGATCGGATATGACGAGGAAACAACTAGAGGCTTATTCGG 422  
1083 CGCAATAGCAGGTTTCATAGAAATGTTGGGAGGAAATGATGAGCGTTGTTAGCGTTT 482  
423 CAGGATCAAAATTTCTGAGGCGACAGGACAGCAGATCTTAAAGCACTCAAGCAGC 542  
1143 CAGGATCAAAATTTCTGAGGCGACAGGACAGCAGATCTTAAAGCACTCAAGCAGC 1202  
543 CATGACCAAAATCAATGGGAATGGAAGGGAATCGAGAGCAAGCAAGAAATTCGA 602  
1203 CATGACCAAAATCAATGGGAATGGAAGGGAATCGAGAGCAAGCAAGAAATTCGA 1262  
603 TCAAAATCGAAAAGGAATTTCTCAGAAAGTAGAAGGGAATTCAGAGCTCGAGAAATAGCT 662  
1263 TCAAAATCGAAAAGGAATTTCTCAGAAAGTAGAAGGGAATTCAGAGCTCGAGAAATAGCT 1322  
663 TGAACACACTAAATAGATCTCTGCTTTACATGCGGAGCTTCTTGCTGCTTGAGAA 722  
1323 TGAACACACTAAATAGATCTCTGCTTTACATGCGGAGCTTCTTGCTGCTTGAGAA 1382  
723 TCAACATCAANTTGACCTGACTGACTCGGAATGGAACAAGCTGTTGAAAAAACAAGAG 782  
1383 TCAACATCAANTTGACCTGACTGACTCGGAATGGAACAAGCTGTTGAAAAAACAAGAG 1442  
783 GCAACTGAGGAAATGCTGGAAGAGATGGGCAATGTTGCTTCAAAATATACCAAAATG 842  
1443 GCAACTGAGGAAATGCTGGAAGAGATGGGCAATGTTGCTTCAAAATATACCAAAATG 1502  
843 TGACAACGCTTGATAGATCAATGAGAAATGTAATGACCATGATGTATACAGAGA 902  
1503 TGACAACGCTTGATAGATCAATGAGAAATGTAATGACCATGATGTATACAGAGA 1562  
903 CGAAGCATTTAAACAACCGGTTTCACATCAAAAGGTGTTGAACTGGAAGTCTGGATACAGAGA 962  
1563 CGAAGCATTTAAACAACCGGTTTCACATCAAAAGGTGTTGAACTGGAAGTCTGGATACAGAGA 1622

963 CTGATCCGCTGATTTCTTCCATATCATGCTTTGCTTGGTGTTCGTCGG 1022  
1623 CTGATCCGCTGATTTCTTCCATATCATGCTTTGCTTGGTGTTCGTCGG 1682  
1023 GTTCATCATGTGGGCTGCGAGAGAGCAACATTTAGTGCAACATTTGATGAGTGA 1082  
1683 GTTCATCATGTGGGCTGCGAGAGAGCAACATTTAGTGCAACATTTGATGAGTGA 1742  
1083 TTAGTAATTTAAACACCTTGTTCGTG 1110  
1743 TTAGTAATTTAAACACCTTGTTCGTG 1770

## RESULT 6

US-09-004-422-54  
Sequence 54, Application US/09004422  
Patent No. 6337070  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/004,422  
FILING DATE: January 8, 1998  
CLASSIFICATION: 530  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
INFORMATION FOR SEQ. ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1777 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: A2/Aichi/2/68  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPOTYPE:  
TISSUE TYPE:

CELL TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-09-004-422-54

Query Match 78.2%; Score 868; DB 4; Length 1777;  
Best Local Similarity 100.0%; Pred. No. 2.1e-277;  
Matches 868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 TATTGATACCTGATTTCTGAATGATCATCTCCAAATGAGAGATTCCTCAATACAGCC 302  
DB 903 TATTGATACCTGATTTCTGAATGATCATCTCCAAATGAGAGATTCCTCAATACAGCC 962  
QY 303 CTTTCAAAAGCTAAACAGATCATATGAGAGATGCCCCAATATGTTAAGCAAAACAC 362  
DB 963 CTTTCAAAAGCTAAACAGATCATATGAGAGATGCCCCAATATGTTAAGCAAAACAC 1022  
QY 363 CCTGAAGTTGGCAACAGATGCGGGAATGTACCAAGAAACAACTAGAGGCTATTGCG 422  
DB 1023 CCTGAAGTTGGCAACAGATGCGGGAATGTACCAAGAAACAACTAGAGGCTATTGCG 1082  
QY 423 CGCAATAGCAGGTTTCTGAATAATGTTGGAGGAATGATGAGAGGTTGGTACGTTT 482  
DB 1083 CGCAATAGCAGGTTTCTGAATAATGTTGGAGGAATGATGAGAGGTTGGTACGTTT 1142  
QY 483 CAGGATCAAAATTTCTGAGGACAGAGACAGAGATCTTAAAGCACTCAACGAGC 542  
DB 1143 CAGGATCAAAATTTCTGAGGACAGAGACAGAGATCTTAAAGCACTCAACGAGC 1202  
QY 543 CATGACCAAAATCAATGGAATTTGAACAGAGGTAATCGAAGACGAGAGAAATTCGA 602  
DB 1203 CATGACCAAAATCAATGGAATTTGAACAGAGGTAATCGAAGACGAGAGAAATTCGA 1262  
QY 603 TCAATCGAAAGGATTTCTCAGAAATTAAGGGAATTCAGAGACTCGAGAAATACGT 662  
DB 1263 TCAATCGAAAGGATTTCTCAGAAATTAAGGGAATTCAGAGACTCGAGAAATACGT 1322  
QY 663 TGAAGACATAAATAGATCTCTGCTTTACAAATGCGAGACTCTTGCGCTTGAGAGA 722  
DB 1323 TGAAGACATAAATAGATCTCTGCTTTACAAATGCGAGACTCTTGCGCTTGAGAGA 1382  
QY 723 TCAACATACAAATTGACCTACTGACTCGGAATGAACAAGCTGTTGAAAAACAAGAG 782  
DB 1383 TCAACATACAAATTGACCTACTGACTCGGAATGAACAAGCTGTTGAAAAACAAGAG 1442  
QY 783 GCAACTGAGGAAAAATGCTGGAAGAGATGGGCAATGTTGCTTCAAAATATACCAAAAG 842  
DB 1443 GCAACTGAGGAAAAATGCTGGAAGAGATGGGCAATGTTGCTTCAAAATATACCAAAAG 1502

QY 843 TGACAAGCTTGATGATGATCAATCAAGAAATGATCTATGACCATGATGATACAGAGA 902  
DB 1503 TGACAAGCTTGATGATGATGATCAATCAAGAAATGATCTATGACCATGATGATACAGAGA 1562  
QY 903 CGAAGCATTAACACCGGTTTCAATGATCAAAAGGTTGAACGAGTCTGGATACAAAGA 962  
DB 1563 CGAAGCATTAACACCGGTTTCAATGATCAAAAGGTTGAACGAGTCTGGATACAAAGA 1622  
QY 963 CTGATCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1022  
DB 1623 CTGATCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1682  
QY 1023 GTTCAATCATGTCGCGCTGCGAGAGAGCAACATTAGTGCACATTGATGATGATGAT 1082  
DB 1683 GTTCAATCATGTCGCGCTGCGAGAGAGCAACATTAGTGCACATTGATGATGATGAT 1742  
QY 1083 TTAGTAATTAATAAACACCTGTTGTTCTG 1110  
DB 1743 TTAGTAATTAATAAACACCTGTTGTTCTG 1770

RESULT 7  
US-08-453-848-6  
Sequence 6, Application US/08453848  
Patent No. 5858368  
GENERAL INFORMATION:  
APPLICANT: Smith, Gale Eugene  
APPLICANT: Volnovitz, Franklin  
APPLICANT: Wilkinson, Bethanie Eident  
APPLICANT: Voznesensky, Andrei I.  
APPLICANT: Hackett, Craig Stanley  
TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA  
TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/453,848  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/120,607  
FILING DATE: 13-SEPT-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE//DOCKET NUMBER: MGS10ICIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-873-8794  
TELEFAX: (404)-873-8795  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1793 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Influenza virus





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? LOCATION: 1 to 18
? FEATURE:
? NAME/KEY: coding region for AcNPV 61k protein signal
? NAME/KEY: sequence
? LOCATION: 19 to 72
? FEATURE:
? NAME/KEY: SmaI restriction site
? LOCATION: 76 to 81
? FEATURE:
? NAME/KEY: coding region for mature rHA
? LOCATION: 73 to 1728
? FEATURE:
? NAME/KEY: KpnI restriction site
? LOCATION: 1771 to 1777
? FEATURE:
? NAME/KEY: BglII restriction site
? LOCATION: 1776 to 1782
? FEATURE:
? NAME/KEY: universal translation termination signal
? LOCATION: 1783 to 1793
? US-09-169-027-6

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Query Match          69.8%; Score 774.8; DB 3; Length 1793;
Best Local Similarity 94.2%; Pzed. No. 1.7e-246;
Matches 816; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

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? 244 ATTGATACCTGTATTGTAATGCATCACTCCAAATGGAGAGATGCCAATGACAAGCCC 303
? 898 ATTGGCACCCTGCAGTTTGAATGATCATCTCCAAATGGAGATGCCAATGACAAGCCC 957
? 304 TTTCAAAACGTAACAGATCACAATATGAGAGATGCCAATGATGTAAGCAAAACACC 363
? 958 TTTCAAAATGTAACAGATCACAATATGAGAGATGCCAATGATGTAAGCAAAACACC 1017
? 364 CTGAAGTGGGCAACAGATGATGCGGATGTACCAAGAAACAACTAGAGCGCTATTGGC 423
? 1018 CTGAATTTGGCAACAGATGATGCGGATGTACCAAGAAACAACTAGAGCGCTATTGGC 1077
? 424 GCAATAGCAGGTTTCAGAAAATGTTGGAGGAGATGATGAGCGTTGATCGGTTTC 483
? 1078 GCAATCGCAGGTTTCAGAAAATGTTGGAGGAGATGATGAGCGTTGATCGGTTTC 1137
? 484 AGGCATCAAAATTTCTG/GGGCAGACAGACAGAGATCTTAAAGCACTCAAGCAGCC 543
? 1138 AGGCATCAAAATTTCTG/GGGCAGACAGACAGAGATCTTAAAGCACTCAAGCAGCA 1197
? 544 ATCGACCAAAATTCGAAATTTGAACAGGGTAAATCGAGACAGACAGAAATTCAT 603
? 1198 ATCGACCAAAATTCGAAATTTGAACAGGGTAAATCGAGACAGACAGAAATTCAT 1257
? 604 CAATCGCAAAAGGAATTTTCAGAGATGAGAGAGATTCAGACCTCGAGAAATACGTT 663
? 1258 CAATCGCAAAAGGAATTTTCAGAGATGAGAGAGATTCAGACCTCGAGAAATACGTT 1317
? 664 GAAGACACTAAATAGATCTCTGCTTACAAATGGGAGCTTCTGTCGCTCGAGAAAT 723
? 1318 GAAGACACTAAATAGATCTCTGCTTACAAATGGGAGCTTCTGTCGCTCGAGAAAT 1377
? 724 CAACATACAAATGACCTTACTGACTCGGAAATGAACAGCTTTTGAAAAACAAGGAG 783
? 1378 CAACATACAAATGACCTTACTGACTCGGAAATGAACAGCTTTTGAAAAACAAGGAG 1437
? 784 CAACATGAGGAAATAGCTGAGAGATGGGCAATGGTGGTCAAAATATACCAAAATGT 843
? 1438 CAACATGAGGAAATAGCTGAGAGATGGGCAATGGTGGTCAAAATATACCAAAATGT 1497
? 844 GACAACGCTTGCAATGATCAATTCAGAAATGTTACTTATGACCATGATGATATACAGAG 903
? 1498 GACAATGCTGCTGATAGGCTTCATTCAGAAATGGAATTTATGACCATGATGATATACAGAG 1557
? 904 GAAGCATTAACACCGCTTTTCAATCAAAAGTGTGGAATGATGATGATGATATACAGAG 963
? 1558 GAAGCATTAACACCGCTTTTCAATCAAAAGTGTGGAATGATGATGATGATATACAGAG 1617

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? 964 TGAATCTGTGATTTCTTTGCAATATCATGCTTTTGTGCTTTGTGCTGCGG 1023
? 1618 TGATCTTATGATTTCTTTGCAATATCATGCTTTTGTGCTTTGTGCTGCGG 1677
? 1024 TTCATCATGTGGGCTGCGAGAGGCAACATTAGTGCACATTTGATGATGAT 1083
? 1678 TTCATCATGTGGGCTGCGAGAGGCAACATTAGTGCACATTTGATGATGAT 1737
? 1084 TAGTATTAACACCGCTTTGTTCT 1109
? 1738 ---TAATTAACACCGCTTTGTTCT 1760

RESULT 9
US-08-453-848-14
? Sequence 14, Application US/08453848
? Patent No. 5858368
? GENERAL INFORMATION:
? APPLICANT: Smith, Gale Eugene
? APPLICANT: Volkovitz, Franklin
? APPLICANT: Wilkinson, Bethanie Eident
? APPLICANT: Voznesensky, Andrei I.
? TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA
? TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES
? NUMBER OF SEQUENCES: 31
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Patrea L. Pabst
? STREET: 2800 One Atlantic Center
? STREET: 1201 West Peachtree Street
? CITY: Atlanta
? STATE: GA
? COUNTRY: USA
? ZIP: 30309-5450
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/453,848
? FILING DATE: 30-MAY-1995
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/120,607
? FILING DATE: 13-SEPT-1993
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Pabst, Patrea L.
? REGISTRATION NUMBER: 31,284
? REFERENCE/DOCKET NUMBER: MGS10ICIP
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (404)-873-8794
? TELEFAX: (404)-873-8795
? INFORMATION FOR SEQ ID NO: 14:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1757 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Influenza virus
? INDIVIDUAL ISOLATE: A/Shandong/9/93 rHA
? NAME/KEY: polyhedrin mRNA leader (partial)
? LOCATION: 1 to 18
? FEATURE:
? NAME/KEY: coding region for AcNPV 61k protein signal
? NAME/KEY: sequence

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: LOCATION: 19 to 72
: FEATURE:
: NAME/KEY: SmaI restriction site
: LOCATION: 76 to 81
: FEATURE:
: NAME/KEY: coding region for mature rHA
: LOCATION: 73 to 1728
: FEATURE:
: NAME/KEY: KpnI restriction site
: LOCATION: 1735 to 1740
: FEATURE:
: NAME/KEY: BglII restriction site
: LOCATION: 1741 to 1746
: NAME/KEY:
: LOCATION:
: NAME/KEY: universal translation termination signal
: LOCATION: 1747 to 1757
US-08-453-848-14

Query Match      68.2%; Score 756.6; DB 2; Length 1757;
Best Local Similarity 94.1%; Pred. No. 1.9e-240;
Matches 786; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 244 ATTGATACCTGTTATTTGTAATGCATCTCAATGAGAGATTCCCAATACAGACC 303
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DB 901 ATTGGCACTGCAGTTCTGAATGCATCTCCAAATGAGAGATTCCCAATACAGACC 960
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QY 304 TTTCAAAACGTAACACATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 961 TTTCAAAATGTAAACAGATACATATATGAGATGAGATGAGATGAGATGAGATGAGAT 1020
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 364 CTGAAGTTGGACAGAGGATCGGAATGTACCGAGAAACAACTAGAGGCTATTTCGCG 423
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1021 CTGAAGTTGGACAGAGGATCGGAATGTACCGAGAAACAACTAGAGGCTATTTCGCG 1080
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 424 GCATACGAGTTTCATGAGAAATGTTGGAGGAAATGATAGAGGTTGGTTCGTTTC 483
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1081 GCATACGAGTTTCATGAGAAATGTTGGAGGAAATGATAGAGGTTGGTTCGTTTC 1140
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QY 484 AGGCATCAAAATTCAGAGGACAGACAGACAGATCTTAAAGCACTCAACAGACG 543
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DB 1141 AGGCATCAAAATTCAGAGGACAGACAGACAGATCTTAAAGCACTCAACAGACG 1200
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QY 544 ATGACCAAAATCAATGGGAATTTGAACAGGTAATCGAAGACAGACAGAAATTCAT 603
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1201 ATGACCAAAATCAATGGGAATTTGAACAGGTAATCGAAGACAGACAGAAATTCAT 1260
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QY 604 CAAATCGAAAAGAAATTCGAGAGTAGAAGGAGAAATTCAGAGACTCGAAGAAATACGTT 663
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DB 1261 CAAATCGAAAAGAAATTCGAGAGTAGAAGGAGAAATTCAGAGACTCGAAGAAATACGTT 1320
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QY 664 GAAGACACTAAATAGATCTCTGCTTACAAATGGGAGCTTCTGCTGCTGAGAGAT 723
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DB 1321 GAAGACACTAAATAGATCTCTGCTTACAAATGGGAGCTTCTGCTGCTGAGAGAT 1380
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QY 724 CAACATCAATTTGACTGACTGACTCGGAATGAACAAGCTTTTGAAGAAAACAAGGAG 783
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DB 1381 CAACATCAATTTGACTGACTGACTCGGAATGAACAAGCTTTTGAAGAAAACAAGGAG 1440
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QY 784 CAACTGAGGGAATTCGTAAGAGATGGCAATGCTTCTTCAAAATTTACCAAAATGT 843
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QY 844 GACAACTGTCATAGAGTCAATCAGAAAGTGTATGACATGATGATGATGATGATGATGAT 903
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DB 1501 GACAACTGTCATAGAGTCAATCAGAAAGTGTATGACATGATGATGATGATGATGATGAT 1560
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QY 904 GAAGCATTTAAACAACCGGTTTCAGATCAAAAGTGTGAAGTGAAGTGTGAAGTGAAGTGAAG 963
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QY 1024 TTCATCATGTGGCGCTGCCAGAGCAACAATAGTCAACATTTGATTGAG 1078
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RESULT 10
US-09-169-027-14
: Sequence 14, Application US/09169027
: Patent No. 6245532
: GENERAL INFORMATION:
: APPLICANT: Smith, Gale Eugene
: APPLICANT: Voliovitz, Franklin
: APPLICANT: Wilkinson, Bethanie Eident
: APPLICANT: Voznesensky, Andrei I.
: APPLICANT: Hackett, Craig Stanway
: TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA
: TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Patrea L. Pabst
: STREET: 2800 One Atlantic Center
: STREET: 1201 West Peachtree Street
: CITY: Atlanta
: STATE: GA
: COUNTRY: USA
: ZIP: 30309-3450
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/169,027
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/453,848
: FILING DATE: 30-MAY-1995
: APPLICATION NUMBER: 08/120,607
: FILING DATE: 13-SEPT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Pabst, Patrea L.
: REGISTRATION NUMBER: 31,284
: REFERENCE/DOCKET NUMBER: MGS101CIP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (404)-873-8794
: TELEFAX: (404)-873-8795
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1757 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Influenza virus
: INDIVIDUAL ISOLATE: A/Shandong/9/93 rHA
: FEATURE:
: NAME/KEY: polyhedrin mRNA leader (partial)
: LOCATION: 1 to 18
: FEATURE:
: NAME/KEY: coding region for AcNPV 61k protein signal
: NAME/KEY: sequence
: LOCATION: 19 to 72
: FEATURE:
: NAME/KEY: SmaI restriction site
: LOCATION: 76 to 81
: FEATURE:
: NAME/KEY: coding region for mature rHA
: LOCATION: 73 to 1728
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 19:23:49 ; Search time 56.4921 Seconds  
(without alignments)  
8672.640 Million cell updates/sec

Title: US-09-918-568-57

Perfect score: 1110

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Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2\_6/pdata/2/ina/backfiles1.seq : \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	1110	100.0	1110	US-08-229-781-57	Sequence 57, Appl
2	1110	100.0	1110	US-08-630-918-57	Sequence 57, Appl
3	1110	100.0	1110	US-09-004-422-57	Sequence 57, Appl
4	868	78.2	1777	US-08-229-781-54	Sequence 54, Appl
5	868	78.2	1777	US-08-630-918-54	Sequence 54, Appl
6	868	78.2	1777	US-09-004-422-54	Sequence 54, Appl
7	774.8	69.8	1793	US-08-453-848-6	Sequence 6, Appl
8	774.8	69.8	1793	US-09-169-027-6	Sequence 6, Appl
9	756.6	68.2	1757	US-08-453-848-14	Sequence 14, Appl
10	756.6	68.2	1757	US-09-169-027-14	Sequence 14, Appl
11	751.8	67.7	1757	US-08-453-848-20	Sequence 20, Appl
12	751.8	67.7	1757	US-09-169-027-20	Sequence 20, Appl
13	745.4	67.2	1701	US-09-232-468A-21	Sequence 21, Appl
14	745.4	67.2	1701	US-09-784-984B-17	Sequence 17, Appl
15	645.2	58.1	666	PCT-US94-01149-1	Sequence 1, Appl
16	642	57.8	666	PCT-US94-01149-3	Sequence 3, Appl
17	641.4	57.8	918	PCT-US94-01149-9	Sequence 9, Appl
18	631.8	56.9	918	PCT-US94-01149-58	Sequence 58, Appl
19	630.2	56.8	670	PCT-US94-01149-7	Sequence 7, Appl
20	605.2	54.5	1762	US-09-506-286B-10	Sequence 10, Appl
21	605.2	54.5	1762	US-09-506-286B-10	Sequence 10, Appl
22	603.6	54.4	1762	US-08-105-483-284	Sequence 284, App
23	603.6	54.4	1762	US-08-105-483-300	Sequence 300, App
24	603.6	54.4	1762	US-08-709-209-284	Sequence 284, App
25	603.6	54.4	1762	US-08-709-209-300	Sequence 300, App
26	603.6	54.4	1762	US-08-458-101-284	Sequence 284, App
27	603.6	54.4	1762	US-08-458-101-300	Sequence 300, App

28	602	54.2	1762	4	US-09-506-286B-7	Sequence 7, Appl
29	602	54.2	1762	4	US-09-762-861B-7	Sequence 7, Appl
30	581.2	52.4	1698	3	US-09-232-478-15	Sequence 15, Appl
31	581.2	52.4	1698	4	US-09-785-055-15	Sequence 15, Appl
32	579.8	52.2	1695	4	US-09-506-286B-12	Sequence 12, Appl
33	579.8	52.2	1695	4	US-09-762-861B-12	Sequence 12, Appl
34	576.6	51.9	1695	4	US-09-506-286B-9	Sequence 9, Appl
35	576.6	51.9	1695	4	US-09-762-861B-9	Sequence 9, Appl
36	418.4	37.7	690	5	PCT-US94-01149-11	Sequence 11, Appl
37	418.4	37.7	690	5	PCT-US94-01149-11	Sequence 11, Appl
38	329	29.6	329	1	US-08-229-781-37	Sequence 37, Appl
39	329	29.6	329	1	US-08-630-918-37	Sequence 37, Appl
40	329	29.6	329	4	US-09-004-422-37	Sequence 37, Appl
41	320.2	28.8	6802	4	US-08-809-513A-6	Sequence 6, Appl
42	311.6	28.1	334	1	US-08-229-781-38	Sequence 38, Appl
43	311.6	28.1	334	1	US-08-630-918-38	Sequence 38, Appl
44	311.6	28.1	334	4	US-09-004-422-38	Sequence 38, Appl
45	306.2	27.6	1759	1	US-08-105-483-279	Sequence 279, App

## ALIGNMENTS

RESULT 1  
US-08-229-781-57  
; Sequence 57, Application US/08229781  
; Patent No. 5589174  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/229,781  
FILING DATE: April 19, 1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1110 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: A2/Aichl/2/68  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:

HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-229-781-57

Query Match 100.0%; Score 1110; DB 1; Length 1110;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTAGAGCAAGCAGGCGATATTTATATCATGAGACCATGCTTGTAGCTAC 60  
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QY 481 TTCAGGATCAAAATTTCTGAGGCGACAGCAGCAGAGATCTTAAAGACCTAAGCA 540  
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QY 781 AGGCAACTGAGGAAATGCTGAAGAGAGTGGGCAATGCTGCTTCAAAATATACACAAA 840  
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QY 1081 TATTAGTAAATTAACACACCTTGTGTTCTG 1110  
DB 1081 TATTAGTAAATTAACACACCTTGTGTTCTG 1110

RESULT 2.  
US-08-630-918-57  
Sequence 57, Application US/08630918  
Patent No. 5631350  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESS: Wendelroth, Lind & Penack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,918  
FILING DATE: April 5, 1996  
CLASSIFICATION: 530  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993.  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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12843.535 Million cell updates/sec

Title: US-09-918-568 57

Perfect score: 1110

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/p/odata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/p/odata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/p/odata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/p/odata/1/pubpna/US07\_PUBCOMB.seq:\*  
5: /cgn2\_6/p/odata/1/pubpna/US07\_PUB.seq:\*  
6: /cgn2\_6/p/odata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/p/odata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/p/odata/1/pubpna/US09\_PUBCOMB.seq:\*  
9: /cgn2\_6/p/odata/1/pubpna/US09\_PUBCOMB.seq:\*  
10: /cgn2\_6/p/odata/1/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/p/odata/1/pubpna/US09\_PUBCOMB.seq:\*  
12: /cgn2\_6/p/odata/1/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/p/odata/1/pubpna/US10\_PUBCOMB.seq:\*  
14: /cgn2\_6/p/odata/1/pubpna/US10\_PUBCOMB.seq:\*  
15: /cgn2\_6/p/odata/1/pubpna/US60\_NEW\_PUB.seq:\*  
16: /cgn2\_6/p/odata/1/pubpna/US60\_PUBCOMB.seq:\*  
17: /cgn2\_6/p/odata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	IB	ID	Description
1	1110	100.0	1110	9	US-09-918-568-57	Sequence 57, Appl
2	868	78.2	1777	9	US-09-918-568-54	Sequence 54, Appl
3	329	29.6	329	9	US-09-918-568-37	Sequence 37, Appl
4	321	28.9	1711	13	US-10-099-619-1	Sequence 1, Appl
5	311.6	28.1	334	9	US-09-918-568-38	Sequence 38, Appl
6	305.2	27.5	334	9	US-09-918-568-40	Sequence 40, Appl
7	301.8	27.2	329	9	US-09-918-568-39	Sequence 39, Appl
8	295.4	26.6	329	9	US-09-918-568-41	Sequence 41, Appl
9	254.2	22.9	1754	9	US-09-918-568-27	Sequence 27, Appl
10	252.6	22.8	1135	9	US-09-918-568-49	Sequence 49, Appl
11	248.2	22.7	1783	9	US-09-918-568-46	Sequence 46, Appl
12	248.2	22.4	1728	9	US-09-918-568-28	Sequence 28, Appl
13	160.4	14.5	429	9	US-09-918-568-32	Sequence 32, Appl
14	157.4	14.2	424	9	US-09-918-568-31	Sequence 31, Appl
15	157	14.1	442	9	US-09-918-568-29	Sequence 29, Appl
16	152.6	13.7	424	9	US-09-918-568-30	Sequence 30, Appl

17	137.2	12.4	409	9	US-09-918-568-34	Sequence 34, Appl
18	134.6	12.1	394	9	US-09-918-568-36	Sequence 36, Appl
19	134.6	12.1	400	9	US-09-918-568-33	Sequence 33, Appl
20	134.6	12.1	410	9	US-09-918-568-35	Sequence 35, Appl
21	42	3.8	2981	14	US-10-242-056-56	Sequence 56, Appl
22	39.6	3.6	440	11	US-09-918-995-15008	Sequence 15008, A
23	39.6	3.6	1059	10	US-09-911-345-3	Sequence 3, Appl
24	38.6	3.5	10906	9	US-09-956-004-63	Sequence 63, Appl
25	38	3.4	414	14	US-10-123-155-418	Sequence 418, Appl
26	38	3.4	414	15	US-10-146-731-418	Sequence 418, Appl
27	37.4	3.4	592	13	US-10-027-632-215470	Sequence 215470, A
28	37.4	3.4	671	14	US-10-184-644-346	Sequence 346, Appl
29	37.4	3.4	1049	10	US-10-184-634-346	Sequence 346, Appl
30	37.4	3.4	1049	10	US-09-833-381-855	Sequence 855, Appl
31	37.4	3.4	1052	11	US-09-764-891-7527	Sequence 7527, Ap
32	37.4	3.4	1052	11	US-09-764-881-191	Sequence 191, Appl
33	37.4	3.4	1077	11	US-09-764-881-1210	Sequence 1210, Ap
34	37.4	3.4	1077	11	US-09-764-881-1210	Sequence 70, Appl
35	36.8	3.3	592	13	US-10-027-632-298985	Sequence 84403, A
36	36.8	3.3	2100	10	US-09-834-975-862	Sequence 862, Appl
37	36.8	3.3	2100	10	US-09-834-975-957	Sequence 957, Appl
38	36.8	3.3	2100	10	US-09-834-975-964	Sequence 964, Appl
39	36.8	3.3	2100	10	US-09-834-975-1008	Sequence 1008, Ap
40	36.8	3.3	15714	9	US-09-764-869-2355	Sequence 2355, Ap
41	36.8	3.3	15714	14	US-10-091-504-2355	Sequence 2355, Ap
42	36.8	3.3	696	9	US-09-770-149-281	Sequence 281, Appl
43	36.6	3.3	1160	14	US-10-123-155-234	Sequence 234, Appl
44	36.2	3.3	1160	15	US-10-146-731-234	Sequence 234, Appl
45	36.2	3.3	1160	15	US-10-146-731-234	Sequence 234, Appl

## ALIGNMENTS

RESULT 1  
US-09-918-568-57  
Sequence 57, Application US/09918568  
Patent No. US20020054882A1  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/918,568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX: <unknown>  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1110 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL: <unknown>  
ANTI-SENSE: <unknown>  
FRAGMENT TYPE: <unknown>  
ORIGINAL SOURCE:  
ORGANISM: A2/Alch1/2/68  
STRAIN: <unknown>  
INDIVIDUAL ISOLATE: <unknown>  
DEVELOPMENTAL STAGE: <unknown>  
HAPLOTYPE: <unknown>  
TISSUE TYPE: <unknown>  
CELL TYPE: <unknown>  
CELL LINE: <unknown>  
ORGANELLE: <unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <unknown>  
CLONE: <unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <unknown>  
MAP POSITION: <unknown>  
UNITS: <unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 57:  
US-09-918-568-57

Query Match 100.0%; Score 1110; DB 9; Length 1110;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGAGCAAGCAGGGGATATCTATTAATCATGAGACCATGCTTGGAGCTAC 60  
DB 1 CTAGAGCAAGCAGGGGATATCTATTAATCATGAGACCATGCTTGGAGCTAC 60  
QY 61 ATTTCTGTGCTGTGGCCGACAGACCTTCAGAGAAATGACAAGACAGACGCTG 120  
DB 61 ATTTCTGTGCTGTGGCCGACAGACCTTCAGAGAAATGACAAGACAGACGCTG 120  
QY 121 TGCCTGGACATCATGCGGTGCAAGAGCAACACTAGTGAATAATCAGATGATG 180  
DB 121 TGCCTGGACATCATGCGGTGCAAGAGCAACACTAGTGAATAATCAGATGATG 180  
QY 181 ATTAAGTACTAATGCTAGTACGCTAGCTCCTCAACGGGAAATATGCAAC 240  
DB 181 ATTAAGTACTAATGCTAGTACGCTAGCTCCTCAACGGGAAATATGCAAC 240  
QY 241 AATATGATACCTGATTTCTGAATGATCACTCCAATGAGAGCATTCACATAC 300  
DB 241 AATATGATACCTGATTTCTGAATGATCACTCCAATGAGAGCATTCACATAC 300

QY 301 CCCTTCAAAACGTAACAGATCATATGAGAGCATGCCCAAGATATGTTAGCAAAAC 360  
DB 301 CCCTTCAAAACGTAACAGATCATATGAGAGCATGCCCAAGATATGTTAGCAAAAC 360  
QY 361 ACCCTGAAGTGGCAACAGGATGGGAATGTACAGAGAAACAACTAGAGGCTATTC 420  
DB 361 ACCCTGAAGTGGCAACAGGATGGGAATGTACAGAGAGAAACAACTAGAGGCTATTC 420  
QY 421 GCGGCAATGACAGGTTCTATGAAATATGTTGGAGGGAATGATAGCGTTGCTAG 480  
DB 421 GCGGCAATGACAGGTTCTATGAAATATGTTGGAGGGAATGATAGCGTTGCTAG 480  
QY 481 TTCAGGATCAAAATTTCTGAGGGCAGAGCAGAGCAGATCTTAAAGCATCAAGCA 540  
DB 481 TTCAGGATCAAAATTTCTGAGGGCAGAGCAGAGCAGATCTTAAAGCATCAAGCA 540  
QY 541 GCCATGACCAAAATCAATGGAATTTGAACAGGTAATCGAAGACGAGCAAGAAATTC 600  
DB 541 GCCATGACCAAAATCAATGGAATTTGAACAGGTAATCGAAGACGAGCAAGAAATTC 600  
QY 601 CATCAATGCAAAAGGAATTCAGAGATGAGAGGAGAAATTCAGGACCTGAGAAATAC 660  
DB 601 CATCAATGCAAAAGGAATTCAGAGATGAGAGGAGAAATTCAGGACCTGAGAAATAC 660  
QY 661 GTTGAAGACATTAATATGATCTGTGCTTACATGCGAGCTTCTGCTGCTGAG 720  
DB 661 GTTGAAGACATTAATATGATCTGTGCTTACATGCGAGCTTCTGCTGCTGAG 720  
QY 721 AATCAACATCAATTGACCTGACTGCTGGAATGAACAGCTGTTGAAAAAACAAG 780  
DB 721 AATCAACATCAATTGACCTGACTGCTGGAATGAACAGCTGTTGAAAAAACAAG 780  
QY 781 AGGCAACATGAGGAAATGCTGAAGATGGCAATGTTCTTCAAAATATACACAAA 840  
DB 781 AGGCAACATGAGGAAATGCTGAAGATGGCAATGTTCTTCAAAATATACACAAA 840  
QY 841 TGTGACACGCTTGCATAGATCAATCAGAAATGTTAGCAATGATGTTACAGA 900  
DB 841 TGTGACACGCTTGCATAGATCAATCAGAAATGTTAGCAATGATGTTACAGA 900  
QY 901 GACGAAGCATTTAACAACCGGTTTCAGATCAAAAGGTTGAAGTGTGATACAAA 960  
DB 901 GACGAAGCATTTAACAACCGGTTTCAGATCAAAAGGTTGAAGTGTGATACAAA 960  
QY 961 GACTGATCCGTGATTTCTTGGCATATCATGCTTTGCTTGTGTTGCTG 1020  
DB 961 GACTGATCCGTGATTTCTTGGCATATCATGCTTTGCTTGTGTTGCTG 1020  
QY 1021 GGGTTCATCATGTGGCCTGCGAGAGGCAACATTAAGTCAACATTTGATTTGAGTG 1080  
DB 1021 GGGTTCATCATGTGGCCTGCGAGAGGCAACATTAAGTCAACATTTGATTTGAGTG 1080  
QY 1081 TATTAGTAATTAACACCCCTGTTCTG 1110  
DB 1081 TATTAGTAATTAACACCCCTGTTCTG 1110

RESULT 2  
US-09-918-568-54  
Sequence 54, Application US/09918568  
Patent No. US2002005482A1  
GENERAL INFORMATION:  
APPLICANT: yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESS: Wenderoth, Lind & Ponack, L.L.P.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.

ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: us/09/918,568  
FILING DATE: 02 Aug-2001  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1777 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL: <Unknown>  
ANTI-SENSE: <Unknown>  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: A2/A1011/2/68  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>  
CELL LINE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUE: IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 54:  
US-09-918-568-54

Query Match 78.2%; Score 868; DB 9; Length 1777;  
Best Local Similarity 100.0%; Pred. No. 2.1e-252;  
Matches 868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 243 TATTGATACCTGTATTTCTGAATGATCATCTCCAAATGAAGATTTCCCATGACAGACC 302  
DB TTTTATGATACCTGTATTTCTGAATGATCATCTCCAAATGAAGATTTCCCATGACAGACC 962  
QY 303 CTTTCAAAACGTTAAACAGATCATATGAGATGCCCCCAAGTATGTTAAAGCAAAACAC 362  
DB CTTTCAAAACGTTAAACAGATCATATGAGATGCCCCCAAGTATGTTAAAGCAAAACAC 1022  
QY 363 CCGAAGTTGGCAACAGGATGGGGAATGACAGAGAAACAACTAGAGCCCTATTTCGG 422  
DB CCGAAGTTGGCAACAGGATGGGGAATGACAGAGAAACAACTAGAGCCCTATTTCGG 1082  
QY 423 CGCAATAGCAGGTTTCTATAGAAATGTTGGAGGGAATGATGACGCTTGATCGGTTT 482  
DB CGCAATAGCAGGTTTCTATAGAAATGTTGGAGGGAATGATGACGCTTGATCGGTTT 1142  
QY 483 CAGGCATCAAAATTTCTGAGGGCACAGACAGACAGATCTTAAAGCACTCAAGCAGC 542  
DB CAGGCATCAAAATTTCTGAGGGCACAGACAGACAGATCTTAAAGCACTCAAGCAGC 1202  
QY 543 CATGACCAATATCAATGGGAAATTTGAACAGGTAATGAAACAGACAGAGAAATTCGA 602  
DB CATGACCAATATCAATGGGAAATTTGAACAGGTAATGAAACAGACAGAGAAATTCGA 1262  
QY 603 TCAATATGAAAGAAATTTCTCAGAGATGAGAGGAGAAATTCAGACCTCGAGAAATTCGT 662  
DB TCAATATGAAAGAAATTTCTCAGAGATGAGAGGAGAAATTCAGACCTCGAGAAATTCGT 1322  
QY 663 TGAAGACACTAAATATGATCTGCTTCAATGCGGAGCTTCTGCTGTGAGAA 722  
DB TGAAGACACTAAATATGATCTGCTTCAATGCGGAGCTTCTGCTGTGAGAA 1382  
QY 723 TCAACATACAAATGACCTGCTGCTGCGGAAATGAAACAGCTTTGAAAAAACAAGAG 782  
DB TCAACATACAAATGACCTGCTGCTGCGGAAATGAAACAGCTTTGAAAAAACAAGAG 1442  
QY 783 GCAACTGAGGAAATGCTGTAAGATGAGGCAATGCTTCTGCTTCAATATACCAACAATG 842  
DB GCAACTGAGGAAATGCTGTAAGATGAGGCAATGCTTCTGCTTCAATATACCAACAATG 1502  
QY 843 TGACAAAGCTTGCATAGAGTCAATCAGAAATGCTACTTATGACCATGATGTATACAGAGA 902  
DB TGACAAAGCTTGCATAGAGTCAATCAGAAATGCTACTTATGACCATGATGTATACAGAGA 1562  
QY 903 CGAAGCATTTAAACACCGGTTTCAGATCAAAAGGTTGAGCACTGATGATACACAGAGA 962  
DB CGAAGCATTTAAACACCGGTTTCAGATCAAAAGGTTGAGCACTGATGATACACAGAGA 1622  
QY 963 CTGATCTCTGTGATTTCTTCTTCCATATCATCTTTTCTGTTGTTGCTGG 1022  
DB CTGATCTCTGTGATTTCTTCTTCCATATCATCTTTTCTGTTGTTGCTGG 1682  
QY 1023 GTTCATCATGTGGGCTGCGCAGAGAGCAACATTAGTGCACATTTGCAATTTGAGTGA 1082  
DB GTTCATCATGTGGGCTGCGCAGAGAGCAACATTAGTGCACATTTGCAATTTGAGTGA 1742  
QY 1083 TTAGTAATTTAAACACACCTTTGTTCTG 1110  
DB TTAGTAATTTAAACACACCTTTGTTCTG 1770

RESULT 3  
US-09-918-568-37  
Sequence 37, Application us/09918568  
Patent No. US20020054882A1  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING

## ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)

NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/918,568  
FILING DATE: 02-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/228,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993

ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 329 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL: <Unknown>  
ANTI-SENSE: <Unknown>  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: A2/Aichi/2/68

STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL LINE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>

FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:

PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-09-918-568-37

Query Match 29.6%; Score 329; DB 9; Length 329;  
Best Local Similarity 100.0%; Pred. No. 2,5e-89;  
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 ATGACAGCCCTTTCAAAAGTAAACATGATGATGAGACATGCCCAAGATGTTA 352  
|||||  
DB 1 ATGACAGCCCTTTCAAAAGTAAACATGATGATGAGACATGCCCAAGATGTTA 60  
|||||  
QY 353 AGCAAAACACCTGAAAGTTGGCAACAGGATCGGAATGTACAGAGAACAACACTAGAG 412  
|||||  
DB 61 AGCAAAACACCTGAAAGTTGGCAACAGGATCGGAATGTACAGAGAACAACACTAGAG 120  
|||||  
QY 413 GCCTATCGGCGCAATAGACAGTTTCATGAAATGTTGGAGGAAATGATAGCGTT 472  
|||||  
DB 121 GCCTATCGGCGCAATAGACAGTTTCATGAAATGTTGGAGGAAATGATAGCGTT 180  
|||||  
QY 473 GGTACGTTTCAGGCATCAAAATTCGAGGCGACAGCAAGCAGACAGATCTTAAAGCA 532  
|||||  
DB 181 GGTACGTTTCAGGCATCAAAATTCGAGGCGACAGCAAGCAGACAGATCTTAAAGCA 240  
|||||  
QY 533 CTCACAGCAGCATCGACCAATCAATGGGAATGGAAGGTAATCGAGAAGCAAGC 592  
|||||  
DB 241 CTCACAGCAGCATCGACCAATCAATGGGAATGGAAGGTAATCGAGAAGCAAGC 300  
|||||  
QY 593 AGAAATTCATCAATCGAAAAGAAATTC 621  
|||||  
DB 301 AGAAATTCATCAATCGAAAAGAAATTC 329  
|||||

RESULT 4  
US-10-099-619-1  
Sequence 1, Application US/10099619  
Publication No. US20020168384A1  
GENERAL INFORMATION:  
APPLICANT: CLAESSENS, JOHANNES AJ  
APPLICANT: WALTER, FUCHS  
TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS VACCINE  
FILE REFERENCE: 20010010US  
CURRENT APPLICATION NUMBER: US/10/099,619  
CURRENT FILING DATE: 2002-03-15  
PRIOR APPLICATION NUMBER: EP012009759  
PRIOR FILING DATE: 2001-03-15  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 1711  
TYPE: DNA  
ORGANISM: AVIAN INFLUENZA VIRUS  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (11)..(1705)  
OTHER INFORMATION: ISOLATE A/ITALY/445/99 (H7/N1)  
US-10-099-619-1

Query Match 28.9%; Score 321; DB 13; Length 1711;  
Best Local Similarity 63.3%; Pred. No. 1,9e-86;  
Matches 517; Conservative 0; Mismatches 285; Indels 15; Gaps 1;

QY 280 GGACGATCCCAATGACAGCCCTTCAAAACGTAACAGATCACAATATGAGCATGC 339  
|||||  
DB 893 GGGACAATATATAGTAATTTGCCCTTCAGAACATAATATAGCAGGCAATGGAATGT 952  
|||||  
QY 340 CCCAAGTATGTTAAGCAAAACACCTGAGTTGGCAACAGGAGTGCGAATGTACAGAG 399  
|||||

Db 953 CCGAGATATGTTAAGTAAAGAGACTCTGCTGCGCAACAGGAGTGAAGAAATGTTCCGAA 1012  
OY 400 AACCAACT-----AGAGGCTATATTCGGCCAAATAGCAGGTTTCATGAA 444  
Db 1013 ATTCCAAAGAGATCGTGTGAGAGAGAGGCTATTTGCTATATAGGGGTTTCATGAA 1072  
OY 445 AATGTTGGGAGGAAATGATAGACGTTGTGACGTTTCAGGCATCAAAATTCGAGGC 504  
Db 1073 AATGATGGGAGAGTGTGATGATGGGTGATGCTTCAGGCATCAAAATGACAAAGA 1132  
OY 505 ACAGGACAGCAGCAATCTTTAAAGACATCAAGCAGCCATCGACCAATCAATGGAA 564  
Db 1133 GAGGGAAGCTCTCAATTACAAAGACCCCAATCAACATTCATCAAGTAAGAGAAA 1192  
OY 565 TTGAACAGGTAATCAAGAGACGAGAAATTCATCAAAATCGAAAGAAATTCATCA 624  
Db 1193 TTGAACGGCTTATTAATAAACTAACCAACATTTGATTAATAGCATGAATTCAT 1252  
OY 625 GAAGTAGAGGAGAAATTCAGAGACCTCGAGAAATACGTTGAAGACACTTAAATAGATCTC 684  
Db 1253 GAGGTTGAAAAGCAATTTGCAATGTGATAAATGACAGAGATTCATGACAGAGT 1312  
OY 685 TGCTCTTACAAATCGAAGCTTCTTGCTCTGAGAAATCAACATACATTCAGCTACT 744  
Db 1313 TGCTCTTACAAATCGAAGCTTCTTGCTCTGAGAAATCAACATACATTCAGCTACT 1372  
OY 745 GACTCGGAATGAGCAAGCTGTTGAAAAAACAAGGAGGCACTGAGGAAATGCTGAA 804  
Db 1373 GACTCGGAATGAGCAAGCTGTTGAAAAAACAAGGAGGCACTGAGGAAATGCTGAA 1432  
OY 805 GAGATGGGCAATGTTGCTTCAAAATATACCAAAATGAGACAGGTTCCATAGAGTCA 864  
Db 1433 GAGATGGGCAATGTTGCTTCAAAATATACCAAAATGAGACAGGTTCCATAGAGTCA 1492  
OY 865 ATCAGAAATGTTGTTGACCATGATGTATACAGAGCAGCAATTAACAACCGTTT 924  
Db 1493 ATTAAGAAACACATATGATACAGCAAGTACAGGAAAGGCAAAATAGATATA 1552  
OY 925 CAGATCAAAAGTGTGATGAGAGTCTGATACAAAGTGTGATGCTGATTCCTT 984  
Db 1553 CAGATGAGCCCATCAAAATGAGAGGCTGATACAAAGTGTGATGCTGATTCCTT 1612  
OY 985 GCCATATCATCTTTTCTGTTGTTGTTGCTGAGGTTTCATCATGAGGCTGCCAG 1044  
Db 1613 GGGGCAATCATCTTTTCTGTTGTTGTTGCTGAGGTTTCATCATGAGGCTGCCAG 1672  
OY 1045 AGAGCAACATTTGATCAACATTTGATGAGTGT 1081  
Db 1673 AATGAAACATGCGGTTCATATTTGTATATAGTTT 1709

RESULT 5  
US-09-918-568-38  
Sequence 38, Application US/09918568  
Patent No. US2002005482A1  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wendejoh, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Disquette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/918,568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: <unknown>  
PRIORITY DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 334 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL: <unknown>  
ANTI-SENSE: <unknown>  
FRAGMENT TYPE: <unknown>  
ORIGINAL SOURCE:  
ORGANISM: A/Fukuoka/C29/85  
STRAIN: <unknown>  
INDIVIDUAL ISOLATE: <unknown>  
DEVELOPMENTAL STAGE: <unknown>  
HAPLOTYPE: <unknown>  
TISSUE TYPE: <unknown>  
CELL TYPE: <unknown>  
CELL LINE: <unknown>  
ORGANELLE: <unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <unknown>  
CLONE: <unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <unknown>  
MAP POSITION: <unknown>  
UNITS: <unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-918-568-38

Query Match 28.1%; Score 311.6; DB 9; Length 334;  
Best Local Similarity 95.8%; Pred. No. 4,9e-84;  
Matches 320; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
OY 293 ATGACAGCCCTTTCAAAACGTAACAGATCATATGAGAGATGCCCAAGTATGTTA 352  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 1 ATGACAAACCCCTTTCAAAATGTAAACAGATCATATATGGGCGATGTCCAGGTATGTTA 60  
QY 353 AGCAAAACACCCCTGAAGTTGGCAACAGGGATGGGATGTACAGAGAAACAACTAGAG 412  
Db 61 AGCAAAACACCTGTGAATTTGGCAACAGGGATGGGATGTACAGAGAAACAACTAGAG 120  
QY 413 GCGTATTCGGCGCAATATGAGGTTTTCATATAGAAATGGTTGGAGGGAATGATAGCGTT 472  
Db 121 GCATATTCGGCGCAATATGAGGTTTTCATATAGAAATGGTTGGAGGGAATGATAGCGTT 180  
QY 473 GGTAGCGTTTCAGGCTCAAAATTTGAGGGCACAGACAGACAGATCTTAAAGCA 532  
Db 181 GGTAGCGTTTCAGGCTCAAAATTTGAGGGCACAGACAGACAGATCTTAAAGCA 240  
QY 533 CTCAGACAGCCATCGACCAATTCATGGAATTTGAACAGGGTATTCGAGAGAGCAAGC 592  
Db 241 CTCAGACAGCCATCGACCAATTCATGGAATTTGAACAGGGTATTCGAGAGAGCAAGC 300  
QY 593 AGAAATTCATCAATTCGAAAAAGGAATTTCTCAGA 626  
Db 301 AGAAATTCATCAATTCGAAAAAGGAATTTCTCAGA 334

## RESULT 6

US-09-918-568-40  
Sequence 40, Application US/09918568  
Patent No. US20020054882A1

## GENERAL INFORMATION:

APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 Inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/918,568  
FILING DATE: 02-Aug-2001

## CLASSIFICATION: &lt;Unknown&gt;

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/228,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993

## ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX: <Unknown>

## INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:  
LENGTH: 334 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL: <Unknown>

ANTI-SENSE: <Unknown>  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: A/ibarak1/90  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-918-568-40

## Query Match

27.5%; Score 305.2; DB 9; Length 334;

Best Local Similarity 94.6%; Pred. No. 4.3e-82;

Matches 316; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 293 ATGACAAACCCCTTTCAAAATGTAAACAGATCATATGAGAGATGCCCAAGTATGTTA 352  
Db 1 ATGACAAACCCCTTTCAAAATGTAAACAGATCATATGAGAGATGCCCAAGTATGTTA 60  
QY 353 AGCAAAACACCCCTGAAGTTGGCAACAGGGATGGGATGTACAGAGAAACAACTAGAG 412  
Db 61 AGCAAAACACCTGTGAATTTGGCAACAGGGATGGGATGTACAGAGAAACAACTAGAG 120  
QY 413 GCGTATTCGGCGCAATATGAGGTTTTCATATAGAAATGGTTGGAGGGAATGATAGCGTT 472  
Db 121 GCATATTCGGCGCAATATGAGGTTTTCATATAGAAATGGTTGGAGGGAATGATAGCGTT 180  
QY 473 GGTAGCGTTTCAGGCTCAAAATTTGAGGGCACAGACAGACAGATCTTAAAGCA 532  
Db 181 GGTAGCGTTTCAGGCTCAAAATTTGAGGGCACAGACAGACAGATCTTAAAGCA 240  
QY 533 CTCAGACAGCCATCGACCAATTCATGGAATTTGAACAGGGTATTCGAGAGAGCAAGC 592  
Db 241 CTCAGACAGCCATCGACCAATTCATGGAATTTGAACAGGGTATTCGAGAGAGCAAGC 300  
QY 593 AGAAATTCATCAATTCGAAAAAGGAATTTCTCAGA 626  
Db 301 AGAAATTCATCAATTCGAAAAAGGAATTTCTCAGA 334

## RESULT 7

US-09-918-568-39

Sequence 39, Application US/09918568

Patent No. US20020054882A1

## GENERAL INFORMATION:





FILED DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 329 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL: <Unknown>  
ANTI-SENSE: <Unknown>  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: A/Suita/1/90  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>  
CELL LINE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-09-918-568-41  
Query Match 26.6% Score 295.4 DB 9 Length 329:  
Best Local Similarity 93.6% Pred No. 4e-79 Indels 0 Gaps 0:  
Matches 308: Conservative 0; Mismatches 21; Indels 0; Gaps 0:  
QY 293 ATGACAAAGCCCTTCAAAAAGTAAACAAGATCATATGAGACATGCCCAAGATGTGTTA 352  
DB 1 ATGACAAAGCCCTTCAAAAAGTAAACAAGATCATATGAGACATGCCCAAGATGTGTTA 60  
QY 353 AGCAAAACACCTCTGAAGTTGGCAACAGAGGATGCGGAATGTACCAAGAAACAACCTAGAG 412  
DB 61 AGCAAAACACCTCTGAAGTTGGCAACAGAGGATGCGGAATGTACCAAGAAACAACCTAGAG 120  
QY 413 GCCATTGCGGCAATAGCAGGTTTCATAGAAATGTTGGAGGAGGATGATAGACGGTT 472  
DB 121 GCATATTGCGGCAATAGCAGGTTTCATAGAAATGTTGGAGGAGGATGATAGACGGTT 180  
QY 473 GGTACGGTTTCAGGATCAAAATTTCTGAGGCGACAGACAAGCAGACAGATCTTAAAGCA 532

DB 181 GGTACGGTTTCAGGATCAAAACTGTGAGGCGACAGACAAGCAGACATCTTAAAGCA 240  
QY 533 CTCAGACAGCCATCGACCAATCATATGGAATTCAGAGGTAATCGAGACGACG 592  
DB 241 CTCAGACAGCCATCGACCAATCATATGGAATTCAGAGGTAATCGAGACGACG 300  
QY 593 AGAAATTCATCAATCGAAAGGAATTC 621  
DB 301 AGAAATTCATCAATCGAAAGGAATTC 329  
RESULT 9  
US-09-918-568-27  
Sequence 27, Application US/09918568  
Patent No. US20020054882A1  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/918-568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004-422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1754 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL: <Unknown>  
ANTI-SENSE: <Unknown>  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: A/Suita/1/89  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>  
CELL LINE: <Unknown>

ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-918-568-27

Query Match 22.98; Score 254.2; DB 9; Length 1754;  
Best Local Similarity 57.78; Pred. No. 3.5e-66;  
Matches 454; Conservative 0; Mismatches 333; Indels 0; Gaps 0;

244 ATGTATACCTGTTTGTGATGATCATCTCCCAATGGAAGCATTCCTCCATGCAAGCCC 303  
885 ATGGATGAATGTACAGCGAAGTGTCAAAACCCAGAGCTTTAAACATGCTTCTCT 944  
304 TTTCAAACGTAACAGATGATGAGCATGCGCCCAAGTATGTTAAGCAAAACACC 363  
945 TTCCAGATGTACACCAAGTCAATAGAGAGTGTCCAAAGTATGTCAGAGATACAAA 1004  
364 CTGAATGTGGCAACAGATGCGGAATGTACAGAGAAACAACCTAGAGCCATTGCGC 423  
1005 TTATAGATGTGTACAGTAAAGAAATCCCATTCATCCAGAGGTTTGTGGA 1064  
424 GCAATGACAGGTTTCATGAAATGTTGGAGGAGATGATGACGTTGTACGCTTC 483  
1065 GCCATTGCGGTTTCAATGAGGGGGGTGACTGATGATGATGATGATGATGATGAT 1124  
484 AGGCATCAAAATTTCTGAGGACAGGACAGCATGCTTTAAAGCACTCAAGCAGCC 543  
1125 CATCATCAGATGATGAGGATGCTGCTGCGGATCAAAAAGCAACGAATATGCC 1184  
544 ATGACCAATCATGATGAAATGAAACAGGATATGAGAGAGCAAGCAATTCAT 603  
1185 ATTACGGAATTCAAACAAAGGTAATTCGTATGAGAAATGAACTCAATTCACA 1244  
604 CAATGAAAGGAATTCCTGAGAGTAAAGGAGATTCAGAGCTCCGAGAAATCGT 663  
1245 GCTGTGGCAAGAAATCAACAAATTTAGAAAGAGATGAAATCTTAATTAAGATT 1304  
664 GAAGACACTAAATAGTCTCTGCTTACATGCGAGCTTCTTCTGCTGCGTGAAT 723  
1305 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1364  
724 CAACATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 783  
1365 GAAAGGACTTTGATTTTCATGACTCAAAATGTGAAATCTGTATGAGAAAGTAAAGC 1424  
784 CAACGTGAGGAAATGCTGAGAGATGGGCAATGTTGCTCAAAATATACCAATATG 843  
1425 CAATTTAAGATATATGCAAGAAATAGGATGAGGCTGTTTGAATTCACCAAGATG 1484  
844 GACACGCTTGATAGTGTCAATCAGAAATGTAATGATGATGATGATGATGATGATGAT 903

1485 AACATGAATGATGAGAAAGTGTGAAATAAGAACTATGATATCCAAATATTCGAG 1544  
904 GAGCATTTAAACACCGGTTTCAGATCAAAAGGTGATGATGATGATGATGATGATGAT 963  
1545 GAATCAAAAGTAAACAGGAGGAAAAATGAGGAGTGAATGAAATCAATGAGAGTCTAT 1604  
964 TGATCCTGTGATTCCTTTCATATCATGCTTTTGTGCTTGTGCTTGTGCTGAGG 1023  
1605 CAGATTCGTGCGCATCTACTACTGCTGCGCAGATTCACGTGCTTGTGCTGCTGAGG 1664  
1024 TTCATCA 1030  
1665 GCAATCA 1671

RESULT 10  
US-09-918-568-49  
Sequence 49, Application US/09918568  
Patent No. US20020054882A1  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/918,568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/729,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1135 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL: <Unknown>  
ANTI-SENSE: <Unknown>  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: A/Okuda/57  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>

HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>  
CELL LINE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 49:  
US-09-918-368-49

Query Match 22.8%; Score 252.6; DB 9; Length 1135;  
Best Local Similarity 56.6%; Pred. No. 8.3e-66;  
Matches 512; Conservative 0; Mismatches 384; Indels 9; Gaps 2;

QY 215 GCTCTCAACGGGAAATATGCAACAAATATGATACCTGTATTTCTGAATGCATCAGTC 274  
DB 227 GATCGGAGATCATGTAAGAAAGAAACACTTGAGAACTGAGACCAATGCAAAATC 286  
QY 275 CAATGGAAGCTTTCCCATGACACCCCTTTCAAAAGCTAAACAGATCAGATATAGAG 334  
DB 287 CTTGGGAGCAATTAATACAACTTCTTTTACAAATGTCACCCACAGCAATAGAGTG 346  
QY 335 CATGCCCAAGTATGTAAGCAAAACACCTGAAGTTGGCAACAGGATGCGAATGTAG 394  
DB 347 AGTGCCCAATATATTAATAATGCGAAGTTGTTGACCAACAGGACTAAGGAATGTC 406  
QY 395 CAGAGAAACAAGTAGAGGCTATTGCGGCAATAGCAGGTTTCATAGAAAATGTTGGG 454  
DB 407 CCCAGATTGAATCAAGAGGATGTTGGGCAATAGCTGTTTATAGAAAGAGGATGGC 466  
QY 455 AGGGAATGATAGAGGTTGTTGAGGTTTCAGGCATCAAAATTCAGAGGCAAGCAAG 514  
DB 467 AAGGATGTTGACGGTTGTTGATGATACCATGACAGCAATGACAGGATAGGGATAG 526  
QY 515 CAGCAGATCTTAAAGACACTCAAGCAGCATGACCAATCAATGGGAATGGAACAGG 574  
DB 527 CAGCAGACAAGAAATCACTCAAAAGGCAATTTGATGGAATCAACCAAGGAATTCG 586  
QY 575 TAAATGAGAGCAGACAGAAATTCATCAATGCAAAAGAAATTCAGAGTAGAG 634  
DB 587 TGATTTGAAAGATTAACACCCCAATTTGAAGCTGTTGGAAAGAAATTCGTAATAG 646  
QY 635 GGAGATTCAGGAGCTCGAGAAATACGTTGAAGACACTAATATCTCTGCTTACA 694  
DB 647 AAAAGCTGGAACCTTGAACAAAAGATGGAAGAGGGTTCTAGATGTTGACATACA 706  
QY 695 ATGCGAGACTTCTGCTCGAGAAATCAACATACATACATGAGCTGAGCTGGAAA 754  
DB 707 ATGCTGAGCTTTTACTTCTGATGAAATGAGAGACACTTACTTTCTATGATTTAATG 766  
QY 755 TGAACAGCTGTTGAAAAAACAGAGGCAACTGAGGAAAAATCTGAAAGATGGCA 814

DB 767 TCAAGAACTGTATAGTAAGTCAAGATGACAGTACAGAGCAACGCTCAAGAACTAGGAA 826  
QY 815 ATGCTGCTTCAAAATATACCAAAATGTGACAAAGCTTGATAGATCAATCAAGAA 874  
DB 827 ATGATGTTTAAATTTATATCAAAATGATGATGATGATGATGATGATGATGATG 886  
QY 875 GTACTATAGCAGTATGATATACAGAGCAAGCAATTAACACCGCTTGATAGTCAAG 934  
DB 887 GGCATATATATATCCCAAGTATGAGAGAGCTTAACTAAATGAAATATAATCAAG 946  
QY 935 GTGTGAACCTGAAGTGTGATCAAAAGACGTGATCCTGATTTCCCTTCCATATCAT 994  
DB 947 GGGTAAATTTAGCAGCATGGGGTTTATCAAAATCCTTGCCATTTATGCTACATAG 1006  
QY 995 GCTTTTG---CTTTGCTGTTTTCGCTGGGTTATATATGAGGCTCCAGAGAGCA 1051  
DB 1007 GTTCATATGCACTGCAATCATGATGCGGATCTCTTCTGGGTGCTCCAAACGGCT 1066  
QY 1052 ACATTAGTCAACATTTGATTTGATGTA-----TTAGAAATTAACACACCTTGT 1105  
DB 1067 CTCTGAGTGCAAGATCTGATATATATATATATATATATATATATATATATAT 1126  
QY 1106 TTCTG 1110  
DB 1127 TTCTG 1131

RESULT 11  
US-09-918-568-46  
Sequence 46, Application US/09918568  
Patent No. US2002005482A1  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESS: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/918,568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1783 base pairs

TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOHETICAL: <unknown>  
ANTI-SENSE: <unknown>  
FRAGMENT TYPE: <unknown>  
ORIGINAL SOURCE:  
STRAIN: A/Okuda/57  
INDIVIDUAL ISOLATE: <unknown>  
DEVELOPMENTAL STAGE: <unknown>  
HAPLOTYPE: <unknown>  
TISSUE TYPE: <unknown>  
CELL TYPE: <unknown>  
CELL LINE: <unknown>  
ORGANELLE: <unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <unknown>  
CLONE: <unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <unknown>  
MAP POSITION: <unknown>  
UNITS: <unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 46;  
US-09-918-568-46

Query Match 22.7% Score 252.4; DB 9; Length 1783;  
Best Local Similarity 56.8%; Pred. No. 1.3e-65;  
Matches 507; Conservative 0; Mismatches 376; Indels 9; Gaps 2;

QY 228 GAAATATGACAACTTTGATACCTGATTTCTGATGCATCCTCCAAATGGAGCAT 287  
|||||  
DB 885 GAAATGAGAGGAACTTTGAGAACTGTGAGACCAATGCCAAATCTCTTTGGAGCAAT 944  
|||||  
QY 288 TCCCAATGACAGCCCTTCAAAAGCTAAACAGATCACATATGAGAGATGCCCAAGTA 347  
|||||  
DB 945 AAATCAACATCTTCAATGTCACCCACTCACATATGATGAGTGCCCAATA 1004  
|||||  
QY 348 TGTATGACAAACCTTTGAGTTGGCAAGGATGCCGAATGTACACAGAAACAAAC 407  
|||||  
DB 1005 TGTAAATTCGAGAGTTGGCTTATGACACAGACTAAGAGATGTTCCCAAGATTGATC 1064  
|||||  
QY 408 TAGAGCCATATCGGCACATAGCAGTTTCATAGAAATGTTGGAGGGAATGATAGA 467  
|||||  
DB 1065 AAGAGATGTTGGGTCATAGCTGTTTATAGAGAGAGATGCCAAGAAATGTTGA 1124  
|||||  
QY 468 CGGTGTAGCGTTTCAGCATCAAAATTTGAGGGCAGACAGACAGACAGATCTTAA 527  
|||||  
DB 1125 CGGTGTATGATGATCATCAGACATGACAGGGATCAGGGTATCCACAGCAAGA 1184  
|||||  
QY 528 AAGCATCAGACGCCATCGACCAATATGGGAATTTGACAGGTTATTCGAGAGAC 587  
|||||  
DB 1185 ATCCACTCAAAAGCAATTTGATGGAATCACCACAGGTTAAATTTCTGATGAAAGAT 1244  
|||||  
QY 588 GAAGAGAAATTCATTAATCGAAAGAAATTTCTCAGAGTGAAGGAGAAATTCAGA 647  
|||||

DB 1245 AAACACCAATTTGAACCTTTGGGAAAGAAATTCGTAACCTTAGAGAAAGACTGAGAA 1304  
|||||  
QY 648 CCTGAGAAATACCTTTGAGACACTAAATATGATCTGTGCTTACATATGGGAGCTTCT 707  
|||||  
DB 1305 CTTGACAAAAGATGAGAGCGGTTCTGATGATGTGACATACATGCTGAGCTTTT 1364  
|||||  
QY 708 TGTGCTCTGGAGATCAACATCAATTTGACCTGACCTGCGGAATGAAACAGCTGT 767  
|||||  
DB 1365 AGTTCTGATGAAATATGAGAGACACTTTCATTTGATGATTTCTAATGTCAGAAATCTGTA 1424  
|||||  
QY 768 TGAATAAACAAGAGGAGCACTGAGGAAATGCTGAAGAGATGGCAATGTTCTTCAA 827  
|||||  
DB 1425 TAGTAAGTCAAGATGACGCTGAGAGACAAAGCTCAAGAACTAGAAATGATGTTTGA 1484  
|||||  
QY 828 AATATCCACAATGTGACAAAGCTTGCATATGATGATCAATGAAATGATCTATAGCA 887  
|||||  
DB 1485 ATTTATCACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1544  
|||||  
QY 888 TGTATATACAGAGAGAGCATTAACAAACCGGTTTCAGATCAAGGTTGTAAGTGA 947  
|||||  
DB 1545 TCCCAAGTATGAGAGAGAGCTTAACATAATGAAATGAAATGAAAGGGAATTAATGAG 1604  
|||||  
QY 948 GTCTGATACAAAGACTGATCTGTGATTTCTTCCATATCATGCTTTTGG---CT 1004  
|||||  
DB 1605 CAGCATGGGGTTTATCAAAATCCTTGCCATTTATGATAGTACAGTATGATGATGATGAT 1664  
|||||  
QY 1005 TTGTGTTGTTTGTGGGCTTATCATGATGAGGCTCCACAGAGGCAACATTAAGTCA 1064  
|||||  
DB 1665 GGCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1724  
|||||  
QY 1065 CATTTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1110  
|||||  
DB 1725 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1776  
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RESULT 12  
US-09-918-568-28  
Sequence 28, Application US/09918568  
Patent No. US20020054882A1  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/918, 568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367

?		REFERENCE/DOCKET NUMBER:	<Unknown>
?		TELECOMMUNICATION INFORMATION:	
?		TELEPHONE:	202-721-8200
?		TELEFAX:	202-721-8250
?		TELEX:	<Unknown>
?		INFORMATION FOR SEQ ID NO: 28:	
?		SEQUENCE CHARACTERISTICS:	
?		LENGTH:	1728 base pairs
?		TYPE:	nucleic acid
?		STRANDEDNESS:	double
?		TOPOLOGY:	linear
?		MOLECULE TYPE:	cDNA to genomic RNA
?		HYPOTHETICAL:	<Unknown>
?		ANTI-SENSE:	<Unknown>
?		FRAGMENT TYPE:	<Unknown>
?		ORIGINAL SOURCE:	
?		ORGANISM:	A/1zum1/5/65
?		STRAIN:	<Unknown>
?		INDIVIDUAL ISOLATE:	<Unknown>
?		DEVELOPMENTAL STAGE:	<Unknown>
?		HAPLOTYPE:	<Unknown>
?		TISSUE TYPE:	<Unknown>
?		CELL TYPE:	<Unknown>
?		CELL LINE:	<Unknown>
?		ORGANELLE:	<Unknown>
?		IMMEDIATE SOURCE:	
?		LIBRARY:	<Unknown>
?		CLONE:	<Unknown>
?		POSITION IN GENOME:	
?		CHROMOSOME/SEGMENT:	<Unknown>
?		MAP POSITION:	<Unknown>
?		UNITS:	<Unknown>
?		FEATURE:	
?		NAME/KEY:	
?		LOCATION:	
?		IDENTIFICATION METHOD:	
?		OTHER INFORMATION:	
?		PUBLICATION INFORMATION:	
?		AUTHORS:	
?		TITLE:	
?		JOURNAL:	
?		VOLUME:	
?		ISSUE:	
?		PAGES:	
?		DATE:	
?		DOCUMENT NUMBER:	
?		FILING DATE:	
?		PUBLICATION DATE:	
?		RELEVANT RESIDUES IN SEQ ID NO:	
?		SEQUENCE DESCRIPTION:	SEQ ID NO: 28;
?		US-09-918-568-28	
?		Query Match	22.4%; Score 248.2; DB 9; Length 1728;
?		Best Local Similarity	56.5%; Pred. No. 2,3e-64;
?		Matches 482; Conservative	0; Mismatches 368; Indels 3; Gaps 1;
Oy	245	TTGATACCTCGTATTTCGTGAATGCATCACCCTCCAAATGGAGCATTTGCCAATGCAAGCCTT	304
Dd	876	TTGGGACACTGTGAGACCAATGCCAACACTCTTTTGAGGACCAATAATACACACTTAACCTT	935
Oy	305	TTCAAACGTAAACAAGATCACATATGAGCATGTGCCCAAGTAGTGTAGCAAAAACACC	364
Dd	936	TTCAACAATGTCCACCCACACTGACAAATAGAATGAGTGGCCCCAAATATGTAAATGGAGAAAT	995
Oy	365	TGAAGTTGCCACAGGAGATGCGGAATGTAACGAGAAACAACACTGAGAGCCTATTGGCGC	424
Dd	996	TGCTCTTACCAACAGGACTPAAGGAATGTTCCCAGATTGAATCAAGAGAGATTGTTGGGG	1055
Oy	425	CATAGCAGAGTTTCATAGAAAATGTTGGGAGGAGATGATAGCGTTGGTAGCGTTTCA	484
Dd	1056	CATAGCTGCTTTATAGAGAGAGATGGCAAGGAATGTTGATGTGGTAGATACC	1115
Oy	485	GGCATCAAAATTCGTGAGGCGACAGACAAAGCAGAGATCTTAAAGCACTCAAGCACA	544

Db	1116	ATCACAGCAATTCACCAGGGATTCAGGGTATGCGACGACACAAAGATTCACCTCAAAAGCAT	1175
Qy	545	TCGACCAATTCATGGGAAATTTGAACAGGGTATTCGAGACGACGAGAGAAATTCATC	604
Db	1176	TTGATGCAATCACACACAAAGGAAATTTCTGTGATGAAAGATGAAACCCCAATTTGAG	1235
Qy	605	AAATGAAGAAGAAATTCACAGAGTAGAGGAGAGATTCAGAGCTCGAGAAATTCGTTG	664
Db	1236	CTGTTGGGAAAGAAATTCATTAATTTAGAGAAAAGACTGAGACCTTGACACAAAAGATG	1295
Qy	665	AAGACATTAATAATAGATCTCTGGTCTTCAATGCGAGCTTCTTGCTCGAGAAATC	724
Db	1296	AAGAGGGGTTTCTAGATGTGTGACATCAATGCTGAGCTTCTAGTTCTGATGAAATG	1355
Qy	725	AACATCAATGACCTGACCTGACCTCGGAAATGAACACCTGTTTGAATAAACAGAGGC	784
Db	1356	AGAGGACCTTGACTTCATGATTTCTTAATGTCAAGAACCTGTATGATATAAGTCAGAAATG	1415
Qy	785	AACTGAGGAAATATGCTGAGAGATGAGGCAATGTTGCTTCAATAATATACCAAAATG	844
Db	1416	AGCTGAGAGACACGCTCAAGAGACTAGAGAAATGATGTTTGAATTTATACCAATGTG	1475
Qy	845	ACAACGCTTGCATGATGATCAATCAGAAATGCTACTTATGACATGATGATATACAGACG	904
Db	1476	ACGATGAATGCATGAATAGTGTGAAAAAGGGAGCTATGATATCCCAAGATGAGAGAG	1535
Qy	905	AAGCATTAACACCGCTTCAGATCAAGAGTGTGAATCAGTCAAGTCTGATACAAAGACT	964
Db	1536	AATCTAACTAAATGAAATGAATCAAGAGGTAATTAAGCAGCATGGGGCTTTACC	1595
Qy	965	GGATTCCTGTGATCTCTTTCCTCCATATCATGCTTTTGG--CTTGTGTTTGTTCGTGG	1021
Db	1596	AAATCTTGCCATTATATCTACAGTTGACGGTCTCTGTACCTGCAATCATGATGGCTG	1655
Qy	1022	GGTTCATCATGTGGGCTGCCAGAGAGCAACATTAGTGCACATTTGCATTGGAGTGT	1081
Db	1656	GGATCTCTTCTGTGGATGCTCCAAAGGGCTCTGCACTGCAAGATCTCATATGATTTG	1715
Qy	1082	ATTAGTAATTAATA 1094	
Db	1716	AATTTATTTTATA 1728	

RESULT 13

US-09-918-568-32

Sequence 32, Application US/09918568

Patent No. US20020054882A1

GENERAL INFORMATION:

APPLICANT: Yoshinobu OKUNO et al.

TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.

STREET: 2033 K Street, N.W., #800

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/918,568

FILING DATE: 02-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/004,422

FILING DATE: January 8, 1998

APPLICATION NUMBER: 08/443,862

RESULT 14  
 US-09-918-568-31  
 Sequence 31, Application US/09918568  
 Patent NO. US20020054882A1  
 GENERAL INFORMATION:  
 APPLICANT: Yoshihobu OKUNO et al.  
 TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
 NUMBER OF SEQUENCES: 38  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
 STREET: 2033 K Street, N.W., #800  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20006  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
 COMPUTER:  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/918,568  
 FILING DATE: 02-Aug-2001  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/004,422  
 FILING DATE: January 8, 1998  
 APPLICATION NUMBER: 08/443,862  
 FILING DATE: May 22, 1995  
 APPLICATION NUMBER: 08/229,781  
 FILING DATE: April 19, 1994  
 APPLICATION NUMBER: 08/054,016  
 FILING DATE: April 29, 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warren M. Cheek, Jr.  
 REGISTRATION NUMBER: 33,367  
 REFERENCE/DOCKET NUMBER: <Unknown>  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-721-8200  
 TELEFAX: 202-721-8250  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 31:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 424 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to genomic RNA

HYPOTHETICAL: <Unknown>  
ANTI-SENSE: <Unknown>  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: A/Yamagata/120/86  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-918-568-31

Query Match 14.2% Score 157.4; DB 9; Length 424;  
Best Local Similarity 60.8%; Pred. No. 3.5e-37;  
Matches 257; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

301 CCCTTTCAAAACGTAACAGATGACATATGAGCATGCCCAAGTATGTTAAGCAAAAC 360  
1 CTTTCCAGAAATGTACACCCAGTACACATAGAGAGAGTGCACAAAGTATGTACAGAGTACA 60  
361 ACCCTGAAGTTGGCAACAGGATGGGATGTACCCAGAGAACAACTAGAGGCTATTTC 420  
61 AATTAGAGATGTTACAGAGACTAAGAACATCCCATTCATTCATCCAGAGTTTGT 120  
421 GCGCAATAGCAGGTTTCATAGAAAATGGTTGGAGAGATGATTAACGGTTGTACGG 480  
121 GGAGCATTTGCCGTTTCATTTCAAGGGGCTGACTGGAATGATGATGATGATGATGAT 180  
481 TTCAGCATCAAAATTTCTGAGGCAACAGCAAGCAAGCATCTTAAAGCACTCAAGCA 540  
181 TATCATCATCAGATGACAGAGATCTGCTATGCTGCGATCAAAAAGCAACAAAT 240  
541 GCCATCGACCAATCAATGGGAAATTTGAACAGGATATGAGACAGCAAGCAAAATTC 600  
241 GCCATTAACGGGATTAACAAGGAAATTTCTGATGAGAGAAATGAACACTCAATTC 300  
601 CATCAATCGAAGAAATTTCTCAGAGTAGAAGGAAATTCAGAGACTCGAATATAC 660  
301 ACAGCTGTGGGAAAGATTTCAACAATTAAGAAAGATGAAATTAATAAATA 360  
661 GTTGAAGACACTAAATAGATCTCTGTTTACATGCGAGACTTCTTCTGCTGAG 720  
361 GTTGTATGATGATTTCTGTGACATTTGGACATATATGACAGATTTGTTGTTCTACTGAA 420  
721 AAT 723

Db 421 AAT 423

RESULT 15  
US-09-918-568-29  
Sequence 29, Application US/09918568  
Patent No. US20020054882A1  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/918,568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/228,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 442 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL: <Unknown>  
ANTI-SENSE: <Unknown>  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: A/PR/8/34  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>



FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION SEQ ID NO: 29:  
US-09-918-568-29

Query Match 14.8; Score 157; DB 9; Length 442;  
Best Local Similarity 60.8; Pred. No. 4.7e-37;  
Matches 262; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

QY 301 CCTTTCAAAACGTAAACAAAGATCAGATATGAGCATGCCCAAGTATGTTAAGCAAAAC 360  
DB 1 CCTTTCAGAAATATTAACCCAGTCACAAATAGAGAGTCCCAAAATACGTACAGAGTCCC 60  
QY 361 ACCCTGAAGTTGGCAACAGGATGCCGATGACCAAGAACAACTAGAGGCTATTC 420  
DB 61 AAATTGAGATGGTTTCAGACTAAGCAACATCCCGTCATCAATCCAGAGGCTATTT 120  
QY 421 GGCATATAGCAGATTCATAGAAATGTTGGAGGAGATGATAGCGGTGTGATCGT 480  
DB 121 GGAGCCATTCGCCGTTTATTGAAAGGGGATGGACTGGAATGATGATGATGATGAT 180  
QY 481 TTGAGGCATCAAAATCTGAGGGCACAGCAAGACAGATCTTAAAGCACTCAAGCA 540  
DB 181 TATCATCATCAGATTAACAGGATCAGGCTATGACGCGATCAAAAAGCACACAAAT 240  
QY 541 GCCATGACCAATTCATGGGAATTCAGACAGGTAATCGAAGAGCAAGCAAAATTC 600  
DB 241 GCCATTAAACGGATTTCAAAACAAGGTAACTGTATCGAGAAATGAACACTCAATTC 300  
QY 601 CATCAATCGAAAGCAATTCAGAGTAGAAGGGAATTCAGGACTCGAAGAAATAC 660  
DB 301 ACAGCTGTGGTAAATATTCACAAATTCAGAAAAAGATGAGAAATTTAAATAAAAA 360  
QY 661 GTTGAAGACACTAAATAGATCTCTGTGCTTACATGCGGAGCTCTTGTGCTCTGAG 720  
DB 361 GTTGAATGATGATTTTGTGACATTTGACATATATATGACAAATTTGTTAGTTCTACTGAA 420  
QY 721 AATCAACATCAATTCGA 737  
DB 421 AATGAAGGACTCTGGA 437

Search completed: August 9, 2003, 19:22:43  
Job time : 180.294 secs

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1	833	46.7	1741	7	US-60-470-920-19	Sequence 19, Appl
2	489.4	27.4	1214	7	US-60-470-920-21	Sequence 17, Appl
3	467.4	26.2	1220	7	US-60-470-920-17	Sequence 21, Appl
4	103.6	5.8	1884	1	PCT-US03-12228-94	Sequence 94, Appl
5	49.2	2.8	124326	7	US-60-487-610-19458	Sequence 19458, A
6	48.4	2.7	40-42952	7	US-60-487-610-42952	Sequence 42952, A
7	48.4	2.7	201	7	US-60-487-610-42953	Sequence 42953, A
8	48	2.7	201	7	US-60-487-610-42923	Sequence 42923, A
9	45.2	2.5	19646141	5	US-09-947-914-42	Sequence 42, Appl
10	44.8	2.5	201	7	US-60-487-610-42954	Sequence 42954, A
11	41.8	2.3	1837	7	US-10-286-897-4024	Sequence 4024, Ap
12	41.8	2.3	3423	5	US-10-105-837-126	Sequence 126, App
13	41.8	2.3	3423	5	US-10-286-897-452	Sequence 452, App
14	41.8	2.3	11116	5	US-10-286-897-1473	Sequence 1473, Ap
15	41.6	2.3	160592	7	US-60-487-610-19887	Sequence 19887, A
16	40.4	2.3	564	5	US-10-603-113-2884	Sequence 2884, Ap
17	40.2	2.3	3802	5	US-10-603-113-11955	Sequence 11955, A
18	40.2	2.2	300	5	US-10-085-783A-47731	Sequence 47731, A
19	40	2.2	1777	5	US-10-042-417A-51	Sequence 51, Appl
20	40	2.2	2435	5	US-10-357-930-22563	Sequence 22563, A
21	40	2.2	2435	5	US-10-357-930-44993	Sequence 24993, A
22	40	2.2	2435	5	US-10-357-930-25291	Sequence 25291, A
23	40	2.2	2435	5	US-10-357-930-28380	Sequence 28380, A
24	38.6	2.2	13831263	5	US-09-947-914-147	Sequence 41, Appl
25	38.4	2.2	11176	5	US-10-603-114-1147	Sequence 1147, Ap
26	38	2.1	54233	7	US-60-485-450-12257	Sequence 12257, A

27	37.2	2.1	6837	7	US-60-487-610-42930	Sequence 42930, A
28	37	2.1	6837	7	US-10-357-930-25433	Sequence 25433, A
29	37	2.1	152321	7	US-60-485-450-12128	Sequence 12128, A
30	36.8	2.1	337	6	US-10-085-7834-47736	Sequence 47736, A
31	36.6	2.1	1314	6	US-10-273-573-2516	Sequence 2516, A
C	31	2.1	179131	5	US-09-947-914-46	Sequence 46, App
32	36.4	2.0	201	7	US-60-487-610-10158	Sequence 10158, A
33	36.4	2.0	9517	7	US-60-487-610-636	Sequence 636, App
C	34	2.0	27112	7	US-60-485-450-11992	Sequence 11992, A
35	36.4	2.0	1215	6	US-10-603-113-6183	Sequence 6183, App
36	36.2	2.0	201007	7	US-60-487-610-19435	Sequence 19435, A
37	36	2.0	93427	7	US-60-485-450-12224	Sequence 12224, A
38	35.8	2.0	412	6	US-10-085-7834-50134	Sequence 50134, A
39	35.6	2.0	508	6	US-10-085-7834-45358	Sequence 45358, A
40	35.6	2.0	1512	6	US-10-603-113-6178	Sequence 6178, App
41	35.6	2.0	2433	6	US-10-621-901-46	Sequence 46, App
C	42	2.0	500	6	US-10-357-930-23194	Sequence 23194, A
43	35.4	2.0	7677	6	US-10-357-930-29060	Sequence 29060, A
44	35.4	2.0	7677	6	US-10-357-930-29060	Sequence 29060, A
C	45	2.0	79786	1	PCT-US02-38582-175	Sequence 175, App

## ALIGNMENTS

```

RESULT 1
US-60-470-920-19
; Sequence 19, Application US/60470920
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine, J.
; APPLICANT: Villalta, Adriane
; APPLICANT: Wlooch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Gaell, Andrew J.
; TITLE OF INVENTION: DNA Influenza Vaccine Compositions
; FILE REFERENCE: 1530.0640000
; CURRENT APPLICATION NUMBER: US/60/470,920
; CURRENT FILING DATE: 2003-05-16
; NUMBER OF SEQ. ID NOS.: 45
; SOFTWARE: Patentln version 3.2
; SEQ. ID NO. 19
; LENGTH: 1741
; TYPE: DNA
; ORGANISM: Influenza A virus
; US-60-470-920-19

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Query Match	46.78; Score 833; DB 7; Length 1741;
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Matches 1180; Conservative 0; Mismatches 520; Indels 15; Gaps 2.

QY	42	CAAAACATAGGCCATCATTTATCTCATATCTCTGTTCACACAGTGAAGAGGAGCCAGAT	107
	5	CAAAATGAGAAATATAGTCTCTCTTCTTGSCAACAGTCAGTCTTGTTAAATGATGCAT	64
Db			
QY	102	ATGCATGTCATACCATGCCCATAATTTCCACAGAGAAGTGCACACATTTTGAACGGAA	167
	65	TTGCATTGGTTACCATGCAAAACACATCGACACAGAGGTTGACACAAATAATGAGAAAGAA	124
Db			
QY	162	CGCATCTGACATCATGCCAGCAATCCCTTGAGAGAACCCATTAACGGAAAGTTATGAA	222
	125	TGTTACTGTTACACATGCCCCAAGACATATCTGAAAGGACACACAAACGGGAAGCTCTGCA	188
Db			
QY	222	ACTAAACGGAATCCCTCCACTTGAACCTAGAGGAGACTGTAGCAATGGCCGATGGCTCTTGG	281
	185	TCTAAATGGAGTGAAGAACCTCTCATTTTTCAGGAGATTGTAGTACGTGATGGCTCTCGG	244
Db			
QY	282	AAATCCAAATGTATAGGCTTCTTAGTGTGCCAGAACGGTCTATATATTGGAGAAAGA	341
	245	AAACCTTATGTGTGAGCAATTCATCAATGTGCGGAAATGGCTCTTAACATAGCGAGAGGC	304
Db			
QY	342	AAACCCGAGAGAGCGTTGTGTTATCCAGGACGCTCAATATATGAAGAATTGAACA	401
	305	CAGTCCAGCAATGACCTCTGTATTACAGAGGGAATTTACAGACATATGAAGAATCGAAGACA	364

QY	402	TCCTCCAGCAGCGGTGAACATTTCGCGAAGTAAGATTCTCGCCGCAACATATGATGATG--	459
Db	365	CCATTGACGACGATTAACCATTTTGGAGAAATTCAGATATATCCCAAAAGTCTTGCTC	424
QY	460	-ACACGCAATPACAACTGAGGTTTCAGCGGCTCGCGGTCTGTATATCATCAT	518
Db	425	CATCTATGATGCTCTCAATCAGGGGTGAGCTACGATGTCCATACCTTTGGGGAGTCTCC	484
QY	519	TTTCAGAACATGTCGTGCGCTGCAAGGAAGAGATCAGATTAATCCGGTTGCCAAGATC	578
Db	485	TTTCAGAAATGTGTATGTGCTTTTCAAAAGAACAGTGCATATACCACAAATTAAGAGAG	544
QY	579	GTACACAAATPACAGCGGAGAACAAATGCTAATTAATTTGGGGGTCCACCATTCCATTGA	638
Db	545	CTACATATATACCACCAAGAAAGATCTTTGGTACTGTGGGGATTACCATCTTAATGA	604
QY	639	TGAGACGAGAACAAAGCAATTTGTACAGAAATGTGGGAACCTAATGTTCCGTAGGCATTC	698
Db	605	TCCGGCAGGCGAGACAAAGCTCTATCAAAATCCAACCCCTACATTTTCCGTGGGAATTC	664
QY	699	AACATTGAACAAAGGTCAACCCACAGAAATPAGCAACAGGCTTAAGTAATGAGCAAG	758
Db	665	AACACTGAACCGAGATGTGTTCCAAATPAGTACTAAGCCCAAGTAAAGCGCAAG	724
QY	759	AGGTGAATGGAATTTCTTTGGACCTCTTGGAATATGTGGACACCATTAATTTTGAGAG	818
Db	725	TGGAGAAAGGAGTCTCTTGACATTTTAAAGCCGAATGATGCCATCAATTTCCAGAG	784
QY	819	TACTGGTAAATTAATGGACACAGAGATGAGATTCAAAATPAGAAAGAGATGATGACAG	878
Db	785	TAATGGAAATTTTCATTTGCCCGCAAGATATGCATACAAATTTGTCAAGAAAGGGACTCAAC	844
QY	879	GATCATGAAACAGAAAGAACCTTGAGAACTGTGAGACCAATGGCCAAACTCTTTGG	938
Db	845	AATTTATGAAAGTGAATTTGGAATTTGGTAACTGCAACACCAAGTGTCAAACTCCAA	904
QY	939	AGCATTAATTAACACTTACCTTTTCACATGTCACCCACATGACAAATAGTGATGAGTCCC	998
Db	905	GCGCATTAACCTTAGATGCTCATTCACAACTATACCCCTTCACCATCGGGGAATGCC	964
QY	999	CAAAATATGTAAATCGGAGAAAGTTGGTCTTACCAACAGCAATAGGAATGTTCCCGCAT	1051
Db	965	CAAAATATGTGAATCAACAGATATAGTCTTGCGATGCACTCAGAAATATACCCTCAAG	1022
QY	1059	TG-----AATCAAGAGATTTGTTGGGCAATAGCTGTTTATGAAAGAGG	1100
Db	1025	GGAGAGAAAGAAAGAAAGAGGAGCTATTTGAGCTATAGAGGTTTTATGAGGAGG	1084
QY	1107	ATGGCAAGGAATGTTTGAAGGTTGGTATGATACCATCAACCAATAGACAGAGATCAG	1166
Db	1085	ATGGCAGGGCATGTGATGATGTTGGTATGTGATACCAATACCATGAGCAGGCGAGTGG	1144
QY	1167	GTATGACACAGCAAAAGATCAGCTCAAAAGCAATTTGATGGAATCACCACAGGTAA	1222
Db	1145	ATAGCTTCAGCAAAAGATCCACTCAAAAGCCAATAGATGAGTCACCAATTAAGTCAA	1204
QY	1227	TTCTGTATGAAAAGATTAACACCCCAATTTGAACTTTGGGAAAGAAATGCGTAATCT	1288
Db	1205	CTCGATCTATTAAACAAATGAAACACTCAGTTTGAAGCCGTTGGAAGGAAATTTAATPACT	1264
QY	1287	AGAGAAAAGACTGAGAACTTGAAACAAAGATGGAAGACGGGTTCTAGATGTGTGAC	1344
Db	1265	AGAAAGAGATAGAGAAATTTAAACAGAAATGGAAGCGGATTTCTTAATGTGTGGAC	1322
QY	1347	ATACAATGCTGAGCTTTTATGTTCTGATGGAATATGAGAGACACTTTCATGATTC	1406
Db	1325	TTTACAATGCTAACTTCTGTTCTCATGAAAATGAGAACTCTCGACTTCATGACTC	1388
QY	1407	TAAATGTCAAGATCTGTATGTAAGTACAGATGAGCTGAGACACATGTCAAAGACT	1466
Db	1385	AAATGTCAAGAACTTTTACGACAGAGTCCGACTACAGCTTATAGGATTAATGCCAAGAACT	1444
QY	1467	AGGAATGATGTTTTGAATTTTATACAAATGTGATGATGAAATTCATGAATAGTGTCA	1526

Accession	Sequence	Length
Db	1445 GGGTAATGGTTGTTTCGAAATTTCTATCACAAATGTATATGCAATATATGGAAGCTTAA	1504
QY	1527 AAACGGGACATATGATTTATCCCACTATGAGAGAGAGTCTAACTAAATAGAAATGAAT	1586
Db	1505 AAACGGACGATAGACTACCCGACATATTCAGAGAAACAGACATAACAGAGAGAAAT	1564
QY	1587 CAAAGGGTAAATATGACAGCATGGGGTTTATCAATCCCTGCATTATAGTACAGT	1646
Db	1565 AAGTGAATAAATTTGGAATCATGGCAATCCACCAATATGTCATTTTATTCACAGT	1624
QY	1647 AGCAGTCTCTATGTACATGGGCATATATGGCTGGGATCTCTTCCTGGGTGCTCCAA	1706
Db	1625 GGGCAGTTCCCTAGACACTGGCATAATAGTACCTGTCTATCTTTATGGATGTGCTCCA	1684
QY	1707 CGGCTCTCTGACATGCAGATCTGCATATGATTAT	1741
Db	1685 TGGATCGTTACATGCAGAAATTTGGATTTAAATTT	1719

```

RESULT 2
US-60-470-920-21
: Sequence 21, Application US/60470920
GENERAL INFORMATION:
: APPLICANT: Luke, Catherine, J.
: APPLICANT: Vialta, Adrian
: APPLICANT: Wloch, Mary K.
: APPLICANT: Evans, Thomas G.
: APPLICANT: Geall, Andrew J.
: TITLE OF INVENTION: DNA Influenza Vaccine Compositions
: FILE REFERENCE: 1530,0640000
: CURRENT APPLICATION NUMBER: US/60/470,920
: CURRENT FILING DATE: 2003-05-16
: NUMBER OF SEQ. ID NOS: 45
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 21
: LENGTH: 1714
: TYPE: DNA
: ORGANISM: Influenza A virus
: US-60-470-920-21

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Query Match	27.48;	Score 489.4;	DB 7;	Length 1714;
Best Local Similarity	56.58;	Pred. No. 1.3e-139;		
Matches 978; Conservative	0;	Mismatches 736;	Indels 17;	Gaps 3;

QY	GC AAAAGCAGGGGTTTACCATAG AAAAAACCAACCAACAAATGGCCATCTTTATCTC	66
Db	1 GCAAAAAGCAGGGGAATTAC - TTTAACTGCAAAAAATGGAACAAATATCATTAATTAAGCTA	58
QY	67 ATTCTCCTCTTCACAGCACTGAGAGGGGNCAGATATCATTTGGATVACCATGCCAATAAT	126
Db	59 CTACTGTGTGTAACACAGCAAGCAATGCAGTTAAATCTGCACTGGGCCACACAGTCAACAAAC	118
QY	127 TCACAGAGAGAGTGCACACAACTTCTAGAGCGGAACGTCACTGTGACTCATATGCCAAGAC	186
Db	119 TCCACAGAAACTGTGGACACGCTTAACAGAAACCAATGTTCTCTGTGACACATGCCAAAGAA	178
QY	187 ATTCCTTGAGAGACCCATTAAGGGAAGTTATGCAAACTAAAGGGAATCCCTCCACTTGAA	246
Db	179 TTGCTCCACACAGACATATATGGAATGCTGTGTGCACAAACCTCGGACATCCCTTCATTT	238
QY	247 CTAGGGAGACTGAGCAATTGCGGATGAGGCTCTCTGGAAATCCAAATATGTATAGCGTTCTA	306
Db	239 CTAGACACATGACATATTTAAGAGACATAGTCTATATGGCAACCTTCTTGTGACCTGCTTGG	298
QY	307 AGTGTCCAGAAACGCTCCTATATATTTGAGAGAAAGAAAACCCGAGAGACGGTTTGTGTAT	366
Db	299 GGAGGAGAGAGATGGTCTACATCGTCCGAAGATCATACAGTGTAAATGGAACGTTTAC	358
QY	367 CCAGGAGAGCTTAATGATTTATGAGAAATTTGAAACATCTCCTCAGACAGCGTGAACATTTTC	426
Db	359 CCTGGGAATGTAGAAAACCTAGAGGAACCTCGAGACACTTTTGTGTTCCGCTACTCTCTAC	418

QY	427	GAGAAAGTAAAGATCTTCCCAAAAGATGATGACACAGCATACAAACAGTGGACGTCA	486
Db	419	CAAGAAATCCAAATCTTCCAGACACAACCTGG-----AATGTACTTACA	464
QY	487	CGGCGCTGCGCGGTCTGTGGTAATTCATCATTTTTCAGGAACATGTGCTGGCTGCACAAG	546
Db	465	CTGGAAACAGACAGAGCATGTGTCA--GGTTCATTTCTACAGAGTAAATGATGTGCTGCATCA	523
QY	547	GAGGATACAGTTATTCGGTTGGCCAAAGATCTGTCAACATATACAAAGCGGAGAAACAATG	606
Db	524	AAGAGCGGTTTTTACCTGTTCCTAAGACGCCCAATATACAAATATACAGGGGAAAGCATTT	583
QY	607	CTAATTAATTTGGGGGTGTCACCATTCCTGATGATGACAGAAAGAACAATTTGACCAG	666
Db	584	CTTTTCGTGTGGGCTACATCATCCACCACCTACATATACCGAACAATTTTGTACATA	643
QY	667	AATGTGGACCTATCTTCCGTAGGACATTCACATATGAAACAAAAGSTCAACCCACAA	726
Db	644	AGAAACGACAAACATCAAGCGTGACAAACAAGATTTGAATAGACCTTCAAAACAGTG	703
QY	727	ATAGCAACAAAGCCCTTAAGTAATGAGCAAGAGGTAAATGAAATCTCTTGGACCTTC	786
Db	704	ATAGGGCCAAAGCCCTTGTCTCATGTCTGCAAGSAAACATTTGATTTATTGTGGSTA	763
QY	787	TTGGATATGTGGACATCCATAAATTTTGAAGTACTGTTAATCTAATTTGCACAGATAT	846
Db	764	CTAAAAACCGGCCCAATCATTCGAGTAGATTCACATGGAATCTAATGTCTCCATGTAT	823
QY	847	GGATTCAAATATATGTAAGTAAGATAGTTCAGAGATCATGAATAACGAAGAACACTTGAG	906
Db	824	GGACACGTTCTTTCAGAGAGGACCATGAAAGAAATCTGAAGACATGATTTTAAAGTGCT	883
QY	907	AACGTGTAGACCAATATCCCAACTCTCTTTGGAGCAATTAATACAACTTATCTTTTCAC	966
Db	884	AATGTGTAGTGAATGTCTACAGATCGAAAGAGTGCTTAAACAGTACATGTGCATTTCCAC	943
QY	967	AATGTCCCAACATGACATATAGTGTAGTGGCCCCCAATATGTAAAAATCGSAGAAATGGTC	1022
Db	944	AATATCATTAATATGTCTATTTTGAACCTGGCCCCCAATATGTAAAGTTAATAGTTCAAA	1003
QY	1027	TTAGCAACAGACTAATATGATATGTTCCCCAGATTGATATCAAGAGATTTTGGGGCATA	1086
Db	1004	CTGGCAGTCGGTCTGAGSAGACGTGGCTGTATGATCAATACAGAGACTTTTGGAGCCATA	1065
QY	1087	GCTGCTTTTATAGAAGAGAGATGGCAGAAATGTTGACGGTGTGTATGATACCATCAC	1148
Db	1064	GCTGATTCATAGAAGAGAGGTGGCCAGAGCTAGCTGCTGTATGTAGTTCACAGAT	1123
QY	1147	AGCAATGACCGAGGATTAGGGTATGACACAGACAAGAAATCATCTCAAAAGGCAATTTGAT	1206
Db	1124	TCAATATGATCAAGGGTTGTGTATGGCTGTACATATAGGATTTAATCTCAAAAGGCAATTTAT	1185
QY	1207	GGAAATCAACAAGATTAATTTCTGTGATTGAAGAAATAAACACCCCAATTTGAAGCTGT	1266
Db	1184	AAAATTAATCATCAAGCTGAATTAATTAATAGTCCAAAGATGAACAAGCAATATGAATAATTT	1243
QY	1267	GGGAAGAATCCGTAATCTTATGAGAAAAGATGTGAGAACTTGAAACAAABAATGTGAGAC	1328
Db	1244	GATATGATATTCAGTGGTTGTAACCTAGCTCAATATGATCAATTAATTAATTAATTTGATGAC	1303
QY	1327	GGGTTTTCAGATGTGTATGACATTAACATGCTAGCTTTAGTTAGTTCGATGGAAATGAGAGG	1386
Db	1304	CAATATACAAGCGTATATGGCATATATATGACAAATTTGTAATGACTTGAATAATCAAAAA	1365
QY	1387	ACACTTGAATCTTATGTTCTTAATGTCAAGATCTGTATAGTAAAGTCAAGATGCAGCTG	1448
Db	1364	ACACTCGATGAGCATGATGCGCAAGCTGAACAATCTAATTAATCAAGGTGAAAGGGCACTG	1423
QY	1447	AGAGACACATCAAGAACTATGAGAAATGATTTTGAATTTTATCACAAAATGATGATAT	1506
Db	1424	GGCTCCAAATGCTATAGTAAGATGGGAAGGCTGTTCCAGCTATACCAATTAATTTGTATGAT	1483
QY	1507	GAAATGATGAATAGTGTCAAAAAACGGGACATATGATTTATCCCAAGTATGAAGAAGACTCT	1566

Db 1484 CAGTGCATGGAAACAATTCCGACACGGGACCCTATATATAGAGAAAGTATAGAGAGCAATCA 1543

Qy 1567 AAATTAATATAGAAATGAATCAATCAAGGGTAAATTTAGACAGCATGGGGGTTTATCAATC 1626

Db 1544 AGACTAGAAAGGCGAAGAAATAGAGGGGGTTTAACTGGATCTGAGGGCACTACAAAATC 1603

Qy 1627 CTTCGCATTTATGCTACAGTAGAGGTTTCTATGTCACGTGGCAATCATGATGGCGGATC 1686

Db 1604 CTCACCATTTTATGACCTGTGCGCTCATCTCTTGTGCTTGGATGGAATGGGGTTTGCTGCTTC 1663

Qy 1687 TCTTCTGGGTGTGCTCCAACGGGCTCTGTCAGTGCAGAGATTCGATATGTA 1737

Db 1664 CTGTTCTGGGCATGTCCATGATCTTTCCAGATGCAACATTTTATATATAA 1714

```

RESULT 3
US-60-470-920-17
: Sequence 17, Application US/60470920
: GENERAL INFORMATION:
: APPLICANT: Luke, Catherine, J.
: APPLICANT: Vialta, Adrian
: APPLICANT: Wlooch, Mary K.
: APPLICANT: Evans, Thomas G.
: APPLICANT: Geall, Andrew J.
: TITLE OF INVENTION: DNA Influenza Vaccine Compositions
: FILE REFERENCE: 1530.0640000
: CURRENT APPLICATION NUMBER: US/60/470,920
: CURRENT FILING DATE: 2003-05-16
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO: 17
: LENGTH: 1220
: TYPE: DNA
: ORGANISM: Influenza A virus
US-60-470-920-17

```

Query Match	26.2%	Score 467.4	DB 7	Length 1220
Best Local Similarity	62.8%	Pred. NC. 6e-133		
Matches 745, Conservative	0	Mismatches 436	Indels 6	Gaps 1

QY	76	TTTCACAGCAGTGAAGGAGACCAATATGCTTGTGGATACCAATGCCAATTAATTCACAG	135
Dp	34	TTTCAGGTAAATAATGCAGACACAAATATGTTAGGTACCATGGGAATTAOTCAACGCAC	93
QY	136	AAGTCGACACAAATTCATAGAGCGGACGTCACCTGTACCTATGCGCAAGACATCTTGAG	195
Dp	94	ACTGTTGACACAGTACTCGAAAAGATGTACCCGTGACACACTCTGTTAACTCTCTCGAA	153
QY	196	AAGGCCATTAAGGAAAGTTATGCAACTAAGGAAATCCCTCCTACTTGAACATGAGGGAC	255
Dp	154	GACAGCCACAACGGABAACTATGTTAAATTAAGAAAGATAGCCCATTAACAATTTGGGAAA	213
QY	256	TGTAGCAATTTGCCGATGGCTCTTTGGAATTCAAAAATGTGATAGCTTCTTAAGTGTCCA	315
Dp	214	TGTAAATATGCGCGATGGCTCTTGGGAAACCGGAATTCGATTTACTGCTCACAGCAGAC	273
QY	316	GAACGGTCTTATATTTGGAGAAAGAAACCCGAGAGACGGTTTGTATTCCAGCGACG	375
Dp	274	TCATGGTCTTATATTTAGTAAACATCCAGATCAAGATGGAAATCTATCCACGGAGAT	333
QY	376	TTCAATGATTAATGAAGATGAACATCTCTCTCGACGGCGTGAACAACTTTCGACAAAGTA	435
Dp	334	TTTCACTCACTATGAGAACTGAGGGACAAATTGACGTCAAGTGTATCTGTTGAAAAATTC	393
QY	436	AAGATTTGCCCAAGAATGATGG-----ACACAGCATCAACAACTGAGAGTTTCACGG	489
Dp	394	GAATATTTTCCAGACAGACGCTCGTGGCCCAATCATGAACAACCAAGGTGTAACGGCA	453
QY	490	GCCTCGCCGGTGTGTGTAATCCATCTTTTTCAGGAACATGGTCTGGCTGACAAAGAA	549
Dp	454	GCATGGTCTATATGGGGAGCAAGCATGTTTATTCAGAAATTTGGCTGTGCTGACAAACAG	513

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QY 550 GGATCAGATTATCCGGTTGCCAAGAGATCCGACAAATACACGCGGAGAAATGCTA 609
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 514 GGAAGCTCATACCAAAAGCTTACGAGAGCTCTATGTAACATTAAGGGAAAGTCCCTT 573
QY 610 ATAAATTTGGGGGTGCACCATCCATTGATGAGACAGAAACAAATCTGTACAGAAAT 669
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 574 GTACTATGGGGTGTTCATCATCCCGCTACCGGTCTGTATCAACAGAGCTCTATCAGAAAT 633
QY 670 GTGGAAACCTATGTTTCCGTAAGCAGATCAACATTTGAACAAAGGTCACCCGAAATA 729
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 634 GCAGATGCTTATGCTCTGTAGAGGTCAATAAATATTAACAGAGATTCACCCGAAATA 693
QY 730 GCACAAAGGCTTAAGTAATGAGCAAGAGGTGATGATGATCTCTGTGACCTCTTG 789
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 694 GCAGCGAGACCAAGTAAGAGGTCAAGCTGGAGATGAATCTTACTGGACATTTACTA 753
QY 790 GATATGTGGACACCATAAATTTTGAGAGTACTGATTAATTTGACACAGATATGGA 849
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 754 GAACCCGGAGACCAATTAACATTTGAGGCAACTGGAATCTAATAGCACCATGCTATGCT 813
QY 850 TTCAAAATATCGAAAAGAGTACTTCAGGATCATGAAAACAGAGAACACTTGAGAAC 909
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 814 TTGCACTGANTAGAGTCTGTGATCGGTATCATCTTCAGACGACAGTGCATGAT 873
QY 910 TGTGAGACCAAAATGCCAAATCTCTTGGAGCAATTAATTAACATTAACCTTTTCAAT 969
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 874 TGTAAACAGAGTGTCAAAACCCCATGCTGTATTAACAGCACTCTCCCTTCCAAAT 933
QY 970 GTCCACCCACTGCAATAGTGTAGTGCAGGCCCAATATGTAATAATCGAAGATGCTTTA 1029
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 934 ATACATCCAGTCAATAGAGAGTGCACCAAAATACGTCAAGATACCAATTTGAGATG 993
QY 1030 GCAACGAGCAATAGATGTTCCCGAGATGATCAAGAGATTTGTTGGGCAATGCT 1089
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 994 GCTACGAGCAATGAAGAAATCTTCAATTCATTAATCAAGGGGTATTTTGGAGCATGCC 1053
QY 1090 GGTTTTATAGAAAGAGATGCGCAAGATGTTGAGGTGATGATACCATGACAGC 1149
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1054 GGTTTTATGAGGGGATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1113
QY 1150 AATGACGAGGATGAGGATGATGAGCAGACAAAGAAATCCACTCAAAAAGCATTTGATGA 1209
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1114 AATGAACAGGATGAGGATGATGAGCAGATCAAAAAAGCACAATAATGCCATTTGACGGG 1173
QY 1210 ATACCAACAGATTAATCTGTGATTAAGATTAACACCAATTT 1256
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1174 ATTAACAAACAGATTAATCTGTGATTAAGATTAACACCAATTT 1220

```

RESULT 4  
PCT-US03-12728-94  
Sequence 94, Application PC/TUS0312728

```

GENERAL INFORMATION:
APPLICANT: MedImmune Vaccines, Inc.
APPLICANT: Hoffman, Erich
APPLICANT: Jin, Hong
APPLICANT: Lu, Bin
APPLICANT: Kemble, George
APPLICANT: Duke, Greg
TITLE OF INVENTION: MULTI PLASMID SYSTEM FOR THE PRODUCTION OF INFLUENZA VIRUS
FILE REFERENCE: 26-00027005/PC
CURRENT APPLICATION NUMBER: PCT/US03/12728
CURRENT FILING DATE: 2003-04-25
PRIORITY FILING DATE: 2003-04-25
PRIORITY FILING DATE: 26-04-2002
PRIORITY FILING DATE: 60/394,983
PRIORITY FILING DATE: 09-07-2002
PRIORITY FILING DATE: 60/410,576
PRIORITY FILING DATE: 12-09-2002
PRIORITY FILING DATE: 60/419,802
PRIORITY FILING DATE: 18-10-2002
PRIORITY FILING DATE: 60/420,708
PRIORITY FILING DATE: 23-10-2002

```

```

PRIOR APPLICATION NUMBER: 60/457,699
PRIOR FILING DATE: 24-03-2003
PRIOR APPLICATION NUMBER: 60/462,361
PRIOR FILING DATE: 10-04-2003
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn version 3.1
SEQ ID NO 94
LENGTH: 1884
TYPE: DNA
ORGANISM: Influenza B virus
PCT-US03-12728-94

```

```

Query Match 5.8%; Score 103.6; DB 1; Length 1884;
Best Local Similarity 51.0%; Pred. No. 2e-21;
Matches 244; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

```

```

QY 1065 AAGAGGATGTTGGGCAATAGCTGTTTATGAAGAGATGCGAAGATGCTTGA 1124
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1116 AAGGGTGTCTCGAGCTATATGCTGTTTCTTGAAGAGAGTGGAAAGATGATTCG 1175
QY 1125 CGTTGGTATGATACCATCAACAGCAATGACCGAGTACGCTATGACAGACAAAGA 1184
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1176 AGTTGGCAGGATACACATCTCATGAGACATGAGTGCAGTGGCAGACCTTAA 1235
QY 1185 ATCCACTCAAAAGCATTTGATGATGATCAACCAAGTAATTTGTGATTAAGAAAT 1244
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1236 GAGTACCAAGAGCTTAACAAAGATTAACAAATAATCTCAATTTTAAAGTACCTAGA 1295
QY 1245 AACACCCCAATTTGAAGCTGTTGGAAAGATTTGCTTAATTAAGAAAGATGAGAGA 1304
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1296 AGTAAGAAATCTTCAAGACTTAAGCGGTGCAATGATGATCAACAAAGATGCTGGA 1355
QY 1305 CTGGAACAAAGATGAGAACCGGTTTCTAGATGTTGAGACATACATGATGACCTTTT 1364
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1356 GCTGATGAGAAAGTGGATGATCTCAAGCTGATTAACATTAAGCTCCCAATAGACTTGC 1415
QY 1365 AGTTGATGAAATGAGAGGACACTTGTCTTCAATTTCAATGATCAAGATCTGTA 1424
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1416 AGTCTGCTTCTTCAACAGAGATTAATTAACAGTGAAGTGAAGTCTTGTGCACTTGA 1475
QY 1425 TAGTAAGTCAGATGACGCTGAGACAAACGTCAAAGTAAGTAAGTAAGTGTGTA 1484
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1476 AAGAAACAGTAAGAAATGCTGGGCCCTCTGCTGTAGACATAGGAAGTGTGCTGA 1535
QY 1485 ATTTTATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1542
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1536 AACCAACAAATGCAACACAGACTTGCCTAGACAGAGATGATGCTGCTGACCTTAAT 1593

```

RESULT 5  
US-60-487-610-19458

```

GENERAL INFORMATION:
APPLICANT: CARGILL, Michelle
APPLICANT: HUANG, Hongjin
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19458
LENGTH: 124326
TYPE: DNA
ORGANISM: Homo sapiens
US-60-487-610-19458

```

```

Query Match 2.8%; Score 49.2; DB 7; Length 124326;
Best Local Similarity 55.6%; Pred. No. 0.00058;
Matches 90; Conservative 2; Mismatches 70; Indels 0; Gaps 0;

```

[illegible]

```

RESULT 6
US-60-487-610-42952
: Sequence 42952. Application US/60487610
: GENERAL INFORMATION:
: APPLICANT: CARGILE, Michels
: APPLICANT: HUANG, Hongjin
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: LAYER FIBROSIS IN HEPATITIS C VIRUS-
: TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C1001469
: CURRENT APPLICATION NUMBER: US/60/487,610
: CURRENT FILING DATE: 2003-07-17
: NUMBER OF SEQ ID NOS: 97101
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 42952
: LENGTH: 201
: TYPE: DNA
: ORGANISM: Homo sapiens
US-60-487-610-42952

```

[illegible]

```

RESULT 7
US-60-487-610-42953
: Sequence 42953, Application US/60487610
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: HUANG, Hongji
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-
: TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL001469
: CURRENT APPLICATION NUMBER: US/60/487,610
: CURRENT FILING DATE: 2003-07-17
: NUMBER OF SEQ ID NOS: 97141
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 42953
: LENGTH: 201
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-60-487-610-42953

```

Query Match	2.7%	Score 48.4	DB 7	Length 201
Best Local Similarity	56.2%	Pred. No. 6.3e-05		
Matches 91	Conservative 0	Mismatches 71	Indels 0	Gaps 0

OY    1A94    AAGATGATCATGAATGCATGAMTAGHGTAAAGAGGGACATATGATTATCCCAAGTA    1553

Dd    31    CACTTGTGATCAGAGTTCCAGACCACCCTTGCGCAACATGTTAAACCTCATCTATATA    90

OY    1554    TGAGAAGAGAGCTCTAACTAAATAGAAATGAAATCAAAGGGGTAAATTTGAGCAGCATGG    1613

Dd    91    AAAAAAAAAAAAAAATAATTAATAATTAATAATTAATAAAAAAATTAATAAAAAAGCTTGGCATGGT    150

OY    1614    GGTTCATCAAATCCCTGCCATTTATGCTACAGTACAGGTTTC    1655

Dd    151    GGCACTGTGCTACTCCAGGCACTCCAGAGAGCGTGGAGGCAAGATC    192

```

RESULT 8
US-60-487-610-42923
: Sequence 42923: Application US/60487610
:
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: HUANG, Hongjin
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: LAYER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS
: TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CU001469
: CURRENT APPLICATION NUMBER: US/60/487,610
: CURRENT FILING DATE: 2003-07-17
: NUMBER OF SEQ ID NOS: 97101
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 42923
: LENGTH: 201
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
US-60-487-610-42923

```

[illegible]

```

RESULT 9
US-09-947-914-42
: Sequence 42, Application US/09947914
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig
: TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPS) LOCATED ON
: TITLE OF INVENTION: 21, METHODS OF DETECTION, AND USES THEREOF
: FILE REFERENCE: C0001298
: CURRENT APPLICATION NUMBER: US/09/947,914
: CURRENT FILING DATE: 2001-09-07
: NUMBER OF SEQ ID NOS: 75
: SEQ ID NO 42
: LENGTH: 1946141
: TYPE: DNA
: ORGANISM: HUMAN
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(1946141)
: OTHER INFORMATION: n = A,T,C or G
: US-09-947-914-42

```

Query Match 2.5%; Score 45.2; DB 5; Length 1946141;





```

; LENGTH: 3423
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (53)..(2800)
US-10-105-837-126

```

Query Match	2.88;	Score 41.8;	DB 6;	Length 3423;
Best Local Similarity	48.28;	Pred. No. 0.023;		
Matches 118; Conservative	0;	Mismatches 127;	Indels	0

QY	1191	TCAAAAGGCAATTTGA	TGGAAATCACCAACAAGTAAATTTCTGTGATTGAAAGATTAACAC	1250
Db	1246	TCTGAAATAATTTACA	AGAAAAGTCCTTGAGSATTTGAAGCCCTTTTGTAGTGAGATAGAAATC	1305
QY	1251	CCAATTGTGAAGCTCT	TGGAAAGAATTGGTAACTTAGAGAGAAAAGACTGGAGAATTTGAA	1310
Db	1306	CTTTTAAATACCAT	TGAGGAAAACCTGTAGTAAAAAGGAGAAAAGGCTAGAGAAACAGNA	1365
QY	1311	CAAAAAGATGTGAACA	TGGGTTTCTAGAGTGTGTGACATACACAAAGCTGAGCTTTAGTTCT	1370
Db	1366	TGAGGAATATGTGAA	TAAGCTTTTAGCACACTATGATGAGACAAAGCCAGACCTTTGAGGA	1425
QY	1371	GATGAAAATGAGAG	TACACTTGACTTTCATGTGATTTCAATGTCAAGAATCTGTATTAGAA	1430
Db	1426	AGTGAAAGAGAGAA	TATGAGATCTTCGATGACGACAGATGGTCCACTTTCTGCAGAGCAT	1485
QY	1431	AGTCA 1435		
Db	1486	GGACA 1490		

RESULT 13	
US-10-286-897-452	
Sequence 452, Application US/10268697	
GENERAL INFORMATION	
APPLICANT: Hysq Inc	Nucleic Acid and Polypeptides
TITLE OF INVENTION: Novel	
FILE REFERENCE: 784FLPCT	
CURRENT APPLICATION NUMBER: US/10/286,897	
CURRENT FILING DATE: 2002-11-01	
Prior APPLICATION NUMBER: US/09/488,725	
Prior FILING DATE: 2000-01-21	
Prior APPLICATION NUMBER: US/09/552,317	
Prior FILING DATE: 2000-04-25	
Prior APPLICATION NUMBER: US/09/598,042	
Prior FILING DATE: 2000-06-20	
Prior APPLICATION NUMBER: US/09/620,312	
Prior FILING DATE: 2000-07-19	
Prior APPLICATION NUMBER: US/09/653,450	
Prior FILING DATE: 2000-08-31	
Prior APPLICATION NUMBER: US/09/662,191	
Prior FILING DATE: 2000-09-14	
Prior APPLICATION NUMBER: US/09/693,036	
Prior FILING DATE: 2000-10-19	
Prior APPLICATION NUMBER: US/09/727,344	
Prior FILING DATE: 2000-11-29	
NUMBER OF SEQ ID NOS: 7143	
SOFTWARE: pc_fl_genes_b Versions 1.0	
SEQ ID NO 452	
LENGTH: 3423	
TYPE: DNA	
ORGANISM: Homo sapiens	
FEATURE:	
NAME/KEY: CDS	
LOCATION: (53) ..(2800)	
US-10-286-897-452	

Query Match	2.3%	Score	41.8	DB	6	Length	3423
Best Local Similarity	48.2%	Pred. NO.	0.023				
Matches 118; Conservative	0	Mismatches	127	Indels	0	Gaps	0

OY	1191	TCAAAGCATTGTGTAATCACCAACAGCTAAATTCGTGATTTGGAAAAAATAAACAC	1250
Dd	1246	TCTGAATAATTACACAAAAGTCCCTTGAGATTGAACCCTTTGTTAGTGAGATAGAATC	1305
OY	1251	CCAATTTGAACCTGTGGGAAAAGATTCCGTAACCTAGAGAAAAGACTGGAGAATTGAA	1310
Dd	1306	CTTTTTTAATCCATTGAGGAAAACCTGATGATAAAATGACNAAGGCTAGAGAACAAGAA	1365
OY	1311	CAAAAAGTGAAGACGGGCTTTCATGATGTGTGACATACAAATCGTACGTTTAGTTCCT	1370
Dd	1366	TGAGGAATGTGAGAAAGCTTTTACGCACACTATGATGACAAACCCAGACCTTTGAGCA	1425
OY	1371	GATGAAATATGAGAGACACTTGAACCTTCATGATTCATATGTCAAAGATCTGTATTAA	1430
Dd	1426	AGTGAGAGAAGAAAGATGAGATCTTCGCATAGACAGATGCTCCACTTTCTGCAGACAT	1485
OY	1431	AGTCA 1435	
Dd	1486	GGACA 1490	

```

RESULT 14
US-10-286-897-1473
: Sequence 1473: Application US/10286897
: GENERAL INFORMATION:
: APPLICANT: Hysq Inc
: TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
: FILE REFERENCE: 784F1PCT
: CURRENT APPLICATION NUMBER: US/10/286,897
: CURRENT FILING DATE: 2002-11-01
: PRIOR APPLICATION NUMBER: US/09/488,725
: PRIOR FILING DATE: 2000-01-21
: PRIOR APPLICATION NUMBER: US/09/552,317
: PRIOR FILING DATE: 2000-04-25
: PRIOR APPLICATION NUMBER: US/09/598,042
: PRIOR FILING DATE: 2000-06-20
: PRIOR APPLICATION NUMBER: US/09/620,312
: PRIOR FILING DATE: 2000-07-19
: PRIOR APPLICATION NUMBER: US/09/653,450
: PRIOR FILING DATE: 2000-08-31
: PRIOR APPLICATION NUMBER: US/09/662,191
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: US/09/693,036
: PRIOR FILING DATE: 2000-10-19
: PRIOR APPLICATION NUMBER: US/09/727,344
: PRIOR FILING DATE: 2000-11-29
: NUMBER OF SEQ ID NOS: 7143
: SOFTWARE: pt_FL-genes_b Versions 1.0
: SEQ ID NO 1473
: LENGTH: 11116
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (4532)..(11116)
: US-10-286-897-1473

```

Query Match	2.3%	Score 41.8	DB 6	Length 1116
Best Local Similarity	48.2%	Pred. No. 0.038		
Matches 118, Conservative	0	Mismatches 127	Indels 0	Gaps 0

Oy	1191	TCAAAGGCAATTTGATGGATTCACCAACAGAGTAAATTCGTGATTTGAAAAGATTAACAC	1250
Db	10060	TCTGAAATAATTACCAAGAAAGTCCTTGAGAGATTGAAGCCCTTTGTAGTAGAGATACAAATC	10111
Oy	1251	CCAAATTTGAGCTGTGGGAAACAAATTCGGTAACTTAGAAGAAAGACTGGAGAACTTTGAA	1310
Db	10120	CTTTTAAATATACCTTAGGAGAAACCTGTATATTAATATGACAAAAGGCTAACAGACACGAA	10177
Oy	1311	CAAAAGATGAGAACACGCGTTCTAGATGTGTGGACATACAAATGCTGCAGCTTTTAACTTCT	1370
Db	10180	TGAGAGAAATGATGAAGAAGCTTTTATAGACAGTATGATGAGAAAAGCCACAGCTTTTAGGA	10238



GenCore version 5.1.6  
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OM nucleic - nucleic search: using sw model

Run on: August 10, 2003, 02:11:24 ; Search time 3938.27 Seconds  
(without alignments)  
14835.212 Million cell updates/sec

Title: US-09-918-568-46  
Perfect score: 1783  
Sequence: 1 CGCGTAGCAAAAGCAGGCGT.....ACCCCTGTTCTGCTACGCCG 1783

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , (apext 1.0

Searched: 32997241 seqs, 16383922548 residues

Total number of hits satisfying chosen parameters: 65994482

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Pending\_Patents\_NA\_Main: \*  
1: /cgn2\_6/p/oddata/2/pna/PCRNUS.COMB.seq: \*  
2: /cgn2\_6/p/oddata/2/pna/PCRNUS.COMB.seq: \*  
3: /cgn2\_6/p/oddata/2/pna/US05.COMB.seq: \*  
4: /cgn2\_6/p/oddata/2/pna/US07.COMB.seq: \*  
5: /cgn2\_6/p/oddata/2/pna/US080.COMB.seq: \*  
6: /cgn2\_6/p/oddata/2/pna/US081.COMB.seq: \*  
7: /cgn2\_6/p/oddata/2/pna/US082.COMB.seq: \*  
8: /cgn2\_6/p/oddata/2/pna/US083.COMB.seq: \*  
9: /cgn2\_6/p/oddata/2/pna/US084.COMB.seq: \*  
10: /cgn2\_6/p/oddata/2/pna/US085.COMB.seq: \*  
11: /cgn2\_6/p/oddata/2/pna/US086.COMB.seq: \*  
12: /cgn2\_6/p/oddata/2/pna/US087.COMB.seq: \*  
13: /cgn2\_6/p/oddata/2/pna/US088.COMB.seq: \*  
14: /cgn2\_6/p/oddata/2/pna/US089.COMB.seq: \*  
15: /cgn2\_6/p/oddata/2/pna/US090.COMB.seq: \*  
16: /cgn2\_6/p/oddata/2/pna/US091.COMB.seq: \*  
17: /cgn2\_6/p/oddata/2/pna/US092A.COMB.seq: \*  
18: /cgn2\_6/p/oddata/2/pna/US092B.COMB.seq: \*  
19: /cgn2\_6/p/oddata/2/pna/US093A.COMB.seq: \*  
20: /cgn2\_6/p/oddata/2/pna/US093B.COMB.seq: \*  
21: /cgn2\_6/p/oddata/2/pna/US094.COMB.seq: \*  
22: /cgn2\_6/p/oddata/2/pna/US095A.COMB.seq: \*  
23: /cgn2\_6/p/oddata/2/pna/US095B.COMB.seq: \*  
24: /cgn2\_6/p/oddata/2/pna/US095C.COMB.seq: \*  
25: /cgn2\_6/p/oddata/2/pna/US095D.COMB.seq: \*  
26: /cgn2\_6/p/oddata/2/pna/US096A.COMB.seq: \*  
27: /cgn2\_6/p/oddata/2/pna/US096B.COMB.seq: \*  
28: /cgn2\_6/p/oddata/2/pna/US096C.COMB.seq: \*  
29: /cgn2\_6/p/oddata/2/pna/US096D.COMB.seq: \*  
30: /cgn2\_6/p/oddata/2/pna/US096E.COMB.seq: \*  
31: /cgn2\_6/p/oddata/2/pna/US097A.COMB.seq: \*  
32: /cgn2\_6/p/oddata/2/pna/US097B.COMB.seq: \*  
33: /cgn2\_6/p/oddata/2/pna/US097C.COMB.seq: \*  
34: /cgn2\_6/p/oddata/2/pna/US098A.COMB.seq: \*  
35: /cgn2\_6/p/oddata/2/pna/US098B.COMB.seq: \*  
36: /cgn2\_6/p/oddata/2/pna/US098C.COMB.seq: \*  
37: /cgn2\_6/p/oddata/2/pna/US098D.COMB.seq: \*  
38: /cgn2\_6/p/oddata/2/pna/US099A.COMB.seq: \*  
39: /cgn2\_6/p/oddata/2/pna/US099B.COMB.seq: \*  
40: /cgn2\_6/p/oddata/2/pna/US099C.COMB.seq: \*  
41: /cgn2\_6/p/oddata/2/pna/US099D.COMB.seq: \*  
42: /cgn2\_6/p/oddata/2/pna/US099E.COMB.seq: \*  
43: /cgn2\_6/p/oddata/2/pna/US099F.COMB.seq: \*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1783	100.0	1783	9	US-08-443-862-46
2	1783	100.0	1783	38	US-09-918-568-46
3	1723.4	96.7	1773	10	US-08-573-569-17
4	1718.6	96.4	1773	10	US-08-573-569-35

Sequence 46, Appl  
Sequence 46, Appl  
Sequence 17, Appl  
Sequence 35, Appl

```

5 1606.4 90.1 1728 9 US-08-443-862-28
6 1606.4 90.1 1728 38 US-09-918-568-28
7 908.8 51.0 1135 9 US-08-443-862-49
8 908.8 51.0 1135 38 US-09-918-568-49
9 732.4 41.1 1733 1 PCT-US03-09287-13
10 732.4 41.1 1733 2 PCT-US03-09287-13
11 732.4 41.1 1733 51 US-10-397-635-13
12 728.2 40.8 1738 4 US-07-773-597-14
13 714 40.0 1698 15 US-09-040-944-1
14 714 40.0 1698 15 US-09-045-042-1
15 703.4 39.5 1770 5 US-08-063-818-1
16 695.6 39.0 1754 9 US-08-443-862-27
17 695.6 39.0 1754 38 US-09-918-568-27
18 463.2 26.0 1757 51 US-10-381-085-12
19 460 25.8 1753 51 US-10-381-085-9
20 460 25.8 1753 51 US-10-381-085-11
21 453.8 25.5 1697 51 US-10-381-085-10
22 400 22.4 400 9 US-08-443-862-33
23 400 22.4 400 38 US-09-918-568-33
24 397 22.3 409 9 US-08-443-862-34
25 397 22.3 409 38 US-09-918-568-34
26 382.4 21.4 410 9 US-08-443-862-35
27 382.4 21.4 410 38 US-09-918-568-35
28 379.6 21.3 394 9 US-08-443-862-36
29 379.6 21.3 394 38 US-09-918-568-36
30 373 20.9 924 4 US-07-751-896-1
31 373 20.9 924 4 US-07-837-773-15
32 373 20.9 924 8 US-07-837-773-15
33 372.6 20.9 810 4 US-07-751-896-5
34 372.6 20.9 810 4 US-07-837-773-19
35 372.6 20.9 810 8 US-08-391-315-19
36 368.2 20.7 670 4 US-07-837-773-5
37 368.2 20.7 670 8 US-08-391-315-5
38 361.4 20.3 912 4 US-07-751-896-17
39 361.4 20.3 912 8 US-07-837-773-31
40 361.4 20.3 912 4 US-08-391-315-31
41 318.6 17.9 1777 9 US-08-443-862-54
42 318.6 17.9 1777 38 US-09-918-568-54
43 312.8 17.5 2005 38 US-09-914-658B-3
44 312.8 17.5 4930 38 US-09-914-658B-1
45 312.4 17.5 4610 38 US-09-914-658B-6

```

## ALIGNMENTS

```

Sequence 28, Appl
Sequence 28, Appl
Sequence 49, Appl
Sequence 49, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 14, Appl
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Sequence 27, Appl
Sequence 27, Appl
Sequence 12, Appl
Sequence 9, Appl
Sequence 11, Appl
Sequence 10, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 1, Appl
Sequence 6, Appl

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RESULT 1
US-08-443-862-46
; Sequence 46, Application US/08443862
; GENERAL INFORMATION:
; APPLICANT: Yoshinobu OKUNO et al.
; TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,862
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,781
; FILING DATE: April 19, 1994
; APPLICATION NUMBER: 08/054,016

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; FILING DATE: April 29, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: A/Okuda/57
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL LINE:
; ORGANELLER:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-443-862-46

Query Match 100.0%; Score 1783; DB 9; Length 1783;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCTAGCAAAAGCAGGGGTTATACCATAGAAAACCAAAACCAATGCGCATATT 60
DB 1 CGGCTAGCAAAAGCAGGGGTTATACCATAGAAAACCAAAACCAATGCGCATATT 60
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QY 61 TATTCATTTCTCTTTCACAGAGTGAGAGGACCAAGATGATGATGATGATGATG 120
DB 61 TATTCATTTCTCTTTCACAGAGTGAGAGGACCAAGATGATGATGATGATGATG 120
QY 121 AATAATTCACAGAGAGGTCGACACCAATTCAGAGGGAACGTCACGTGACTCATGCC 180
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QY 121 AATAATTCACAGAGAGGTCGACACCAATTCAGAGGGAACGTCACGTGACTCATGCC 180
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DB 301 CTTGATAGGATGCAATGAGGATTCGGGATGCTCTTGGAAATCCAAATGATAGG 360  
OY 361 TGTATCCAGGACGAGGATTCGGGATGCTCTTGGAAATCCAAATGATAGG 420  
DB 361 TGTATCCAGGACGAGGATTCGGGATGCTCTTGGAAATCCAAATGATAGG 420  
OY 421 CATTGAGGAAGTAAAGATTCGGGATGCTCTTGGAAATCCAAATGATAGG 480  
DB 421 CATTGAGGAAGTAAAGATTCGGGATGCTCTTGGAAATCCAAATGATAGG 480  
OY 481 GGTTCAGGGGCTGCGGAGTTCGGGATGCTCTTGGAAATCCAAATGATAGG 540  
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OY 541 ACAAGGAGGATCAATATTCGGGATGCTCTTGGAAATCCAAATGATAGG 600  
DB 541 ACAAGGAGGATCAATATTCGGGATGCTCTTGGAAATCCAAATGATAGG 600  
OY 601 CAAATGCTAATATTCGGGATGCTCTTGGAAATCCAAATGATAGG 660  
DB 601 CAAATGCTAATATTCGGGATGCTCTTGGAAATCCAAATGATAGG 660  
OY 661 TACCAAGATGAGGACCTATGTTCCGATGAGGACATCAATGAAACAAAGGTCACAC 720  
DB 661 TACCAAGATGAGGACCTATGTTCCGATGAGGACATCAATGAAACAAAGGTCACAC 720  
OY 721 CCAGAAATAGGACAGGCTTAAAGTATGAGGATGAGGATGAGGATGAGGATGAGG 780  
DB 721 CCAGAAATAGGACAGGCTTAAAGTATGAGGATGAGGATGAGGATGAGGATGAGG 780  
OY 781 ACCCTCTGATATGAGGACCATTAATTTGAGAGTATGATGATGATGATGATGATG 840  
DB 781 ACCCTCTGATATGAGGACCATTAATTTGAGAGTATGATGATGATGATGATGATG 840  
OY 841 GAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900  
DB 841 GAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900  
OY 901 CTTGAGAACTGTGAG/CCAATGCGCAACTCTTGGGAGGATGATGATGATGATGATG 960  
DB 901 CTTGAGAACTGTGAG/CCAATGCGCAACTCTTGGGAGGATGATGATGATGATGATG 960  
OY 961 TTTGACAAATGTCAC/CACTGACAAATGATGATGATGATGATGATGATGATGATG 1020  
DB 961 TTTGACAAATGTCAC/CACTGACAAATGATGATGATGATGATGATGATGATGATG 1020  
OY 1021 TTTGCTTTAGCAACAGGACTAAGGATGTTCCAGATGATGATGATGATGATGATG 1080  
DB 1021 TTTGCTTTAGCAACAGGACTAAGGATGTTCCAGATGATGATGATGATGATGATG 1080  
OY 1081 GCAATAGCTGTTTATGAAAGGAGGATGCGCAAGGATGTTGAGGATGATGATGATG 1140  
DB 1081 GCAATAGCTGTTTATGAAAGGAGGATGCGCAAGGATGTTGAGGATGATGATGATG 1140  
OY 1141 CATCAGAGCAATGAC/AGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 1200  
DB 1141 CATCAGAGCAATGAC/AGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 1200  
OY 1201 TTTGATGAAATCACCACCAAGGATGATGATGATGATGATGATGATGATGATGATG 1260  
DB 1201 TTTGATGAAATCACCACCAAGGATGATGATGATGATGATGATGATGATGATGATG 1260  
OY 1261 GCTGTGGGAAAGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320  
DB 1261 GCTGTGGGAAAGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320

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OY 1381 GAGAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440  
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OY 1561 GAGTCTAAATAGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 1620  
DB 1561 GAGTCTAAATAGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 1620  
OY 1621 CAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680  
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OY 1681 GGGATCTCTTCTGGGATGCTGCAAGGATGCTGCAAGGATGCTGCAAGGATGCTGCA 1740  
DB 1681 GGGATCTCTTCTGGGATGCTGCAAGGATGCTGCAAGGATGCTGCAAGGATGCTGCA 1740  
OY 1741 TAAATGATTTATATTAATAAACAACCCCTGTTGCTGAGGCG 1783  
DB 1741 TAAATGATTTATATTAATAAACAACCCCTGTTGCTGAGGCG 1783

RESULT 2  
US-09-918-568-46  
Sequence 46, Application US/09918568  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESS: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/918, 568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004, 422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443, 862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/229, 781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054, 016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200

TELEFAX: 202-721-8250  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 46:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1783 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to genomic RNA  
 HYPOTHETICAL: <Unknown>  
 ANTI-SENSE: <Unknown>  
 FRAGMENT TYPE: <Unknown>  
 ORIGINAL SOURCE:  
 ORGANISM: A/Okuda/57  
 STRAIN: <Unknown>  
 INDIVIDUAL ISOLATE: <Unknown>  
 DEVELOPMENTAL STAGE: <Unknown>  
 HAPOTYPE: <Unknown>  
 TISSUE TYPE: <Unknown>  
 CELL TYPE: <Unknown>  
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 ORGANELLE: <Unknown>  
 IMMEDIATE SOURCE:  
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 AUTHORS:  
 TITLE:  
 JOURNAL:  
 VOLUME:  
 ISSUE:  
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 DATE:  
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 FILING DATE:  
 PUBLICATION DATE:  
 RELEVANT RESIDUES IN SEQ ID NO:  
 SEQUENCE DESCRIPTION: SEQ ID NO: 46:  
 US-09-918-568-46

Query Match 100.0%; Score 1783; DB 38; Length 1783;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGGCTAGCAAAAGCAGAGGGTTATACCATGAAAAACCAAAAGCAAAACCAATGGCCATCATTT 60  
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 361 TGTTCATCAGGACGCTTCAATGATTTATGAAGAAATTAACATCTCTCAGCAGCGTAAA 420  
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 421 CATTTCGAGAAAGTAAAGATTCTGCCAAAGATAGATGAGACAGCATCAACCACTGGA 480  
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 481 GGTTCAGGGGCTGCGCGGTCTGTCTGTAATCCATCTTTTTCAGAACATGTCTGCGTG 540  
 541 ACAAGAGAGGATCAATATATCCGCTTGCAGAAAGATCGTAGACAAATCAAGCGGAGAA 600  
 541 ACAAGAGAGGATCAATATATCCGCTTGCAGAAAGATCGTAGACAAATCAAGCGGAGAA 600  
 601 CAATGCTAATATTTGGGGGCTGCACACATCCATGATGAGACAGAACCAAGAACATTTG 660  
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Db 1441 CAGCTGAGACACACATCAAGAAGCTAGAAATGATGTTTGATTTATCACAATGT 1500  
QY 1501 GATGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560  
Db 1501 GATGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560  
QY 1561 GAGCTTAACTAAATGAAATGAATCAAGGGGTAAATTTGAGCAGCATGGGGTTTAT 1620  
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QY 1741 TAACTCATTTTAAATTAATAAAGACCCCTGTTCTGCTAGCCG 1783  
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RESULT 3  
US-08-573-569-17  
: Sequence 17, Application US/08573569  
: GENERAL INFORMATION:  
: APPLICANT: Maassab, Hunein F  
: TITLE OF INVENTION: Cold-adapted Influenza Virus  
: NUMBER OF SEQUENCES: 40  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Anna M Lewak  
: STREET: 5445 Corporate Drive  
: CITY: Troy  
: STATE: MI  
: COUNTRY: USA  
: ZIP: 48098  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: OPERATING SYSTEM: IBM PC compatible  
: SOFTWARE: Patent In Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/573,569  
: FILING DATE:  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US/08/082,846  
: FILING DATE:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Lewak, Anna M  
: REGISTRATION NUMBER: 38006  
: REFERENCE/DOCKET NUMBER: 2115-00257  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 313-641-1600  
: TELEFAX: 313-641-0270  
: INFORMATION FOR SEQ ID NO: 17:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1773 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: RNA (genomic)  
: ORIGINAL SOURCE:  
: ORGANISM: Influenza virus  
: STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 761  
: STRAIN:

IMMEDIATE SOURCE:  
: CLONE: HA  
: FEATURE:  
: NAME/KEY: mutation  
: LOCATION: replace(144, "u")  
: OTHER INFORMATION: /gene= "HA"  
: OTHER INFORMATION: /note= "u in ca "master" strain; a in w2(3)"  
: OTHER INFORMATION: /citation= (11)  
: FEATURE:  
: NAME/KEY: mutation  
: LOCATION: replace(455, "a")  
: OTHER INFORMATION: /gene= "HA"  
: OTHER INFORMATION: /note= "a in ca "master" strain; g in w2(3)"  
: OTHER INFORMATION: /citation= (11)  
: FEATURE:  
: NAME/KEY: mutation  
: LOCATION: replace(729, "c")  
: OTHER INFORMATION: /gene= "HA"  
: OTHER INFORMATION: /note= "c in ca "master" strain; a in w2(3)"  
: OTHER INFORMATION: /citation= (11)  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: 44..1729  
: OTHER INFORMATION: /product= "hemagglutinin"  
: OTHER INFORMATION: /gene= "HA"  
: OTHER INFORMATION: /note= "hemagglutinin protein"  
: OTHER INFORMATION: /citation= (11)  
: PUBLICATION INFORMATION:  
: AUTHORS: Herlocher, M L  
: AUTHORS: Maassab, H F  
: AUTHORS: Webster, R G  
: TITLE: Molecular and biological changes in the cold  
: TITLE: adapted master strain A/AA/6/60 (H2N2) influenza  
: TITLE: virus  
: JOURNAL: Proceedings of the National Academy of Sciences of the USA  
: DATE: 1993  
: RELEVANT RESIDUES IN SEQ ID NO: 17: FROM 1 TO 1773  
: US-08-573-569-17

Query Match 96.7%; Score 1723.4; DB 10; Length 1773;  
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Matches 1320; Conservative 422; Mismatches 31; Indels 0; Gaps 0;

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Db 61 CAUUCUUCUUUUCACACAGTGAAGAGGAGGAGCAGATTAAGTTCATGACATGCAATTA 120  
QY 126 TTCACAGAGAGGTCGACACAAATTTAGAGCGGAACGTCATGTCATGCAAGGA 185  
Db 121 UUCACAGAGAGGTCGACACAAATTTAGAGCGGAACGTCATGTCATGCAAGGA 180  
QY 186 CATCTTGAGAGAGCCATTAAGCAAGTATGAACCTAAACGATTCCTCCACTGA 245  
Db 181 CAUUCUUCGAGAGACCAUAAAGCAAGUUAUGCAAAACGAAUCCUCCACUUGA 240  
QY 246 ACTAGGGAGCTGATGATTCGCGATGCTCTTGAATTCGAAATGATGATGATGATGAT 305  
Db 241 ACUAGGGAGCTGATGATTCGCGATGCTCTTGAATTCGAAATGATGATGATGATGAT 300  
QY 306 AAGTGTCCAGAAAGGTCCTATATATTGAGAAAGAAACCCGAGAGAGCGTTGTGTTA 365  
Db 301 AAGUUGCCAGAAUUGCCUUAUUAUUGGAGAAAGAAACCCGAGAGAGCGTTGTGTTA 360  
QY 366 TCCAGGAGCTTCAATGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 425  
Db 361 UCCAGGAGCTTCAATGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 420  
QY 426 CGAGAAAGTAAGATTTCTGCCAAAGATAGATGAGACACATATACAAATGAGGTTTC 485

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Db 481 ACAGGCTCGCGGTGTGTGTAATCCATCTTTTTCAGAACATGCTGCTGACAAA 540  
QY 546 GGAAGATCGAGATTATCCGCTGTCAGAACGATCTGTACACATTCAGAGGAGCAAT 605  
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QY 606 GCAATTAATTTGGGGGTGACACATCCATTGATGACAGAAACAAAGAACATGTTGCA 665  
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QY 726 AATAGCAACAAGGCTTAATGTAATGTAAGAGGTAAGATGTAATTCCTTGACCT 785  
Db 721 AATAGCAACAAGGCTTAATGTAATGTAAGAGGTAAGATGTAATTCCTTGACCT 780  
QY 786 CTGTGATGTGGGACACATTAATTTTGGAGTACTGTATGTAATTCCTTGACCT 845  
Db 781 CTGTGATGTGGGACACATTAATTTTGGAGTACTGTATGTAATTCCTTGACCT 840  
QY 846 TGGATTCAAATATTCGAAAAGAGTAGTTCAGGATCATGAAAAACAGAGACATTTGA 905  
Db 841 TGGATTCAAATATTCGAAAAGAGTAGTTCAGGATCATGAAAAACAGAGACATTTGA 900  
QY 906 GAACGTGTGAGCAATATCCAAATCTCTTGGAGCATTAATTCACATTTACTTTTCA 965  
Db 901 GAACGTGTGAGCAATATCCAAATCTCTTGGAGCATTAATTCACATTTACTTTTCA 960  
QY 966 CAATGTCCACCCACTAGTATGATGATGATGATGATGATGATGATGATGATGAT 1025  
Db 961 CAATGTCCACCCACTAGTATGATGATGATGATGATGATGATGATGATGATGAT 1020  
QY 1026 CTGTAGCAGACGCTAAGAGATGTTCCCGAGATGTAATCAAGAGATGTTGGGCAAT 1085  
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RESULT 4  
US-08-573-569-35  
Sequence 35, Application US/08573569  
GENERAL INFORMATION:  
APPLICANT: Maassab, Hunein F  
APPLICANT: Heliocher, Martha L  
TITLE OF INVENTION: Cold-adapted Influenza Virus  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Anna M Lewak  
STREET: 5445 Corporate Drive  
CITY: Troy  
STATE: MI  
COUNTRY: USA  
ZIP: 48098  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/573, 569  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/082, 846  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lewak, Anna M  
REGISTRATION NUMBER: 33006  
REFERENCE/DOCKET NUMBER: 2115-00257  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 313-641-1600  
TELEFAX: 313-641-0270  
INFORMATION FOR SEQ. ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1773 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Influenza virus  
STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)  
IMMEDIATE SOURCE:  
CLONE: HA  
FEATURE:  
NAME/KEY: mutation  
LOCATION: replace(144, "a")  
OTHER INFORMATION: /gene= "HA"  
OTHER INFORMATION: /note= "u in ca "master" strain; a in wt(3)"  
FEATURE: /citation= ([1])  
NAME/KEY: mutation  
LOCATION: replace(455, "g")



OTHER INFORMATION: /gene= "HA"  
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NAME/KEY: mutation  
LOCATION: replace(729, "a")  
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OTHER INFORMATION: /c: citation= ([1])  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 44..1729  
OTHER INFORMATION: /product= "hemagglutinin"  
OTHER INFORMATION: /gene= "HA"  
OTHER INFORMATION: /note= "hemagglutinin protein"  
OTHER INFORMATION: /c: citation= ([1])  
PUBLICATION INFORMATION:  
AUTHORS: Herliocher, M L  
AUTHORS: Maassab, H F  
AUTHORS: Webster, R G  
TITLE: Molecular and biological changes in the cold  
TITLE: adapted master strain A/A/6/60 (H2N2) Influenza  
TITLE: virus  
JOURNAL: Proceedings of the National Academy of Sciences of the USA  
DATE: 1993  
RELEVANT RESIDUES IN SIQ ID NO: 35: FROM 1 TO 1773  
US-08-573-569-35

Query Match 96.48; Score 1718.6; DB 10; Length 1773;  
Best Local Similarity 74.8; Pred. No. 0;  
Matches 1318; Conservative 421; Mismatches 34; Indels 0; Gaps 0;

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DB 61 CAUUCUCCUGUACGACAGTGAAGGGGACACAGATATGATATGATATGATATTA 120  
QY 126 TTCACAGAGAGGTGACACATATTCAGACCGGACAGTCTGACTGATGCGCAAGA 185  
DB 121 UCCACAGAGAGGTGACACATATTCAGACCGGACAGTCTGACTGATGCGCAAGA 180  
QY 186 CATCTCTGAGAGAGCATATAAGGAAAGTTATGCAAACTAAAGCAATCCCTCCACTGA 245  
DB 181 CAUUCUCCUGUACGACAGTGAAGGGGACACAGATATGATATGATATGATATTA 240  
QY 246 ACTAGGGGAGTGTAGATTGCGCGAGTCTCTTGAATCCAAATGTGATAGCTTCT 305  
DB 241 ACUAGGGGAGTGTAGATTGCGCGAGTCTCTTGAATCCAAATGTGATAGCTTCT 300  
QY 306 AAGTGTCCGAGACGTTCTATATATTGAGAAAGAAACCCGAGAGAGCGTTTGTGTA 365  
DB 301 AAGGUDCCAGAAUGTUCUUAUUAUAGGAGAAAGAAACCCGAGAGAGCGTTTGTGTA 360  
QY 366 TCCAGGAGGCTTCAAGGATTATGAAAGTGAACATCTCTCCAGCGGCGTGAACATTT 425  
DB 361 UCCAGGAGGCTTCAAGGATTATGAAAGTGAACATCTCTCCAGCGGCGTGAACATTT 420  
QY 426 CGAAGAAAGTAAAGATCTGCCCAAAGATAGATGACACAGCATCAACAATGAGAGTTC 485  
DB 421 CGAAGAAAGTAAAGATCTGCCCAAAGATAGATGACACAGCATCAACAATGAGAGTTC 480  
QY 486 ACGGCGCTCGCGGCTTCTGTATTCATATTTTTCAGAGACATGCTGTGCTGACAAA 545  
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QY 546 GGAAGATGAGATTACCGGTTGCAAAAGATGATCAACAATCAAGGAGGAGCAAAAT 605  
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QY 606 GCTAATATTTTGGGCTGTGACACATCCCATTTGATGACAGAACAAAGCATTTGTACA 665

DB 601 GCUAAUAAUUGGGGGGUGACACCAUUGAGAGACAGACAAACAAACAUUGUACCA 660  
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DB 661 GAUUGGGGAACCAUUGUUGCCGAGGACCAUUGAAGCAAAAGGUGAACCCAGAGA 720  
QY 726 AATGCAACAAGGCGCTAAGTGAATGAGCAAGGAGGTGAATGGAATCTCTGTGAGCCT 785  
DB 721 AATGCAACAAGGCGCTAAGTGAATGAGCAAGGAGGTGAATGGAATCTCTGTGAGCCT 780  
QY 786 CTTCGATATGTGGGACACATTAATTTTGAAGTACTGTAATCTATATTCACACAGAGA 845  
DB 781 CUUGAUAUUGGGGACACCAUAAUUGAGAGUACUGUAUUCUAUUGCACCAGAGUA 840  
QY 846 TGAATTCAAATATCGAAAGAGGTACTTCAGGATCATGAAACAGAGAGACATTTGA 905  
DB 841 UGGAUUCAAAUAUUGCAAAAGAGGAGUAGUUGGAGCAUAAUUGCAAGAGACACUUGA 900  
QY 906 GAATGTGAGACCAAAATGCCAACTCTTTGGGAGCAATTAATCAACATTTACCTTTCA 965  
DB 901 GAACUGUAGACCAAAUUGCCAAACUCCUUGGGAGCAUAAUUGCAACAUUGCCUUDCA 960  
QY 966 CAATGTCCACCCACTGACATATGAGTATGCTGCCCAAAATATGTAATGAGAGATTGCT 1025  
DB 961 CAUUGUCCACCCACTGACATATGAGTATGCTGCCCAAAATATGTAATGAGAGATTGCT 1020  
QY 1026 CTTCGACCAAGGACTAAGAAATGTTCCCAATTTGAATCAAGAGATTTGTTGGGCAAT 1085  
DB 1021 CUUAGCAACAGGACUAAAGAAUUGUCCCAAGUUGAUCAGAGAGAUUGUUGGGGCAU 1080  
QY 1086 AGCTGTGTTTATTAAGAGAGATGGCAAGAAATGTTGACGGTGTGATACCATCA 1145  
DB 1081 AGCUGUUAUUAAG 1140  
QY 1146 CAGCAATGCCAGGAGTACAGGATATGACAGCAAGAAAGAAATCCATCAAGAGATTTGA 1205  
DB 1141 CAGCAATGCCAGGAGTACAGGATATGACAGCAAGAAAGAAATCCATCAAGAGATTTGA 1200  
QY 1206 TGGATATCCACCAAGGTAATTTCTGTGATTTGAAAGATTAACACCCATTTGAAGCTGT 1265  
DB 1201 UGGAUUCACCAACCAAGGTAATTTCTGTGATTTGAAAGATTAACACCCATTTGAAGCTGT 1260  
QY 1266 TGGGAAGAAATTCGTTAATCTAGAGAAAGCTGAGACCTTGAACAAAGATGAGAGA 1325  
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QY 1626 CTTTGCCATTTATCTCTAGAGAGTGTCTATGATCTGTCATGATGATGATGATGAT 1685  
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CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/443, 962  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/229, 781  
 FILING DATE: April 19, 1994  
 APPLICATION NUMBER: 08/054, 016  
 FILING DATE: April 29, 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warren M. Cheek, Jr.  
 REGISTRATION NUMBER: 33,367  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-8850  
 TELEFAX:  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 49:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1135 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA to genomic RNA  
 HYPOTHEetical:  
 ANTI-SENSE:  
 FRAGMENT TYPE:  
 ORIGINAL SOURCE:  
 ORGANISM: A/Okuda/57  
 STRAIN:  
 INDIVIDUAL ISOLATE:  
 DEVELOPMENTAL STAGE:  
 HAPLOTYPE:  
 TISSUE TYPE:  
 CELL TYPE:  
 CELL LINE:  
 ORGANELLE:  
 IMMEDIATE SOURCE:  
 LIBRARY:  
 CLONE:  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT:  
 MAP POSITION:  
 UNITS:  
 FEATURE:  
 NAME/KEY:  
 LOCATION:  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 PUBLICATION INFORMATION:  
 AUTHORS:  
 TITLE:  
 JOURNAL:  
 VOLUME:  
 ISSUE:  
 PAGES:  
 DATE:  
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 FILING DATE:  
 PUBLICATION DATE:  
 RELEVANT RESIDUES IN SEQ ID NO:

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	Best Local Similarity	98.7%	Pred. Mismatches 3	3-e-239	
	Matches 916	Conservative	0	Indels 12	Gaps 0
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Db	208	AAGTTATCGAATCTAAACCGATCCGGGATCATGAAACGAGAGCAACTTGAGAAGCTGT	267		
QY	913	GAGCCAAATGCGCAATCTCTCTTTGGGAGACATAAATACAACATTCCTTTTACACATGTC	972		

Db	268	GAGACCAAAATGCCAAACCTCCCTTTGGAGACAAATAATACAACTTACCTTTTACCAATGTC	327
QY	973	CACCCACTGACAAATAGTGAAGTCCGCCCAAAATATGTAAATTCGGAAAGTTGGCTTACGA	1032
Db	328	CACCCACTGCAAAATAGGTGAGTGGCCCAAAATATGTAAATTCGGAAAGTTGGCTTACGA	387
QY	1033	ACAGGACTAAGGAATGTTCCCCACATTTGAATCAAGAGATTTGTTGGGGCAATAGTCGGT	1092
Db	388	ACAGGACTAAGGAATGTTCCCCACATTTGAATCAAGAGATTTGTTGGGGCAATAGTCGGT	447
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QY	1273	GAATTCGGTAACTTAGAGAAAAGCTGAGAACCTTGAAACAAAAGATGGAAGACGGGTTT	1332
Db	628	GAATTCGGTAACTTAGAGAAAAGCTGAGAACCTTGAAACAAAAGATGGAAGACGGGTTT	687
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Db	688	CTAGATGTGGGACATCAATGCTGAGACTTCTTACTTCTGATGGAAATTTGAGAGCACCTT	747
QY	1393	GACTTTCATGATTCATATGTCACAAGACTCTGTATGTAAGTCAAGATGCAGATCGAGAGAC	1452
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RESULT 8  
 US-09-918-568--49  
 ? Sequence 49, Application US/09918568  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Yoshinobu OKUNO et al.  
 ? TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
 ? ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
 ? NUMBER OF SEQUENCES: 58  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
 ? STREET: 2033 K Street, N.W., #800  
 ? CITY: Washington  
 ? STATE: D.C.  
 ? COUNTRY: U.S.A.

Query Match	51.0%;	Score 908.8;	DB 38;	Length 1135;
Best Local Similarity	98.7%;	Pred. No. 3.3e-239;		
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QY 1333	CTAGATGTGTGACATACAAATGCTGAGCTTTTACTTCTGATGAGAAATGAGAGCACCTT	1392		
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QY 1393	GACCTTCATGATTCATATGTCACAAATGCTATAGTAAGTCAGAAATGACCTGAGAGAC	1452		
Db 748	GACCTTCATGATTCATATGTCACAAATGCTATAGTAAGTCAGAAATGACCTGAGAGAC	807		
QY 1453	AACGTCAAAGACTAGAGAAATGATGTTTGAATTTTATCCAAATGATGATGAAATGC	1512		
Db 808	AACGTCAAAGACTAGAGAAATGATGTTTGAATTTTATCCAAATGATGATGAAATGC	867		
QY 1513	ATGAAATATGTGAAAAAACGGGACATATGATATGCCAAGTGTGAAGAAAGATCTAAACTA	1572		
Db 868	ATGAAATATGTGAAAAAACGGGACATATGATATGCCAAGTGTGAAGAAAGATCTAAACTA	927		
QY 1573	AATAGAAATGAAATCAAAAGGGGTAAATTTGACAGCATGAGGGGGTWTATCAAAATCCTTGCC	1632		
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QY 1693	TGGGTGTCTCCAAACGGGTCTCTGACAGTCAGAGATGCAATATGATTAAGTCAATTTTA	1752		
Db 1048	TGGGTGTCTCCAAACGGGTCTCTGACAGTCAGAGATGCAATATGATTAAGTCAATTTTA	1107		
QY 1753	TAATTAATAAACACCCCTGTTTCTGCTAG	1780		
Db 1108	TAATTAATAAACACCCCTGTTTCTGCTAG	1135		

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; GENERAL INFORMATION:
; APPLICANT: ZHANG, XIAOLI
; TITLE OF INVENTION: POTENT ONCOLYTIC HERPES SIMPLEX VIRUS FOR CANCER
; TITLE OF INVENTION: THERAPY
; FILE REFERENCE: P02410W0
; CURRENT APPLICATION NUMBER: PCT/US03/09287
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 00/367,788
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 00/410,024
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentlin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1733
; TYPE: DNA
; ORGANISM: Influenza virus
; PCT-US03-09287-13

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Query Match      41.3%; Score 732.4; DB 1; Length 1733;
Best Local Similarity 65.4%; Pred. No. 2e-190;
Matches 1091; Conservative 0; Mismatches 571; Indels 6; Gaps 1;

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QY 136 AAGGTGACACCAATTTAGAGCGGAACGTCACTGTACTCTATGCCAAGACATCTTGAG 195
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DB 186 GACAGCCATATATGGGAAGTCTGACGCTCAACGGGATACCTCCCTACAGACGGGAAG 245
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QY 256 TGTAGCAATTCGGGAAJGCTCTTGAATCCAAATGTATAGGCTTCTAAGTGTCCA 315
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DB 246 TGCATATGTGGCGGAAJGCTCTGGGCAATCCAGAGTGATCTTACTACATCGCAAC 305
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QY 316 GAACGCTCTATATATGGGAAGAAACCCGAGAGCGTTGTGTATCCAGCAGC 375
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QY 376 TTCAATGATTAATGAACATCTCCAGCAGCGTGAACATTTGCGAAGATA 435
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 366 TTGATGATTAATGAACATTAAGAGACACTAAGTTCATTTCTTATTTGAAAAATTT 425
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 436 AAGATTCCTGCCAAGCTAGAT-----GACACAGCAGTACCAACACTGAGGTTCAAG 489
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 426 GAAATTTTCCGAAGCTAAGCTCATGGCCAAATCATGAGACAATAAGGTGTACAGCT 485
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 490 GCTTGGCGGCTGTCTGTATATCATATTTTTCAGGAACATGGTGTGGCTGACAAGGA 549
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 486 GCATGCTCTTACTCTGAGCCAGCAGTTTACCGGAATTTGCTGTGGTAACAAAATA 545
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 550 GGAATGATTAATCCGGTTGGCAAGAGTCTACAAACATCAAGCGGAGAAATGCTA 609
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 546 GGGACTTCATATCCAACTACAGCAATCTATACAGCAACATTAAGGGGAAGAGTCTT 605
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 610 ATATATTTGGGGGTGCTCCATCCCATTTGATGAGACAGAACAAACATTTTACAGAAAT 669
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 606 GTCTCTCTGGGGGTGCTCCACCTCCCAAGTGTGAGTAGAACAAAGTATATACAGAAAT 665
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 670 GTGGGAACCTAATTTTCTGTAGGCACATCAACATTTGAACAAAAGGTCAACCCAGAAATA 729
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 666 GCTGATGATCACTTTTGTAGTGTATGCTCAAAATACAAACGGAAGATTCGCTCGGAATA 725
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 730 GCACAAGGCTTAAGTGAATGCAAGAGTGAATGAAATTTCTTGTACCCCTTGG 789
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 726 GCAGCTAGACTGAAGTTAGAGACAGCAGCGAGCAAGATGACATTAATTTTGAACATTA 785
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 790 GATATGTGGACACCAATAATTTTGAAGAGTACTGTATTAATTTGACACAGAGTATGA 849
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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DB 786 GACCAAGAGACACTATTAACATTTGAAGCCCACTGGGAATTTGATAGACACCATGTATGCT 845
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 850 TTCAAAATATCGAAAAGAGTGTAGGATGATCATGTAAGAAACAGAGAACACTGACAAAC 909
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 846 TTGCAATTAATTAAGGGGTCTGACTGTGATTAATTAACATGATGATGCTCCAGTTCACAAAT 905
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 910 TGTGAGACCAAAATGCCAAATCTCTTTGGGAGCAATAATTAATCAACATTAACCTTTTACAAAT 969
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 906 TGTGACACAAAGGTGTCCAAACCCCTCATGAGGGCTTTGAACAGCACCCTTCCTTTACAAAT 965
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 970 GTCCACCCACTGACAAATAGTGTAGTGTGCCCAAAATATGTAAATTCGGAAGTGTCTTTA 1029
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 966 GTACATCTCTATCACTATTGGAAGAAATGTCCCAAAATAGCTCAAGACACCAAACTAAGATG 1025
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1030 GCACAAGACTAAGAAATGTTCCCACTATGAATCAACAGAGATGTTTGGGCAATAGCT 1089
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1026 GCAACAGGACTTAAGAAATGTCCCATTCATTCAGTCCAGAGACTATTTGGAGCAATTTGCT 1085
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1090 GGTTTATTAAGAGAGAGATGCAAGAAATGTTGACGTTGTGTATGATACATCAGACG 1149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1086 GGATTTCAATTGAGGAGATGACAGCGCATGATGATGATGTACGGGTATCATCATCAG 1145
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1150 AATGACCAAGGATCAGGATATGACAGACAAAGAAATCCACTCAAAAGCAATTTGATGA 1209
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1146 AATGACCAAGGATCAGGATATGCTGTATCAGAAAGACACACAGAAATGCGATCAGCGG 1205
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1210 ATCAACCAAGGAAATTTCTGTATTTGAAGAAATTAACACCCCAATTTGAAGCTGTGGG 1269
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1206 ATCAAGATGAAGGAAATTTGGTAATTAAGAAAGTGAACCTCAATTCACCTAGTGGGC 1265
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1270 AAGAATTCGTTACTTATGAGAAAGAAAGCTGAGAACTTGAACAAAGAAATGGAAGAGCGG 1329
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1266 AAGAATTCATTAATTTAGAAAGAGAAATTTGAATTAAGAAAGTGTGATGATGGA 1325
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1330 TTTCTAGATGTGTGACATCAATGTGACCTTTTAACTGTATGATGAAGAAATGAGAGACA 1389
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1326 TTCTGTGATGTGTGACATCAATGTGACCTGCTCTCACTTGAATTAAGAAAGAACT 1385
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1390 CTGTGACTTCTATGATTTATATGTCAAAGATCTGTATAGTAAAGTCAAGTCAAGTCAAG 1449
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1386 CTGACTCTTATGATCTCAATGTGAAGAAATTAATTAAGAAAGTCAAGTCAAGTCAAG 1445
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1450 GACACGCTCAAGAACTAGGAAGATGATGTTTGAATTTATCAAAATGATGATGAA 1509
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1446 AATTAATCCAAAGAAATTTGGGAATGTTGTTTGAATTTATCAAGTGTGATGATGAG 1505
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1510 TGCATGAATAGTGAAGAAAGCGGACATATGATTTATCCCAAGTATGAAGAGACTTAA 1569
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1506 TGCATGAAGAGTGAAGAAAGCGGACATATGACACTACCCCAAGTATTCAGAAAGTCCAA 1565
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1570 CTAAATGAATGAATCAACAAAGGGTAAATTTGAGCAGCATGGGGGTTTATCAAAATCTT 1629
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1566 TTGAATGGAAGAAAGAAAGACGGGTGAATCAATCAATGAGATTTATCAAAATTTTG 1625
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1630 GCCATTAATCTCAAGTAGAGAGTCTATATCTCACTGCAATCAATGAGGCTGGGATCTT 1689
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1626 GCGATCTATTCACAGTCGCGCAGTGTCTGTAGTCTTGTAGTCTCTCTGGGGGCAATAGC 1685
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1690 TTCTGGTGTGCTCAACGGGCTCTGCACTGTGACAGATGTCATATGA 1737
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1686 TTCTGATGTGCTCTAATGGGTCTATGTCATGCAAGATATGCAATTTAA 1733
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 10
PCT-US03-09287-13
; Sequence 13, Application PC/TUS0309287
; GENERAL INFORMATION:
; APPLICANT: ZHANG, XIAOLI
; TITLE OF INVENTION: POTENT ONCOLYTIC HERPES SIMPLEX VIRUS FOR CANCER
; TITLE OF INVENTION: THERAPY
; FILE REFERENCE: P02410W0

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; CURRENT APPLICATION NUMBER: PCT/US03/09287
; PCT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/367,788
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 60/410,024
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 13
; LENGTH: 1733
; TYPE: DNA
; ORGANISM: Influenza virus
; PCT-US03-09287-13

Query Match      41.1%; Score 732.4; DB 2; Length 1733;
Best Local Similarity 65.4%; Pred. No. 2e-190;
Matches 1091; Conservative 0; Mismatches 571; Indels 6; Gaps 1;

OY 76 TTCACAGCAGTAGAGGGGACGAGATTCATTGGATACCATTAATCCACAGAG 135
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 66 TTCACGTACTGAAACCTGACACCATCTGTGTGGCTACCATCGAACAACCTACAGAC 125
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 136 AAGGTGACACATTTCTAGACGCGAAGCTGCTGTCATGCGAAGAGCATCCTTGAG 195
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 126 ACTGTGACACAGTACTGGAAGAAATGTGACCGTGTGCTACCTAGTGAATTTGCTGAA 185
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 196 AAGACCATPACGGAAGATTATGCAAACTAAACGGAATCCCTGCACTGTAAGGAGAC 255
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 186 GACAGCATATATGGAAACTCTGACCTGACCGGATGCTCCCTACCACTGGGAAG 245
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 256 TGTAGCATGCGGAGTGGCTCTTGGAAATCCAAATGATAGAGCTTCTAAGTGTCCA 315
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 246 TGCATGTGTGGGAGATGGCTCTGCGCAATCCAGAGTGTATCTTCTACTGCTGCAAC 305
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 316 GAACGCTCTATATTTGAGAAAGAAACCCGAGAGACGTTTGTATTCCAGCGAGC 375
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 306 TCATGTCTCTACTATATGAACTTCAACTCAGAAAGGAAACATGCTACCCGCGTGA 365
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 376 TTCATGATTTAGAAATTTGAAACATCTCTCAGACGCTGAAACATTTGCGAAGTA 435
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 366 TTCATGATTTAGAAATTTGAAAGAGAGAGCTAAGTTCATTTCTTGAATAATTTT 425
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 436 AAGATTCTGCCCAAGATAGAT-----GGACACGACATPACACATCGAGGTTCACGG 489
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 426 GAAATTTTCCGAGCAAGCTCATGCGCAATATGAGCACTAAGGTGTTCACGCT 485
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 486 GCGTGGCGGTCTGTGTATCCATCATTTTTCAGACATGCTGTGCTGACAAAGAA 549
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 486 GCATGCTCTTACTCTGTGAGCCAGCAGATTTTACCGGAATTTGCTGTGANTACAAAGAA 545
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 550 GGATCAGATTTATCCGTTGCCAAGAGATGTCACACATTAACAAGCGAGAAATGCTA 609
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 546 GGAATTTCTATATCCAAACTCAGCAATATCATACACACAAATTAAGGGGAAGAGTCTT 605
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 610 ATAATTTGGGGGTGACCATCCCATTTGATGAGACAGAAACAAAGACATTTGTCCAGAT 669
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 606 GTGCTCTGGGGGTGACCAACCTCCCAAGTGTGAGAGACAAAGATCTATACCGAAT 665
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 670 GTGGGAACCTATGTTCCGTAGGACATACATGGAACAAAGGTCAACCCAGAAATA 729
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 666 GCTGATGATGATGTTTCAATTTGATGATGATGATGATGATGATGATGATGATGAT 725
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 730 GCAACAGGCTTAAGGTGATGACAGAGAGTGAATGGAATTTCTTTGAGACCTCTTG 789
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 726 GACGTAGACCTGAAGTTAGAGCAGCGCAGAGATGAATATATATATGACACTATTA 785
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 790 GATATGTGGACACCATTAATTTTGAAGTACTGTAATCTAATTTGACACAGATGGA 849
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 786 GACCAAGAGACATTAATTAATTTGAGAGCCTGGAATTTGATACACCATGATGTCT 845
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 850 TTCAAAATATGAAAAAGAGTATGATGAGGATCATGAAACAGAGACACTGTGAGAC 909
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 846 TTCGATTTGAATTAAGGGGTCTGACTCTGGAATTAATTAATCAATCAATCTCAGTTCAAT 905
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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OY 910 TGTGAGACCAAACTCCAAACTCTTGGAGCAATAATATCAATTAATCTTTCACAAAT 969
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 906 TGTGACCAAGAGTCCAAACCCCATGAGGGCTTTGACAGCAGCCTCTTTCAGAAAT 965
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 970 GTCCACCCACTGACATATAGTGTAGTCCCAAAATATGTAATAATCGAAGAGTGTCTTA 1029
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 966 GTACATCTTATCACTATTTGGAGATATGCCAAATATAGCTCAAGAGCAACCAATAGAAATG 1025
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1030 GCAACAGACTAAGGATTTTCCCAATTTGATTCAGAGAGATTTGTTGGGCAATAGCT 1089
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1026 GCAACAGACTAAGAAATGTCCATCCATCACTGACAGAGACTATTTGGAGCAATGTCT 1085
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1090 GGTTTTATAGAGAGAGATGCGAAGATGTTGAGAGTGTGATGATACCATCAGAC 1149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1086 GGATTTCTATTTAGGAGAGATGACAGCATATATGATGATGATGATGATGATGATGATGAT 1145
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1150 AATGACAGAGATCAGGATATGACAGCAGCAAGAAATCCACTGAAAGGCAATTTGATGGA 1209
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1146 AATGACAGAGATCAGGATATGCTGCTGATCAGAAAGACACAGAAATGATGATGATGATGAT 1205
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1210 ATCACCACAAAGTAAATTTCTGATTTGAAATATTAACACCAATTTTAACTGTTGG 1269
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1206 ATCACAAGTAAAGTAAATTTCTGATTTGAAATATTAACACCAATTTTAACTGTTGG 1265
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1270 AAGAAATTCGTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1329
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1266 AAGAAATTCATTAATTTAGAAAGGAGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTG 1325
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1330 TTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1389
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1326 TTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1385
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1390 CTTCAGCTTATGATTTCTATATGTCAGAAATCTGATATGATATGATATGATATGATATGAT 1449
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1386 CTGACCTTCTATGATTTCTATATGTCAGAAATCTGATATGATATGATATGATATGATATGAT 1445
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1450 GACAGCTCAAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1509
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1446 AATTAATGCCAAAGAAATTTGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1505
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1510 TGCATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1569
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1506 TGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1565
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1570 CTAAATGAAGTAAATCAAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1629
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1566 TTGAATCGAAGAAATTAAGCGGGTGAACCTAGAAATCAATCAATGAGTATTAATCAATTTTG 1625
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1630 GCCATTATGCTACAGTACAGGTTCTATGCTACATGCAATCATGATGATGATGATGATGATGAT 1689
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1626 GCGATCTATTTCCACAGTCCGCGAGTTCTATGCTGATGATGATGATGATGATGATGATGATGAT 1685
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1690 TTCTGGGTGCTCCACAGGGTCTCTGCAAGTCAAGATCTGATATGGA 1737
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1686 TTCTGGGTGCTCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1733
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-10-397-635-13
; Sequence 13, Application US/10397635
; GENERAL INFORMATION:
; APPLICANT: ZHANG, XIAOLIU
; APPLICANT: FU, XUPING
; TITLE OF INVENTION: POTENT ONCOLYTIC HERPES SIMPLEX VIRUS FOR CANCER
; TITLE OF INVENTION: THERAPY
; FILE REFERENCE: P02410052
; CURRENT APPLICATION NUMBER: US/10/397,635
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/367,788
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 60/410,024
; PRIOR FILING DATE: 2002-09-11
```









QY	136	AAGGTCGACACAAATTCVAGGCGGAACGTCACGTGTGACATCATGCCAAGACATCTTGAG	19
Db	94	ACTGTTGACACAGTACTCGAAAAAGATGAGCCGTGACACACTCTGTTAACTGCTCGAA	15
QY	136	AAGACCCATAACGGAAGATTATGCAACTAAACGGAATCCCTCCACTTGAATAGGGAC	25
Db	134	GACACCCACAAACGGAAACTATGTAAATTAAGAAATAGGCCCTTACAAATGGGGAAA	21
QY	236	TGTACCATTTGCCGAGTGGCTCCTTGGAAATCCAAATGGAATAGGCTTCAATGTGCCA	31
Db	214	TGTATATTCGGCGGATGGCTCTTGGGAAACCCGGATGCGATTTACTGTCCACGGAGC	27
QY	316	GAACGCTCTTATATTTGGAGAAAGAAAACCCGAGAGCGGTTTGTATTACAGGAGC	37
Db	274	TCATAGTCTTATTTGTGAAAACATCGAACTCAGAAATGGAACATGTTACCAGAGAT	33
QY	376	TTCAATGATTTATGAAAGATTTAAACATCTCTCGACAGCTGAAACATTTTCGAGAAGTA	43
Db	334	TTCTATCGACTATGAGAACTGAGGAGCAATTTGAGCTCAGTGTATGTTGAAAATTC	39
QY	436	AAGATTCTGCCCCAAGATAGATGG-----ACACAGCATCAACACTGAGGTTTCACG	48
Db	394	GAATATTATTTCCAGACAGACTGCTGGCCCATATCAAAACAAAGATGTAAACGCA	45
QY	490	GCTGCGCGGTGTCTGTTAATCCATCAATTTTTCAGAAACATGGTCTGTGACAAAGAA	54
Db	454	GCAATGCTCTATGGGGGAGCAGACAGTTTTCAGAAATTTGGTATGGCTGACAAAGAG	51
QY	550	GGATCAGATTATCCGGTTGGCCAAAGATCGTACACAAATCAACACGAGAAACAAATGCTA	60
Db	514	GGAAGCTCATACCCAAAGCTTTAGCAAGTCTTATGTGAACATTAAGGAAAGAAATCTT	57
QY	610	ATAATTTGGGGGTGCACCATCCCATGTAGAGACAGAAAGAAACATTTGTACCGAAT	66
Db	574	GTACTATGGGGTGTATCATATCCGCCCTACCGGTACTGATCAACAGATCTCTATTCGAAT	63
QY	670	GTTGGAAACCTATGTTTCCGTAGGCACATCAACATTTGAACAAAAGTCAACCCGCAAAAT	72
Db	634	GCAGATGCTTATGTCTCTGTAGGGTATCAAAATATTAACAGGAGATTTCACCCCGAAATA	69
QY	730	GCACAAAGGCTTAAATGSAATGSCAACAAAGAGTAGATGGAATTCCTTTGACCCCTTGG	78
Db	694	GTAAGCAGACCCAAATAGAGATCAAGTGGAGAGTAACTATTACTGGACATTACTA	75
QY	790	GATATGTGGACACATTAATTTTGTAGACTAGTGTATGCTATTAATGACACAGATATGA	84
Db	754	CAACCCGAGACACATATCAATTTTGTAGGCACTGGAAATCTTAATAGCACCATGATATGCT	81
QY	850	TTCAAAATATCGAAAAAGAGTACTTCAGGATCATGAAACAGAAAGAACACTTGTAGAAC	90
Db	814	TTTCGACTGAATAGAGTTCTGTATCCGGTATCATCTACTGACGACACCACTGATAT	87
QY	910	TGTGAGACCAATTTGCCAAACCTCTTTGGAGCAATAAATACAACTTACCTTTTACAAT	96
Db	874	TGTATACGAAGTGTCAACACCCCATGGTGTATTAACACAGAGCTCCCTTTCCAGAAT	93
QY	970	GTCACCCACTGCATATAGTGAATGCCCAATATGTAAATCGGAGATGGTGTCTTA	102
Db	934	ATACATTCAGTACCAATAGAGAGTGGCCCAAAATACGTACAGAGTACCAAAATTTGGATG	99
QY	1030	GCAACAGACTTAAGAAATGTTCCCCAGATTAATCAATCAAGAGATGTTTGGGGCAATAGCT	108
Db	994	GCTACAGAGACTTAAGAAACATTCATCTATTCATTTCCACAGGGTCTATTTTGGAGCATTTGCC	105
QY	1090	GTTTTATAGAAAGGATGGCAAGAAATGTTGACGTTTGTTATGATACCATCACAGC	114
Db	1054	GTTTTATTTGGGGGGGATGACCTGGAATGATATGATGATGTTATGTTATCATCATCAG	111
QY	1150	AATGACCAAGGATCAGGTTATCGACGACAGCAAAAGATCACTCAAAAGCATTTGATATGA	120
Db	1114	AATCAACAGGATCAGCTATGCGACGGGATCTAAAAAAAGCACAAATATGGCATTTGACGG	117

QY 1210 ATCCACAAGAGTAATTCGTGATGAAAGATAACACCCCAATTGAGCTGTGG 1269  
1174 ATTCACAAGAGTGAAATTTGTATGAGAAATGAAACCCCAATTGACAGCTGGGT 1233  
QY 1270 AAGAAATCGGTACCTAGAGAAAAGACTGGAGACTTGAACAAAAGATGGAAGCGG 1329  
1234 AAAAAATTCACAACCTAGAGAAAGATGAAATTTAAATAAAGAGCTGATGGA 1293  
QY 1330 TTCTAGATGCTGGCATACAAATGCTGAGCTTTTACTGTGAGAAATGAGAGACA 1389  
1294 TTCTGATATTTGGACATATTAATGCAAAATGTTAGTTCTACTGGAATGAAAGACC 1353  
QY 1390 CTGCACTTTCATGATTTAATGTCACAATCTGTATGTAAGTCAAAATGCACTGAGA 1449  
1354 CTGATTTTCATGACCTCAATGTAAGAAATCTGTATGAGAAAGTAAAGCAATTAAAG 1413  
QY 1450 GACACGTCAAAAGAACTAGAGAAATGATGTTTGAATTTATCAAAATGATGATGAA 1509  
1414 AATATGCCAAGTAAATCGGAAATGATGTTTGAATTTATCAAAATGATGATGAA 1473  
QY 1510 TGCAATGATGCTGAAAGAGGACATATGATATCCCAAGTATGAAAGAGTCTAAA 1569  
1474 TGCAATGATGCTGAAAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1533  
QY 1570 CTAATGAAATGAAATGCAAGAGGTAATTTGAGCAGCATGGGGTTTATCAATCTT 1629  
1534 TTGACAGAGAGAGAACTAGATGAGTAAATTTAGATGAGAGAGAGAGAGAGAGAG 1593  
QY 1630 GCCATTTATGCTACATAGAGAGGTTCTATGCTACTGCAATCATGATGCTGGATCTT 1669  
1594 GCGATCTACTCACTTCGCGCAGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1653  
QY 1690 TTCTGGGTGCTCTCCACGGGCTCTCTGAGTGGAGTGGAT 1733  
1654 TTCTGGGTGCTCTCCACGGGCTCTCTGAGTGGAGTGGAT 1697

## RESULT 15

US-08-063-818-1

Sequence 1, Application US/8063818

GENERAL INFORMATION:

APPLICANT: Olsen, Christopher W.

APPLICANT: McGregor, Marilyn W.

APPLICANT: Hotze, Brian

APPLICANT: Hinshaw, Virginia S.

TITLE OF INVENTION: Swine Influenza Virus and Vaccine

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dickstein, Shapiro and Morin

STREET: 2101 L. Street NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/063,818

FILING DATE: 19930520

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Brady Jr., James W.

REGISTRATION NUMBER: 32,115

REFERENCE/DOCKET NUMBER: N0610.002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)785-9700

INFORMATION FOR SEQ. ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1770 base pairs

TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA (genomic)  
US-08-063-818-1

Query Match  
Best Local Similarity 63.9%; Pred. No. 2e-182;  
Matches 1083; Conservative 0; Mismatches 606; Indels 6; Gaps 1;

QY 76 TTCACAGCAGTGAAGGGGACAGATATGCTTGGATGCCAATTAATTCACAGAG 135  
1174 ATTCACAAGAGTGAAATTTGTATGAGAAATGAAACCCCAATTGACAGCTGGGT 1233  
QY 1270 AAGAAATCGGTACCTAGAGAAAAGACTGGAGACTTGAACAAAAGATGGAAGCGG 1329  
1234 AAAAAATTCACAACCTAGAGAAAGATGAAATTTAAATAAAGAGCTGATGGA 1293  
QY 1330 TTCTAGATGCTGGCATACAAATGCTGAGCTTTTACTGTGAGAAATGAGAGACA 1389  
1294 TTCTGATATTTGGACATATTAATGCAAAATGTTAGTTCTACTGGAATGAAAGACC 1353  
QY 1390 CTGCACTTTCATGATTTAATGTCACAATCTGTATGTAAGTCAAAATGCACTGAGA 1449  
1354 CTGATTTTCATGACCTCAATGTAAGAAATCTGTATGAGAAAGTAAAGCAATTAAAG 1413  
QY 1450 GACACGTCAAAAGAACTAGAGAAATGATGTTTGAATTTATCAAAATGATGATGAA 1509  
1414 AATATGCCAAGTAAATCGGAAATGATGTTTGAATTTATCAAAATGATGATGAA 1473  
QY 1510 TGCAATGATGCTGAAAGAGGACATATGATATCCCAAGTATGAAAGAGTCTAAA 1569  
1474 TGCAATGATGCTGAAAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1533  
QY 1570 CTAATGAAATGAAATGCAAGAGGTAATTTGAGCAGCATGGGGTTTATCAATCTT 1629  
1534 TTGACAGAGAGAGAACTAGATGAGTAAATTTAGATGAGAGAGAGAGAGAGAGAG 1593  
QY 1630 GCCATTTATGCTACATAGAGAGGTTCTATGCTACTGCAATCATGATGCTGGATCTT 1669  
1594 GCGATCTACTCACTTCGCGCAGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1653  
QY 1690 TTCTGGGTGCTCTCCACGGGCTCTCTGAGTGGAGTGGAT 1733  
1654 TTCTGGGTGCTCTCCACGGGCTCTCTGAGTGGAGTGGAT 1697



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Core version 5.1.6

Run on: August 9, 2003, 19:11:43 ; Search time 1703.58 Seconds

(without alignments)

15836.045 Million cell updates/sec

Title: US-09-918-568-57

Perfect score: 1110

Sequence: 1 CTAGAGACGAAACAGGGAT.....TAAACACCCCTGTTTCG 1110

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database : EST:\*

1: em\_estba:\*

2: em\_estba:\*

3: em\_estba:\*

4: em\_estba:\*

5: em\_estba:\*

6: em\_estba:\*

7: em\_estba:\*

8: em\_estba:\*

9: em\_estba:\*

10: em\_estba:\*

11: em\_estba:\*

12: em\_estba:\*

13: em\_estba:\*

14: em\_estba:\*

15: em\_estba:\*

16: em\_estba:\*

17: em\_estba:\*

18: em\_estba:\*

19: em\_estba:\*

20: em\_estba:\*

21: em\_estba:\*

22: em\_estba:\*

23: em\_estba:\*

24: em\_estba:\*

25: em\_estba:\*

26: em\_estba:\*

27: em\_estba:\*

28: em\_estba:\*

29: em\_estba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	56.4	5.1	997	29	CNS005TE
C 2	50.6	4.6	878	29	CNS0187R
C 3	49.2	4.4	1101	29	CNS0039G
C 4	47.4	4.3	1159	29	CNS015XR

C 5	47	4.2	1101	29	CNS00KIB	AL077812 Drosophila
C 6	47	4.2	1101	29	CNS017KX	AL081871 Drosophila
C 7	44.2	4.0	662	28	AZ839792	AZ839792 2M0136N02
C 8	44	4.0	901	28	AZ537973	AZ537973 ENTFT76TF
C 9	43.6	3.9	904	28	AZ535715	AZ535715 ENTBS23TF
C 10	43.2	3.9	528	28	BH095442	BH095442 RPT-24-2
C 11	43.2	3.9	1001	29	CNS01400	AL103554 Drosophila
C 12	43	3.9	634	28	AZ967094	AZ967094 2M0237E23
C 13	43	3.9	664	28	AZ724344	AZ724344 RPT-24-1
C 14	42.8	3.8	1201	13	BX399653	BX399653 BX399653
C 15	42.6	3.8	1201	13	BX461310	BX461310 BX461310
C 16	42.4	3.8	936	28	BH160320	BH160320 ENTST12TF
C 17	42.4	3.8	1101	29	CNS0181N	AL108773 Drosophila
C 18	42.4	3.8	1201	13	BX376097	BX376097 BX376097
C 19	42.2	3.8	632	28	AG166064	AG166064 Pan troy1
C 20	41.8	3.8	816	28	AZ528212	AZ528212 ENTDA70TF
C 21	41.8	3.8	1115	9	AL551400	AL551400 AL551400
C 22	41.6	3.7	634	10	BF426967	BF426967 df73f09.y
C 23	41.6	3.7	838	29	CNS03WJ	AL263440 Tetraodon
C 24	41.6	3.7	1101	29	CNS017KE	AL108152 Drosophila
C 25	41.4	3.7	747	28	CNS011RO	AL100640 Drosophila
C 26	41.4	3.7	844	28	AZ675008	AZ675008 ENTBS57TF
C 27	41.2	3.7	500	12	BM279971	BM279971 zah6149.z
C 28	41.2	3.7	604	29	FR0042754	AL130246 Fugu rubr
C 29	41.2	3.7	622	12	BM168204	BM168204 EST570727
C 30	41	3.7	356	28	AO296270	AO296270 HS.2166.B
C 31	41	3.7	816	14	CA463791	CA463791 AGENCOURT
C 32	41	3.7	975	29	CNS060UF	AL115885 T3 end of
C 33	41	3.7	987	29	CNS00418	AL066537 Drosophila
C 34	40.8	3.7	713	29	BX241460	BX241460 Danio rer
C 35	40.8	3.7	822	13	BU620988	BU620988 UI-H-FL1-
C 36	40.8	3.7	867	29	CNS0054A	AL057618 Drosophila
C 37	40.8	3.7	971	29	CNS00297	AL068026 Drosophila
C 38	40.6	3.7	972	14	CD389021	CD389021 AGENCOURT
C 39	40.4	3.6	885	13	BX425603	BX425603 BX425603
C 40	40.4	3.6	974	29	CNS001YT	AL075432 Drosophila
C 41	40.4	3.6	1101	29	CNS00YYG	AL096994 Drosophila
C 42	40.2	3.6	532	14	CA301599	CA301599 ta05d10.
C 43	40.2	3.6	566	28	BH113964	BH113964 RPT-24-2
C 44	40.2	3.6	670	29	AG168925	AG168925 Pan troy1
C 45	40	3.6	500	28	AO374391	AO374391 RPT11-14

## ALIGNMENTS

RESULT 1

CNS005TE/c

LOCUS

DEFINITION

ACCESSION

AL060767

VERSION

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammosser in Pieter de Jong's laboratory in the Department of





REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Ephydroidae; Drosophilidae; Drosophila.  
1 (bases 1 to 1111)  
Genoscope.  
Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs. For further information  
please see <http://www.fruitfly.org> The BDGP Drosophila  
melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
Aaron Mamoser in Pieter de Jong's laboratory in the Department of  
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
NY. The library is named RPc1-98 and was constructed by partial  
EcoRI digestion of Drosophila DNA provided by the BDGP from the  
isogenic strain y; cn bw sp, the same strain used for the BDGP's  
P1 and EST libraries. A more detailed description of the library  
and how to order individual BAC clones, the entire library, or  
filters for hybridization from the BACPAC Resource Center can be  
found at [http://db.cpac.med.buffalo.edu/drosophila\\_bac.htm](http://db.cpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
source  
Location/Qualifiers

1. 1101  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACR08K10"  
/clone\_1b="RPc1-98"  
/note="end : TET3"

BASE COUNT  
ORIGIN  
201 a 64 c 131 g 202 t 503 others

Query Match 4.38; Score 49.2; DB 29; Length 1101;  
Best Local Similarity 17.7%; Pred. No. 0.27;  
Matches 100; Conservative 230; Mismatches 234; Indels 2; Gaps 1;

544 ATGACCAATCAATGGAATGGAACAGGTAATGAGAAAGCAAGCAATTCAT 603  
Db 999 RDGAGAKRDPADATDADGAGRRDGRKRDKRRKGGDDKKKKAKKATKWW 940  
604 CAATCGAAAAAGAAATTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 663  
Db 939 DDDMDKDKMKDGAARRKADDDGAGDDGDKGKADDDDTGKDDDKKDDMDK 880  
664 GAAGACACAAATATATCTGCTGCTTACATCGGAGCTTTGCTGCTGGAAT 723  
Db 879 GTWGDATWMAAATDWWMGWADADMTWMAAADMDMADMDMAMKMDAMAGARTAD 820  
724 CAACATACAAATGACCTGACTGCTGGAATGACAGGAGGAGGAGGAGGAGG 783  
Db 819 RRMGRBRAGRGARARRDKRRDKRDAADDDADATTTTTRTDMDKMTDTW 760  
784 CAACGAGGAGAAATCTGAAGAGATGGGCAATGCTTCAAAATATACCAATG 843  
Db 759 TRWAADRTMDRDDDPRDAGTAGRRMRRTWRMRRTDMDADADTARDDRRR 700  
844 GACAGCGCTGCATATAGTCATACAGATG--TACTATAGCCTATGATATACAG 901  
Db 699 DGADAKGKTKGRRRRRBRATWDRDAMWADAMWTTTDTDDMDKRRRRGAR 640  
902 ACAACATTAACACCGGTTTCAGATCAAGAGTGTGAGAGTGGTATACAAAG 961  
Db 639 RTTARAAMDMWTYKADMAKMDKTRADRRDAADTWDARAKADMDAKARMRARR 580  
962 ACTGATCTGTGAGATTCCTTTGCAATATCATGCTTTTGTGCTGTGTTGCTG 1021  
Db 579 ARAARADRRMTGKTATATWTTWABAAMWAMATTTATWTTTWTGTTTTTTT 520  
1022 GGTTCATCATGGGCTGCGCAGAGGCAACATTTGAGCAATTTGATTTGAGT 1081  
Db 519 TWTTTAAWMAWMTATWAAWMAAAMAAATTTTTTTTTTTTAAWMAWMA 460

Qy 1082 ATAGTAATTAACACCTGTTT 1107  
Db 459 WTTTWTWTTTWTWMAATTTTTTTWT 434

RESULT 4  
CNS015XR/c  
LOCUS  
DEFINITION  
CNS015XR 1159 bp DNA linear GSS 26-JUL-1999  
Drosophila melanogaster genome survey sequence 17 end of BAC  
BACN15017 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AL106041  
GI:5619746  
GSS.  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidae; Drosophilidae; Drosophila.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Genoscope.  
Direct Submission  
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a  
collaboration with the European Drosophila Genome Project (EDGP) -  
<http://www.edgp.edi.ac.uk> - This Drosophila melanogaster BAC  
library (Dros BAC) was made by Alain Billard at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MRC  
project grant. The DNA was prepared from embryos by Alain Bucheton  
and Genevieve Payan. It has been constructed in the vector  
pBelobAC11.

COMMENT

FEATURES  
source  
Location/Qualifiers

1. 1159  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACN15017"  
/clone\_1b="DrosBAC"  
/plasmid="pBelobAC11"  
/note="end : T7"

BASE COUNT  
ORIGIN  
448 a 36 c 7 g 178 t 490 others

Query Match 4.38; Score 47.4; DB 29; Length 1159;  
Best Local Similarity 21.7%; Pred. No. 0.77;  
Matches 95; Conservative 173; Mismatches 167; Indels 3; Gaps 2;

270 CACTCCAAATGAGAGATTCGCCAATGACAAAGCCCTTCAACGTAACAGATCAT 329  
Db 1087 SAIVSVVAAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSA 1028  
330 TGGAGCATGCCCAATATGTTAAGCAAAACACCTGAGTTGCAACAGGATGCG 389  
Db 1027 SASAVSVSAVSVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSA 968  
390 TGTACAGAGAAACAAATAGAGGCTATTGCGGCAATAGCAGGTTTATAGAAA 449  
Db 967 SCHMSCA-ASAAASAVCGKSMASMSAGASVSAASAAASASASASASAS 909  
450 TTGGAGGAGAAATGATGACCGCTTGATGCTTACGATCAAAATTCGAGGCG 509  
Db 908 ASASASVSAVSAVSVVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSA 849  
510 ACAAGCAGAGATCTTAAGAGCACTGACAGCAGCATGCAATCAATGGAATTTGA 569  
Db 848 AVTVVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSA 791  
570 CAGGTAATCGAGAGAGAGAGAAATTCATCAATGGAAGCAATTTTCAGAGT 629  
Db 790 HASRVAVASASRSVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSA 731



Db 910 GAWMTKTRKRGCGGAAAAD-WGRTDWMWMDKRAAAAAGKDGCKKARTWGAAAAA 852

Qy 683 TCTGCTTACATGAGAGAGCTCTTGCGCTCGAGATCAACATACATGACCTGA 742

Db 851 WTKTKATKTKKTKTGRAWMAAGTPTTWDAAATAMKTKRAAAAAGRAAAAMAKDKTKR 792

Qy 743 CTGACTCGGAATGAAACAAAGCTTTGAAA-AAACAGAGAGGCACTGAGGAAATGCG 800

Db 791 GKRKRKRGTDGKGTGKTKTTTWTKTAARARARAAAKWTKTKTDGRARAAAMDWT 792

Qy 801 TGAAGAGAGGCGCAATGCTTCAATATACCAATATGACAAAGCTTGATGATGA 860

Db 731 TTRKATATRDGAAAATATRGAAAAATGKTTDGAATAATAMARRTWTMDWMAAR 672

Qy 861 GTCATCAGAAATGTAATGATGACCATGATGATACAGAGAGAG 907

Db 671 AAGAAWMAKAAAMDAAADAKKKGRRKRAAAATTAARRAKKADR 625

RESULT 7

LOCUS AZ839792/c 662 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0136N02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0136N2 F, genomic survey sequence.

ACCESSION AZ839792

VERSION AZ839792.1 GI:13009700

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 662)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weils,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished

JOURNAL Contact: Robert B. Weiss

COMMENT University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0136 row: N column: 02

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 662.

FEATURES

source

1. 662

Location/Qualifiers

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0136N02"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

BASE COUNT 131 a 116 c 106 g 309 t

ORIGIN

Query Match 4.0%; Score 44.2; DB 28; Length 662;

Best Local Similarity 60.3%; Pred. No. 4.4;

Matches 73; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 556 AATGGAAATTTGACACGAGGTAATGACAGACAGCAAGAAATTCATCAATGAAAG 615

Db 561 AATGAAAGTTGAGGTAAACAGCAATATGACCAAGAAACAGAAATGAGAG 502

Qy 616 GAATTCACAGAGAGAGAGAGAAATTCAGACCTCGAATAATACGTTGAACACTAA 675

Db 501 AAATATCAGATGTTGAGACACACATGCAAGACATGATACATCAGTCAAGAAATGAA 442

Qy 676 A 676

Db 441 A 441

RESULT 8

LOCUS AZ537973/c 901 bp DNA linear GSS 14-NOV-2000

DEFINITION ENTFT76TF Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.

ACCESSION AZ537973

VERSION AZ537973.1 GI:1142468

KEYWORDS GSS.

SOURCE Entamoeba histolytica

ORGANISM Entamoeba histolytica

REFERENCE Eukaryota; Entamoebidae; Entamoeba. 1 (bases 1 to 901)

AUTHORS Loftus,B., Van Aken,S. and Fraser,C.

Determination of clone end sequences from Entamoeba histolytica

Unpublished

JOURNAL Contact: Brendan J Loftus

COMMENT Department of Eukaryotic Genomics

The Institute for Genomic Research

7712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3543

Email: bjoftus@tigr.org

Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library

DNA library

Seq primer: M13-Forward

Class: shotgun

High quality sequence start: 16

High quality sequence stop: 740.

FEATURES

source

1. 901

Location/Qualifiers

/organism="Entamoeba histolytica"

/mol\_type="genomic DNA"

/strain="HMI:IMSS"

/db\_xref="taxon:5759"

/clone\_lib="Entamoeba histolytica sheared DNA"

/note="Vector: PHOS1; Site:1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith,

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g147321141gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."





was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1147321419b1aF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 277 a 132 c 92 g 133 t

Query Match 3.9% Score 43; DB 28; Length 634;  
Best Local Similarity 47.6%; Pred. No. 8.7;  
Matches 127; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

OY 526 AAAAGCACTCAAGCAGCCATGACCAATCAATGGAATGACGGTAAATCGAGAAG 585  
DB 199 AGAGACAAAAAAGAGACATTTCTATCAATCAAGAAACCTCCACAGATGAGTCAA 258  
OY 586 ACGACGAGAAATTCATCAATGAAAGAAATTCAGAGTAGAAGGAGAAATTCAG 645  
DB 259 ATTCTGACATCTATGCTCCAAATGAGTCCACCACATTCATTAAGAACTTTACAA 318  
OY 646 GACCTGAGAAATTCGTTGAAGACACTAAATAGATCTGCTTCAATGCGAGCTT 705  
DB 319 AACCTCAAAACACACACTGAAACCTCACACATTAATGAAATTTAAACCTCCACTTT 378  
OY 706 CTGTGCTCTGAGAAATCAACATATGACCTGACTGAGAAATGAAAGCTG 765  
DB 379 GCCAATGCTGAGCAATTTGATACGAAGATCAACAAAGGCGACATGAAATTAACAGATT 438  
OY 766 TTGAAAAAACAAGAGGCAACTGAGG 792  
DB 439 TATGAACCAATTTGAATTTAACAAGATG 465

RESULT 13  
LOCUS A2724344 664 bp DNA linear GSS 24-JAN-2001  
DEFINITION RPCI-24-145C19.TJ RPCI-24 Mus musculus genomic clone RPCI-24-145C19  
ACCESSION A2724344  
VERSION A2724344.1 GI:12469888  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus. 1 (bases 1 to 664)  
Zhaoh, S., Nierman, W., Malek, J., Shatsman, S., Akiret, B., Levins, M., Tsengaye, G., Geer, K., Krol, M., Shvartsdey, A., Gebregeorgis, E., Russell, D., de Jong, P. and Fraser, C.M.  
Mouse BAC End Sequences from Library RPCI-24  
Unpublished  
Other GSSs: RPCI-24-145C19.TJ  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhaoh@igf.org

Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end page: [http://www.tigr.org/db/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/db/bac_ends/mouse/bac_end_intro.html)  
Plate: 145 row: C column: 19

Seq primer: SP6  
Class: BAC ends.  
Location/Qualifiers  
1. 664  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="RPCI-24-145C19"  
/sex="Male"  
/cell\_type="Spleen/Brain"  
/clone\_lib="RPCI-24"  
/note="Vector: pTRBAC1; Site\_1: BamHI; Site\_2: BamHI; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTRBAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."

BASE COUNT 308 a 138 c 89 g 129 t

Query Match 3.9% Score 43; DB 28; Length 664;  
Best Local Similarity 47.6%; Pred. No. 8.7;  
Matches 127; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

OY 526 AAAAGCACTCAAGCAGCCATGACCAATCAATGGAATGACGGTAAATCGAGAAG 585  
DB 120 AGAGACAAAAAAGAGACATTTCTATCAATCAAGAAACCTCCACAGATGAGTCAA 179  
OY 586 ACGACGAGAAATTCATCAATGAAAGAAATTCAGAGTAGAAGGAGAAATTCAG 645  
DB 180 ATTCTGACATCTATGCTCCAAATGAGTCCACCACATTCATTAAGAACTTTACAA 239  
OY 646 GACCTGAGAAATTCGTTGAAGACACTAAATAGATCTGCTTCAATGCGAGCTT 705  
DB 240 AACCTCAAAACACACACTGAAACCTCACACATTAATGAAATTTAAACCTCCACTTT 299  
OY 706 CTGTGCTCTGAGAAATCAACATATGACCTGACTGAGAAATGAAAGCTG 765  
DB 300 GCCAATGCTGAGCAATTTGATACGAAGATCAACAAAGGCGACATGAAATTAACAGATT 359  
OY 766 TTGAAAAAACAAGAGGCAACTGAGG 792  
DB 360 TATGAACCAATTTGAATTTAACAAGATG 386

RESULT 14  
LOCUS BX399653/c 1201 bp mRNA linear EST 13-MAY-2003  
DEFINITION BX399653 Homo sapiens PLACENTA COR 25-NORMALIZED Homo sapiens cDNA  
ACCESSION BX399653  
VERSION BX399653.1 GI:30629850  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 1201)  
Li, W.-B., Gruber, C., Jesse, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr); Web: [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4309.f. For more information about this cluster, see <http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0D1080C030P1&cluster=4309.f>  
Feng Liang Email: [fliang@life.techn.com](mailto:fliang@life.techn.com) URL: <http://fulllength.invitrogen.com/>  
Faraday Avenue Genoscope, sequence ID: CS0D1080C030P1.



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QY 766 GTCAAGATCTGTATAGTAAAGTCAGAAATCAGCTGAGACACAGCTCAAGAACTAGCA 825  
11 1111111111 1111 11 11 1111111111  
Db 1375 TAGAAGATCTGTATAGTAAAGTAAAGCAATTAAGATATATGCCAAGAAATGCGA 1434  
QY 826 AATGATGTTTGAATTTTTCACAAATGTGATGATGATGATGATGATGATGATGATGAT 885  
1111111111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 1435 AATGATGTTTGAATTTTTCACCAAGTGTGATGATGATGATGATGATGATGATGATGAT 1494  
QY 886 GGGACATATGATATATCCAGATATGAGAGAGCTAACTAAATAGAAATGAATGAAA 945  
1111 11111111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 1495 GGGACATATATATATCCAGATATGAGAGAGCTAACTAAATAGAAATGAATGAAA 1554  
QY 946 GGGTAAATTTGAGAGCATGGGGTTTATCAATCCTTGCATTTATGCTACAGTAGCA 1005  
1555 GGAATGAAATTTAGAAATCAATGGGGTCTATCAGATTCGCGATCTACACGTGCGCC 1614  
QY 1006 GGTCTATGTCACGTGCAATCATGATGCTGGGATCTCTTCTGGGCTGCTCCACGGG 1065  
1615 AGTTCACATGCTGTGTAGTCTCCCTGGGGCAATGAGCTTCTGATGTCTTAATGGG 1674  
Db 1066 TCTCTGAGTCAGAGATCTGCAT 1088  
Db 1675 TCTTTCAGTCAGATATGCAAT 1697

RESULT 12  
US-09-045-042-1  
Sequence 1, Application US/09045042  
GENERAL INFORMATION:  
APPLICANT: TAUBENBERGER, Jeffery K.  
APPLICANT: REID, Ann H.  
APPLICANT: FANNING, Thomas G.  
TITLE OF INVENTION: HEMAGGLUTININ GENE OF THE 1918 INFLUENZA  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BELLAMY, Werten, F.W.  
STREET: 901 North Stuart Street, N.W., Suite 700  
CITY: Arlington  
STATE: VA  
COUNTRY: USA  
ZIP: 22203-1837  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US-09/045,042  
FILING DATE: 19-MAR-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: BELLAMY, Werten, F.W.  
REGISTRATION NUMBER: 27,029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-696-8119  
TELEFAX: 703-696-8116  
INFORMATION FOR SEQ. ID NO.: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1698 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: C-terminal  
ORIGINAL SOURCE:  
ORGANISM: Influenza virus  
STRAIN: Influenza A/South Carolina/1/18 (H1N1)  
IMMEDIATE SOURCE:  
CLONE: Hemagglutinin  
US-09-045-042-1

Query Match 40.1%; Score 455; DB 15; Length 1698;  
Best Local Similarity 70.5%; Pred. No. 2.5e-108;  
Matches 608; Conservative 0; Mismatches 255; Indels 0; Gaps 0;  
QY 226 GGATCCGGGATCATGAAGAGAGAAAGCACTTGAGAACTGTGAGACCAATGCAAACT 285  
11111111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 835 GGATCCGGGATCATGACCTTACAGACGACAGTGATGATGATGATGATGATGATGATGAT 894  
QY 286 CTTTGGGACATTAATACAACTTATCTTTTCACATGTCACCACTGACATAGT 345  
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11111111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 955 GAGTCCCAATATGTCAGAGATGACCAATTTGAGAGTGGCTTACAGGACTAAGAACTT 1014  
QY 406 CCCAGATTGAATCAAGAGATGTTTGGGCAATAGCTGTTTATAGAAGAGATGG 465  
11 11111111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 1015 CCATCTATCAATCCAGAGGCTATTTGAGCCATTCGCGTTTATGAGGGGGATGG 1074  
QY 466 CAAGGAATGCTGACGTTGCTATGATACCATCAGCATGACAGGATGACGCTAT 525  
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Db 1075 ACTGGAATGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1134  
QY 526 GCAGCAGCAAGAGATCCACTCAAAAGCACTTGTGATGATCCCAAGGATTAATCT 585  
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Db 1135 GCAGCAGATCAAAAGACACAAATGCTATGACGGATTCACAAAGGATTAATCT 1194  
QY 586 GTGATGAAAGATTAACACCAATTTGAAGCTTGGGAGAGAAATTCGCTAATTTAGAG 645  
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QY 646 AAAAGACTGAGAACTTGAACAAAGATGGAAGCGGTTTCTAGATGTGACATAC 705  
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QY 826 AATGATGTTTGAATTTTTCACAAATGTGATGATGATGATGATGATGATGATGATGAT 885  
11111111 1111 1111 1111 1111 1111 1111 1111 1111 1111  
Db 1435 AATGATGTTTGAATTTTTCACCAAGTGTGATGATGATGATGATGATGATGATGATGAT 1494  
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QY 946 GGGTAAATTTGAGAGCATGGGGTTTATCAATCCTTGCATTTATGCTACAGTAGCA 1005  
1555 GGAATGAAATTTAGAAATCAATGGGGTCTATCAGATTCGCGATCTACACGTGCGCC 1614  
QY 1006 GGTCTATGTCACGTGCAATCATGATGCTGGGATCTCTTCTGGGCTGCTCCACGGG 1065  
1615 AGTTCACATGCTGTGTAGTCTCCCTGGGGCAATGAGCTTCTGATGTCTTAATGGG 1674  
Db 1066 TCTCTGAGTCAGAGATCTGCAT 1088  
Db 1675 TCTTTCAGTCAGATATGCAAT 1697

RESULT 13  
PCT-US03-09287-13  
Sequence 13, Application PC/TUS0309287  
GENERAL INFORMATION:  
APPLICANT: ZHANG, XIAOLI  
TITLE OF INVENTION: POTENT ONCOLYTIC HERPES SIMPLEX VIRUS FOR CANCER  
US-09-045-042-1



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QY  ATTGAAAAGATAAAACCCCAATTTTGAAGCTTTGGGAAAAGAAATTCCGGTACTTGTAGAAA 648
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Db  ATTGAAAAGATGAACACTCACTATTCTAGTCACTGGGCAAGAAATTCATTAATTGAAAGG 1289
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QY  AGACTGAGAACTTGAACAAAAAGATGAGAACGCGCTTTCTAGATGCTGACATACAAAT 649
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Db  AGAATTTGAAATTTGAATTAATAAAGGTGATGATGATGATTCCTGATGTTTGGACATACAA 1290
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QY  GCTGAGCTTTAGTTCGTGATGAAAATGAGAGACACTTGACTTTCAITGATTCATATGTC 768
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Db  GCCCAACACTGCGTCTACTTGAAGAAAGAAAGAACTAGACTTTCAATGACTCCAAATGTC 1350
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QY  AAGATCTGATTTAGTAAAGTGAAGTGAAGCTGAGCTGAGAGCAACGTCAAAGAACTGSAAT 769
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QY  GGATGTTTGAATTTTATCACAAATGTGATGATGAATGCATGAATAGTGTGAAAACGGG 829
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QY  ACATATGATTTATCCCAAGTATGAAGAAGAGCTTAACCTAAATAGAAATGAAATCAAAAGG 889
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QY  GTAAATTTGACACGATGGGGGCTTTATCAAAATCCTTGCCATTTATGCTAAGTAGACAGGT 949
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Db  GTGAACACTAGAAATCAATGAGAGTTTATCAAAATTTTGGCGACTATTTCCACAGTCGCCAGT 1590
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QY  TCTATGTCACTGCGCAATCATGATGGCTGGGATCTCTTTCTGGGATGTCCTCCAAAGGGCT 1009
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QY  CTGCAGTGCAGGATCTGCATTTGA 1092
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COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/063.818
FILING DATE: 19930520
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Brady Jr., James W.
REGISTRATION NUMBER: 32,115
REFERENCE/DOCKET NUMBER: N0610.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)785-9700
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1770 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-063-818-1

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Query Match 41.4%; Score 470; DB 5; Length 1770;

Best Local Similarity 70.4%; Pred. No. 2,9e-113;

Matches 629; Conservative 0; Mismatches 265; Indels 0; Gaps 0;

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QY 226 GGATCGGGGATCATGAAAGAGAGAACTTGAGAACTGTGAGACCAATGCCAACT 285
DB 867 GAATCTGGTATTAAATTCAGATACCCAGTTCAGATTTGAATAGCACTTGCAACA 926
QY 286 CCTTGGGAGAAATTAACAACATTTCTTTCATGTCACCCACTGACATAGT 345
DB 927 CCCAAGGTGTATTAACACTGCTCCCATTTTCAGATGTACATCCAGCCCAATTTGA 986
QY 346 GAGTGGCCCAATATGTAAATCGAGAACTTGTCTAGCAACAGAGACTAGAAATGT 405
DB 987 GAATGTCAAAAGTATGTCAAAAGCAAAATTTGAGAAATGCTACAGATTAAGAAATATC 1046
QY 406 CCCCAATTTGATTAAGAGATTTGTTGGGCAATAGCTGTTTATGAAGAGAGATG 465
DB 1047 CCGTCTATTCATCTAGAGTCTGTTTGGAGCCATTCGTTTATGAAGGGGGTGG 1106
QY 466 CAAGGATGGTGGTGGTGTATGATACATCACACCAAAATGGGAGGATCAGGAT 525
DB 1107 ACAGGATGTATAGTGGTGTGATGATATCACCAAAATGGGAGGATCAGGATC 1166
QY 526 GCAGCAGACAAGATCCACTCAAAAGGATTTGATGATCACCACCAAGGTAATTTCT 585
DB 1167 GCAGTGCACCAAAAGAGACACAGATGCCATTTGCGGGATTCACATCAAAAGTAATCT 1226
QY 586 GTGATTAAAAAGATTAACCCCAATTTGAGCTGTTGGGAAAGAAATTCGTAATTAAG 645
DB 1227 GTTATTAAAAAGATGAACACACAGTTCACAGCGGGGTAAGAAATTCACACCTTGGAA 1286
QY 646 AAAAGACTGGAGTGAACAAAAGATGAAGGATTCATGATGTGAGCATAC 705
DB 1287 AAGGAATATGAGATTTAAACAAAAGGTTGATGATGTTGAGTGTGGACTTAC 1346
QY 706 AATGCTGAGCTTTAGTTCTGATGAGAAATGAGAGACACTTGCATTCATGATTCAT 765
DB 1347 AATGCCAAGCTTTGTTGTTCTTATGAAATGAAGAACTTTGATTCATGACTCAAT 1406
QY 766 GTCAAGATCTGTATTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 825
DB 1407 GTGAAGAACCTATATGAAGAAAGTAAAGCCAGTCAAGCAATGCCAAGAAATTTGG 1466
QY 826 AATGATGTTTGAATTTTATCACAATGTGATGATGATGATGATGATGATGATGAT 885
DB 1467 AATGATGCTTTGATTTCTATCACAATGTGATGATGATGATGATGATGATGATGAT 1526

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QY 886 GGACATATGATATCCCAAGTAGAAGAGTCTAAACTAATAGAAATGAATCAAA 945
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QY 946 GGGTAAATATGAGCAGATGGGGGTTTATCAATCTTGCCATTTATGCTACATGCA 1005
DB 1587 GGGTAAATATGAGTATCAAAAGAGATTTACAGATTTTGGGATCTATTCAGCTGCC 1646
QY 1006 GGTCTATGTCACATGCAATGATGATGATGATGATGATGATGATGATGATGATG 1065
DB 1647 AGTTCATTTGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1706
QY 1066 TCTCTGAGTGCAGATGCTGCATATGATTAATGATTTTAAATTAATAAACA 1119
DB 1707 TCTTACAGTGCAGATATGATTTAAATTAAGATTTTACAGACATGAGAAAA 1760

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# RESULT 10

US-07-773-597-14

Sequence 14, Application US/07773597

GENERAL INFORMATION:

APPLICANT: INGELS, Stephen C.

APPLICANT: BRIERLEY, Ian

TITLE OF INVENTION: RIBOSOMAL FRAMESHIFT SIGNALS AND USES

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Walter H. Dreyer

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/773.597

FILING DATE: 19920106

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Dreyer, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-55784/RHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 1778 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 33..1730

US-07-773-597-14

Query Match 41.1%; Score 466.8; DB 4; Length 1778;

Best Local Similarity 51.4%; Pred. No. 2e-111;

Matches 469; Conservative 172; Mismatches 267; Indels 4; Gaps 1;

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QY 226 GGATCGGGGATCATGAAAGAGAGAACTTGAGAACTGTGAGACCAATGCCAACT 285
DB 867 GGATCGGGGATCATGAAAGAGAGAACTTGAGAACTGTGAGACCAATGCCAACT 926
QY 286 CCTTGGGAGAAATTAACAACATTTCTTTCATGTCACCCACTGACATAGT 345
DB 927 CCGTCTATTCATCTAGAGTCTGTTTGGAGCCATTCGTTTATGAAGGGGGTGG 986

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STRAIN:  
IMMEDIATE SOURCE:  
CLONE: HA  
FEATURE:  
NAME/KEY: mutation  
LOCATION: replace(144, "u")  
OTHER INFORMATION: /gene= "HA"  
OTHER INFORMATION: /note= "u in ca "master" strain; a in w2(3)"  
OTHER INFORMATION: /citation= ([1])  
FEATURE:  
NAME/KEY: mutation  
LOCATION: replace(455, "a")  
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NAME/KEY: mutation  
LOCATION: replace(729, "c")  
OTHER INFORMATION: /gene= "HA"  
OTHER INFORMATION: /note= "c in ca "master" strain; a in wt2(3)"  
OTHER INFORMATION: /citation= ([1])  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 44..1729 /product= "hemagglutinin"  
OTHER INFORMATION: /gene= "HA"  
OTHER INFORMATION: /note= "hemagglutinin protein"  
OTHER INFORMATION: /citation= ([1])  
PUBLICATION INFORMATION:  
AUTHORS: Herlocher, M L  
AUTHORS: Maassab, H F  
AUTHORS: Webster, R G  
TITLE: Molecular and biological changes in the cold  
TITLE: adapted master strain A/Aa/6/60 (H2N2) influenza  
TITLE: virus  
JOURNAL: Proceedings of the National Academy of Sciences of the USA  
DATE: 1993  
RELEVANT RESIDUES IN SEQ ID NO: 17: FROM 1 TO 1773  
US-08-573-569-17

Query Match 77.8% Score 882.8: DB 10: Length 1773:  
Best Local Similarity 71.8% Pred. No. 7.9e-221:  
Matches 665: Conservative 234: Mismatches 27: Indels 0: Gaps 0:  
QY 208 AAGTTATGCAAACTAAAGCATCCGAGTATGAAAACAGAGAACACTTGAGAGTCT 267  
DB 848 AAAAUAUCGAAAAGAGAGUAGUUCUGGAGUACUAGAAAAGAGAACACUUCAGAACUGU 907  
QY 268 GAGACCAATGCCAACTCTTTGGAGCAATAATACACATTACCTTTCCAAATGTC 327  
DB 908 GAGACCAAAUUGCCAAACUCCUUGGGAGCAUAAUAAUACACAUUCCUUCACAAUUGC 967  
QY 328 CACCCACTGCAATAGTGGAGTGGCCCAATATATGAAATGGGAGAACTTGCTTACCA 387  
DB 968 CACCCACUAGCAAAUAGGAGUAGUCCCAAAUAGUAAAUUGGAGAAUUGUUCUACCA 1027  
QY 388 ACAGAGTAAGAGTGTCCCACTGATGATCAAGAGAGATGTTGGGCAATAGCTGCT 447  
DB 1028 ACAGAGCUAAGAGUAGUCCCAUAGAGAGUAGUUGGGGCAUUAUACUGU 1087  
QY 448 TTTATAGAGAGAGTGGCAAGAAAGTGTGATGATGATACCATCAGCAAT 507  
DB 1088 UUUUAUAGAGAGAGUAGUCCCAUAGAGAGUAGUUGGUUAGUACCAUACAGCAAU 1147  
QY 508 GACCAGGATCAGGCTATGCGAGACAGACAAATCCACTCAAAAGGCTTTGATGATC 567  
DB 1148 GACCAGGAGUAGGAGUAGUCCCAUAGAGAGUAGUUGGUUAGUACCAUACAGCAAU 1207  
QY 568 ACCAACAAGTAAATCTGATGAAAGATAAACACCAATTTGAAGCTGGTGGGAAA 627  
DB 1208 ACCAACAAGUAAUUCUGUAGUAGUAAUAAACACCAUUAUUGAGUUGGAGAAA 1267  
QY 628 GAATTCGTAACCTAGAGAAAGAGCTGAGAACTTGAACAAAGATGGAAGAGCGGTTT 687

DB 1268 GAUUCAGUAAACUUGAGAGAGAGACUGGAGAAUUCUAAACAAAAGAGAGAGCGGUU 1327  
QY 688 CTAGATGTGGACATFACATGCTGAGCTTTTATGTCGATGAGAAATGAGAGACACTT 747  
DB 1328 CUGAGUUGGUGGACUACAAUAGUCCUUCUAGUAGUAGUAGUAGUAGUAGUAGU 1387  
QY 748 GACTTTCATGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 807  
DB 1388 GACUUCUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1447  
QY 808 AACGTCAAGAACTAGAGAAATGATGTTTGAATTTATACAAATGATGATGATGATGAT 867  
DB 1448 AACGUCAAAAGACUAGAGAAUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1507  
QY 868 ATGATAGTGGAAAACGGGACATGATGATGATGATGATGATGATGATGATGATGAT 927  
DB 1508 AUGAAUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1567  
QY 928 AATAGAAATGAATCAAGAGGAGTAAATGAGAGAGATGAGAGGCTTATCAAAATCCTTGC 987  
DB 1568 AAUAGAAUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1627  
QY 988 ATTATGCTACAGTACAGGCTTCTATGTCATGTCATGTCATGTCATGTCATGTCAT 1047  
DB 1628 AUUUAUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAG 1687  
QY 1048 TGGCTGCTCCACAGGCTCTGTCAGTGCAGAGATGATGATGATGATGATGATGAT 1107  
DB 1688 UGGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1747  
QY 1108 TAATTAATAACACCTTCTTCTGCT 1133  
DB 1748 UAAUUAATAACACCCUUGUUCUACU 1773

RESULT 6  
US-08-573-569-35  
Sequence 35, Application US/08573569  
GENERAL INFORMATION:  
APPLICANT: Maassab, Hunein F  
APPLICANT: Herlocher, Martha L  
TITLE OF INVENTION: Cold-adapted Influenza Virus  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Anna M Lewak  
STREET: 5445 Corporate Drive  
CITY: Troy  
STATE: MI  
COUNTRY: USA  
ZIP: 48098  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/573.569  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/082.846  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lewak, Anna M  
REGISTRATION NUMBER: 33006  
REFERENCE/DOCKET NUMBER: 2115-00257  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 313-641-1600  
TELEFAX: 313-641-0270  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1773 base pairs

DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>  
CELL LINE: <Unknown>  
ORGANELLE: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 46:  
US-09-918-568-46

Query Match 80.18; Score 908.8; DB 38; Length 1783;  
Best Local Similarity 98.73; Pred. No. 1.2e-227;  
Matches 916; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY	208	AAGTATGCAAACTA	ACGATCCGGATCATGAAAAAGAGAACTTGGAATGT	267
DB	853	AAATATCGAAGAA	BSITAGTTGAGGATCATGAAAAAGAGAACTTGGAATGT	912
QY	268	GAGACCAATGCCAA	ACTCCTTGGGAGCAATAAATCAACATTACCTTTCAACATGTC	327
DB	913	GAGACCAATGCCAA	ACTCCTTGGGAGCAATAAATCAACATTACCTTTCAACATGTC	972
QY	328	CACCACTGACATA	BSITAGTGCCTCCCAATATGTAATCGAGAACTTGCTTAACA	387
DB	973	CACCACTGACATA	BSITAGTGCCTCCCAATATGTAATCGAGAACTTGCTTAACA	1032
QY	388	ACAGACTAAGAA	TTTCCCAAGATGATCAAGAGATTTTGGGCAATAGCTGT	447
DB	1033	ACAGACTAAGAA	TTTCCCAAGATGATCAAGAGATTTTGGGCAATAGCTGT	1092
QY	448	TTTATAGAGAGAT	TGCAAGAAATGTTGACGTTGTTATGATACATCAGCAAT	507
DB	1093	TTTATAGAGAGAT	TGCAAGAAATGTTGACGTTGTTATGATACATCAGCAAT	1152
QY	508	GACAGGATCAGG	ATGCGAGCAAGAAATCCACTAAAAAGCATTTGATGATC	567
DB	1153	GACAGGATCAGG	ATGCGAGCAAGAAATCCACTAAAAAGCATTTGATGATC	1212
QY	568	ACCAACAAGTAA	TTCTGTGATTGAAAAGATAAACACCAATTTGAAGCTGTGGAAA	627
DB	1213	ACCAACAAGTAA	TTCTGTGATTGAAAAGATAAACACCAATTTGAAGCTGTGGAAA	1272
QY	628	GAATTCGTAAC	TTTGAGAAAGACTGAGAACTTGAAACAAAAAGAGAAAGCGGTTT	687
DB	1273	GAATTCGTAAC	TTTGAGAAAGACTGAGAACTTGAAACAAAAAGAGAAAGCGGTTT	1332
QY	688	CTGATGTGTGAC	ATTCATGCTGAGCTTTTGTCTGATGGAATGAGAGACCTT	747
DB	1333	CTGATGTGTGAC	ATTCATGCTGAGCTTTTGTCTGATGGAATGAGAGACCTT	1392

QY	748	GACTTCATGATCTA	ATGTCAGAACTGTATGTAAGTCGAATGACGTGAGAC	807
DB	1393	GACTTCATGATCTA	ATGTCAGAACTGTATGTAAGTCGAATGACGTGAGAC	1452
QY	808	AACGTCAAGAACT	AGAAATGATGTTTGAATTTATCAAAATGATGATGATGC	867
DB	1453	AACGTCAAGAACT	AGAAATGATGTTTGAATTTATCAAAATGATGATGATGC	1512
QY	868	ATGATAGTGTGAAA	ACGGGACATATGATTATCCCAAGTATGAGAAGCTTAACTA	927
DB	1513	ATGATAGTGTGAAA	ACGGGACATATGATTATCCCAAGTATGAGAAGCTTAACTA	1572
QY	928	AATGAATATGAAT	CAAGGGGTAAATGTAGCAGCATGGGGGTTTATCAATCTTGCC	987
DB	1573	AATGAATATGAAT	CAAGGGGTAAATGTAGCAGCATGGGGGTTTATCAATCTTGCC	1632
QY	988	ATTATGCTACAG	TAGCAGGTTCTATGTCACTGCAATCATGATGCTGGATCTTTC	1047
DB	1633	ATTATGCTACAG	TAGCAGGTTCTATGTCACTGCAATCATGATGCTGGATCTTTC	1692
QY	1048	TGGGTGTCTCCAA	CGGGCTCTGCACTGCAAGATTCGATATGATTAATGATCTTAA	1107
DB	1693	TGGGTGTCTCCAA	CGGGCTCTGCACTGCAAGATTCGATATGATTAATGATCTTAA	1752
QY	1108	TAATTAATAACAC	CCCTGTTCTGCTAG	1135
DB	1753	TAATTAATAACAC	CCCTGTTCTGCTAG	1780

RESULT 5  
US-08-573-569-17  
Sequence 17, Application US/08573569  
GENERAL INFORMATION:  
APPLICANT: Maassab, Hunein F  
APPLICANT: Herliocher, Martha L  
TITLE OF INVENTION: Cold-adapted Influenza Virus  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Anna M Lewak  
STREET: 5445 Corporate Drive  
CITY: Troy  
STATE: MI  
COUNTRY: USA  
ZIP: 48068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/573,569  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/082,846  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lewak, Anna M  
REGISTRATION NUMBER: 33006  
REFERENCE/DOCKET NUMBER: 2115-00257  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 313-641-1600  
TELEFAX: 313-641-0270  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1773 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Influenza virus  
STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI



PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 49:  
US-09-918-568-49

Query Match 100.0%; Score 1135; DB 38; Length 1135;  
Best Local Similarity 100.0%; Pred. No. 3,1e-287;  
Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CTAGCAAAAGCAGGGGTTATACCATAGAAAACCAAAAGCAAAACATGGCCATCTTTAT 60
DB 1 CTAGCAAAAGCAGGGGTTATACCATAGAAAACCAAAAGCAAAACATGGCCATCTTTAT 60
QY 61 CTCATCTCTCTGTTTCACAGAGTGAGAGGGGACCATGATGATGATGATGATGATGATGAT 120
DB 61 CTCATCTCTCTGTTTCACAGAGTGAGAGGGGACCATGATGATGATGATGATGATGATGAT 120
QY 121 AATTCACAGAGAGAGGTTGACACCAATTTCTAGAGCGGAACGTCTGCTGATGATGATGAT 180
DB 121 AATTCACAGAGAGAGGTTGACACCAATTTCTAGAGCGGAACGTCTGCTGATGATGATGAT 180
QY 181 GACATCCTTGAGAGAGGTTGACACCAATTTCTAGAGCGGAACGTCTGCTGATGATGATGAT 240
DB 181 GACATCCTTGAGAGAGGTTGACACCAATTTCTAGAGCGGAACGTCTGCTGATGATGATGAT 240
QY 241 AAAACAGAGAGAGAGGTTGAGAGAGGTTGAGAGAGGTTGAGAGAGGTTGAGAGAGGTTG 300
DB 241 AAAACAGAGAGAGAGGTTGAGAGAGGTTGAGAGAGGTTGAGAGAGGTTGAGAGAGGTTG 300
QY 301 AATACACATTAACCTTTTACCAATGTCACCCACTGACAAATAGTGAATGATGATGATGAT 360
DB 301 AATACACATTAACCTTTTACCAATGTCACCCACTGACAAATAGTGAATGATGATGATGAT 360
QY 361 GTAAATGAGAGAGGTTGAGAGAGGTTGAGAGAGGTTGAGAGAGGTTGAGAGAGGTTGAG 420
DB 361 GTAAATGAGAGAGGTTGAGAGAGGTTGAGAGAGGTTGAGAGAGGTTGAGAGAGGTTGAG 420
QY 421 AGAGATGTTGTTGGGTCATAGTGTGTTTATAGAGAGAGGTTGAGAGAGGTTGAGAGAGGTT 480
DB 421 AGAGATGTTGTTGGGTCATAGTGTGTTTATAGAGAGAGGTTGAGAGAGGTTGAGAGAGGTT 480
QY 481 GGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 481 GGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 TCCACTCAAAAGGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 541 TCCACTCAAAAGGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 601 AACACCCATTTGAAATGTTGTTGGGAAAGAAATTCGTTAACTAGAGAGAGGTTGAGAGAG 660
DB 601 AACACCCATTTGAAATGTTGTTGGGAAAGAAATTCGTTAACTAGAGAGAGGTTGAGAGAG 660
QY 661 TTGAACAAAAGATGAGAGAGGTTTCTAGATGTTGAGACATCAATGCTGAGACTTTTA 720
DB 661 TTGAACAAAAGATGAGAGAGGTTTCTAGATGTTGAGACATCAATGCTGAGACTTTTA 720
QY 721 GTTCTGATGAGAGAGGTTGAGAGAGGTTGATGATGATGATGATGATGATGATGATGATGAT 780
DB 721 GTTCTGATGAGAGAGGTTGAGAGAGGTTGATGATGATGATGATGATGATGATGATGATGAT 780
QY 781 AGTAAGTCAGAGAGGTTGAGAGAGGTTGAGAGAGGTTGAGAGAGGTTGAGAGAGGTTGAG 840
DB 781 AGTAAGTCAGAGAGGTTGAGAGAGGTTGAGAGAGGTTGAGAGAGGTTGAGAGAGGTTGAG 840
QY 841 TTTTATACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 841 TTTTATACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 CCCAAGTATGAGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
DB 901 CCCAAGTATGAGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
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QY 961 AGCATGGGGGTTTATCAATCTTCGTCATTTATGCTACAGAGAGGTTCTATGCTACTG 1020
DB 961 AGCATGGGGGTTTATCAATCTTCGTCATTTATGCTACAGAGAGGTTCTATGCTACTG 1020
QY 1021 GCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 GCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 ATCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1135
DB 1081 ATCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1135
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## RESULT 3

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US-08-443-862-46
; Sequence 46, Application US/08443862
; GENERAL INFORMATION:
; APPLICANT: Yoshinobu OKUNO et al.
; TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,862
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,781
; FILING DATE: April 19, 1994
; APPLICATION NUMBER: 08/054,016
; FILING DATE: April 29, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: A/Okuda/57
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLER:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
```

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Db 181 GACATCTTGAGAGACCATTACGGAAAGTTATGCAAACTAAACGGATCCGGATCANG 240
Qy 241 AAAACAGAGAGAACACTTGAGAACTGTGAGACCAATGCGAAATCTCTTTGGAGCAATA 300
Db 241 AAAACAGAGAGAACACTTGAGAACTGTGAGACCAATGCGAAATCTCTTTGGAGCAATA 300
Qy 301 AATACACATTACCTTTTACAAATGTCCACCACTGACAAATAGGTAGTGTCCCAAAATAT 360
Db 301 AATACACATTACCTTTTACAAATGTCCACCACTGACAAATAGGTAGTGTCCCAAAATAT 360
Qy 361 GTAATATGGGAGAACTGGTCTTAGCAACAGACTAGAGAACTTCCCAAGTTGAATCA 420
Db 361 GTAATATGGGAGAACTGGTCTTAGCAACAGACTAGAGAACTTCCCAAGTTGAATCA 420
Qy 421 AGAGATTTGTTGGGGCAATAGCTGGTTTATGAGAGAGATGCGCAAGAAATGTTGAC 480
Db 421 AGAGATTTGTTGGGGCAATAGCTGGTTTATGAGAGAGATGCGCAAGAAATGTTGAC 480
Qy 481 GGTGTGATGATACCATCAGCAATGACACAGGATCAGGGATGACAGCAAGAA 540
Db 481 GGTGTGATGATACCATCAGCAATGACACAGGATCAGGGATGACAGCAAGAA 540
Qy 541 TCCACTCAAAAGGCAATTTGATGATGATACCAACAGAGTAATTTCTGATGAAAAGATA 600
Db 541 TCCACTCAAAAGGCAATTTGATGATGATACCAACAGAGTAATTTCTGATGAAAAGATA 600
Qy 601 AACACCCCAATTTGAGCTGTTGGGAAAGAAATTCGGTACTTGAAGAAAGACTGGAGAC 660
Db 601 AACACCCCAATTTGAGCTGTTGGGAAAGAAATTCGGTACTTGAAGAAAGACTGGAGAC 660
Qy 661 TTGAACAAAAGATGAGAGACGGGTTTCTAGATGTGTGACATACAACTGAGCTTTTA 720
Db 661 TTGAACAAAAGATGAGAGACGGGTTTCTAGATGTGTGACATACAACTGAGCTTTTA 720
Qy 721 GTTCGATGAGAAAATGAGAGGACACTTGACTTTCATGATTTCAATGTCAAGATCTGTAT 780
Db 721 GTTCGATGAGAAAATGAGAGGACACTTGACTTTCATGATTTCAATGTCAAGATCTGTAT 780
Qy 781 AGTAAGTCAGATGACAGCTGAGAGACAACTCAAGAACTAGAAATGATGTTTGA 840
Db 781 AGTAAGTCAGATGACAGCTGAGAGACAACTCAAGAACTAGAAATGATGTTTGA 840
Qy 841 TTTTATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db 841 TTTTATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Qy 901 CCCAAGTATGAAGAGTCTAACTAAATAGAAATGAATGAAGGGGTAATATGAGC 960
Db 901 CCCAAGTATGAAGAGTCTAACTAAATAGAAATGAATGAAGGGGTAATATGAGC 960
Qy 961 AGCATGGGGGTTTATCAATCTTCCATTTATGCTACAGTAGAGTCTATGTCACGT 1020
Db 961 AGCATGGGGGTTTATCAATCTTCCATTTATGCTACAGTAGAGTCTATGTCACGT 1020
Qy 1021 GCAATCATGATGCTGGGATCTCTTTGCTGCTCCACAGGGTCTCTGACAGTGCAG 1080
Db 1021 GCAATCATGATGCTGGGATCTCTTTGCTGCTCCACAGGGTCTCTGACAGTGCAG 1080
Qy 1081 ATGCGATATGATATATGATATTTATTAATTAATAAACACCTTGTCTGTCTAG 1135
Db 1081 ATGCGATATGATATATGATATTTATTAATTAATAAACACCTTGTCTGTCTAG 1135

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RESULT 2

US-09-918-568-49

Sequence 49, Application US/09918568

GENERAL INFORMATION:

APPLICANT: Yoshinobu OKUNO et al.

TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING

ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.

```

STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 1135 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/Okuda/57
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:

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5 882.8 77.8 1773 10 US-08-573-569-17 Sequence 17, Appl  
6 882.8 77.8 1773 10 US-08-573-569-35 Sequence 35, Appl  
7 838 73.8 1728 9 US-08-443-862-28 Sequence 26, Appl  
8 838 73.8 1728 38 US-09-918-568-28 Sequence 28, Appl  
9 470 41.1 1770 5 US-08-063-818-1 Sequence 1, Appl  
10 466.8 41.1 1778 4 US-07-773-597-14 Sequence 14, Appl  
11 455 40.1 1698 15 US-09-040-944-1 Sequence 1, Appl  
12 455 40.1 1698 15 US-09-045-042-1 Sequence 1, Appl  
13 452.8 39.9 1733 1 PCT-US03-09287-13 Sequence 13, Appl  
14 452.8 39.9 1733 2 PCT-US03-09287-13 Sequence 13, Appl  
15 452.8 39.9 1733 51 US-10-397-635-13 Sequence 13, Appl  
16 447.8 39.5 1754 9 US-08-443-862-27 Sequence 27, Appl  
17 447.8 39.5 1754 38 US-09-918-568-27 Sequence 27, Appl  
18 400 35.2 400 9 US-08-443-862-33 Sequence 33, Appl  
19 400 35.2 400 38 US-09-918-568-33 Sequence 33, Appl  
20 397 35.0 409 9 US-08-443-862-34 Sequence 34, Appl  
21 397 35.0 409 38 US-09-918-568-34 Sequence 34, Appl  
22 382.4 33.7 410 9 US-08-443-862-35 Sequence 35, Appl  
23 382.4 33.7 410 38 US-09-918-568-35 Sequence 35, Appl  
24 379.6 33.4 394 9 US-08-443-862-36 Sequence 36, Appl  
25 379.6 33.4 394 38 US-09-918-568-36 Sequence 36, Appl  
26 373 32.9 924 4 US-07-751-896-1 Sequence 1, Appl  
27 373 32.9 924 4 US-07-837-773-15 Sequence 15, Appl  
28 373 32.9 924 8 US-08-391-315-15 Sequence 15, Appl  
29 372.6 32.8 810 4 US-07-751-896-5 Sequence 5, Appl  
30 372.6 32.8 810 4 US-07-837-773-19 Sequence 19, Appl  
31 372.6 32.8 810 8 US-08-391-315-19 Sequence 19, Appl  
32 368.2 32.4 670 4 US-07-837-773-5 Sequence 5, Appl  
33 368.2 32.4 670 8 US-08-391-315-5 Sequence 5, Appl  
34 361.4 31.8 912 4 US-07-751-896-17 Sequence 17, Appl  
35 361.4 31.8 912 4 US-07-837-773-11 Sequence 31, Appl  
36 361.4 31.8 912 8 US-08-391-315-11 Sequence 31, Appl  
37 293.6 25.9 1697 51 US-10-381-085-10 Sequence 10, Appl  
38 293.6 25.9 1753 51 US-10-381-085-9 Sequence 9, Appl  
39 293.6 25.9 1753 51 US-10-381-085-11 Sequence 11, Appl  
40 280.2 23.2 729 51 US-10-381-085-12 Sequence 12, Appl  
41 263.8 23.2 729 4 US-07-751-896-3 Sequence 3, Appl  
42 263.8 23.2 729 4 US-07-751-899-3 Sequence 3, Appl  
43 263.8 23.2 729 4 US-07-837-773-17 Sequence 17, Appl  
44 263.8 23.2 729 5 US-08-021-535-3 Sequence 3, Appl  
45 263.8 23.2 729 5 US-08-021-617-3 Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-08-443-862-49  
Sequence 49, Application US/08443862  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/443,862  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 15, 1994  
APPLICATION NUMBER: 08/054,016

FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1135 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM: A/Okuda/57  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-443-862-49

Query Match 100.0%; Score 1135; DB 9; Length 1135;  
Best Local Similarity 100.0%; Pred. No. 3, 1e-287;  
Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGCAAAAGCAGGGGTTATACCATAGAAAACCAAAAGCAAAATGGCCATCTTTAT 60  
|||||  
Db 1 CTAGCAAAAGCAGGGGTTATACCATAGAAAACCAAAAGCAAAATGGCCATCTTTAT 60  
|||||  
QY 61 CTCATTCTCTGTTTCACAGCAGTGAAGAGGGACCAATATGCTTGGATACCATGCCAAT 120  
|||||  
Db 61 CTCATTCTCTGTTTCACAGCAGTGAAGAGGGACCAATATGCTTGGATACCATGCCAAT 120  
|||||  
QY 121 AATTCACAGAGAGGTCGACACATTTAGAGCGGAGTCACGTGACTATGCCAAG 180  
|||||  
Db 121 AATTCACAGAGAGGTCGACACATTTAGAGCGGAGTCACGTGACTATGCCAAG 180  
|||||  
QY 181 GACATCTTGAGAGAGCCATACGGAAGGTTATGCAAACTAAACGATCCGGATCAGT 240  
|||||

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 10, 2003, 02:11:24 ; Search time 2506.97 Seconds  
(without alignments)  
14835.212 Million cell updates/sec

Title: US-09-918-568-49  
Perfect score: 1135  
Sequence: 1 CTAGCAAGACGAGGGTTAT.....AACACCCCTGTTCTGCTAG 1135

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32997241 seqs, 16383922548 residues

Total number of hits satisfying chosen parameters: 65994482

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Pending\_Patents\_MN\_Main:\*

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- 2: /cgn2\_6/ptodata/2/pna/PCRTUS\_COMB.seq.old.\*
- 3: /cgn2\_6/ptodata/2/pna/US07\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pna/US080\_COMB.seq.\*
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- 23: /cgn2\_6/ptodata/2/pna/US095B\_COMB.seq.\*
- 24: /cgn2\_6/ptodata/2/pna/US095C\_COMB.seq.\*
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- 27: /cgn2\_6/ptodata/2/pna/US096B\_COMB.seq.\*
- 28: /cgn2\_6/ptodata/2/pna/US096C\_COMB.seq.\*
- 29: /cgn2\_6/ptodata/2/pna/US096D\_COMB.seq.\*
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- 31: /cgn2\_6/ptodata/2/pna/US097A\_COMB.seq.\*
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- 37: /cgn2\_6/ptodata/2/pna/US098D\_COMB.seq.\*
- 38: /cgn2\_6/ptodata/2/pna/US099A\_COMB.seq.\*
- 39: /cgn2\_6/ptodata/2/pna/US099B\_COMB.seq.\*
- 40: /cgn2\_6/ptodata/2/pna/US099C\_COMB.seq.\*
- 41: /cgn2\_6/ptodata/2/pna/US099D\_COMB.seq.\*
- 42: /cgn2\_6/ptodata/2/pna/US099E\_COMB.seq.\*
- 43: /cgn2\_6/ptodata/2/pna/US099F\_COMB.seq.\*

- 44: /cgn2\_6/ptodata/2/pna/US100A\_COMB.seq.\*
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- 47: /cgn2\_6/ptodata/2/pna/US101B\_COMB.seq.\*
- 48: /cgn2\_6/ptodata/2/pna/US102A\_COMB.seq.\*
- 49: /cgn2\_6/ptodata/2/pna/US102B\_COMB.seq.\*
- 50: /cgn2\_6/ptodata/2/pna/US103A\_COMB.seq.\*
- 51: /cgn2\_6/ptodata/2/pna/US103B\_COMB.seq.\*
- 52: /cgn2\_6/ptodata/2/pna/US104A\_COMB.seq.\*
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- 55: /cgn2\_6/ptodata/2/pna/US6001\_COMB.seq.\*
- 56: /cgn2\_6/ptodata/2/pna/US6002\_COMB.seq.\*
- 57: /cgn2\_6/ptodata/2/pna/US6003\_COMB.seq.\*
- 58: /cgn2\_6/ptodata/2/pna/US6004\_COMB.seq.\*
- 59: /cgn2\_6/ptodata/2/pna/US6005\_COMB.seq.\*
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- 61: /cgn2\_6/ptodata/2/pna/US6007\_COMB.seq.\*
- 62: /cgn2\_6/ptodata/2/pna/US6008\_COMB.seq.\*
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- 74: /cgn2\_6/ptodata/2/pna/US6020\_COMB.seq.\*
- 75: /cgn2\_6/ptodata/2/pna/US6021\_COMB.seq.\*
- 76: /cgn2\_6/ptodata/2/pna/US6022\_COMB.seq.\*
- 77: /cgn2\_6/ptodata/2/pna/US6023A\_COMB.seq.\*
- 78: /cgn2\_6/ptodata/2/pna/US6023B\_COMB.seq.\*
- 79: /cgn2\_6/ptodata/2/pna/US6024\_COMB.seq.\*
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- 87: /cgn2\_6/ptodata/2/pna/US6032\_COMB.seq.\*
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- 90: /cgn2\_6/ptodata/2/pna/US6035\_COMB.seq.\*
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- 94: /cgn2\_6/ptodata/2/pna/US6039\_COMB.seq.\*
- 95: /cgn2\_6/ptodata/2/pna/US6040\_COMB.seq.\*
- 96: /cgn2\_6/ptodata/2/pna/US6041\_COMB.seq.\*
- 97: /cgn2\_6/ptodata/2/pna/US6042\_COMB.seq.\*
- 98: /cgn2\_6/ptodata/2/pna/US6043\_COMB.seq.\*
- 99: /cgn2\_6/ptodata/2/pna/US6044\_COMB.seq.\*
- 100: /cgn2\_6/ptodata/2/pna/US6045\_COMB.seq.\*
- 101: /cgn2\_6/ptodata/2/pna/US6046\_COMB.seq.\*
- 102: /cgn2\_6/ptodata/2/pna/US6047\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1135	100.0	1135	US-08-443-862-49	Sequence 49, Appl
2	1135	100.0	1135	US-09-918-568-49	Sequence 49, Appl
3	908.8	80.1	1783	US-08-443-862-46	Sequence 46, Appl
4	908.8	80.1	1783	US-09-918-568-46	Sequence 46, Appl



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: FILE REFERENCE: C1001469
: CURRENT APPLICATION NUMBER: US/60/487,610
: CURRENT FILING DATE: 2003-07-17
: NUMBER OF SEQ ID NOS: 97101
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 19897
: LENGTH: 160592
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: (1)...(160592)
: OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-60-487-610-19897

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Query Match	3.7%;	Score 41.6;	DB 7;	Length 160592;
Best Local Similarity	46.1%;	Pred. No. 0.1;		
Matches 140;	Conservative 0;	Mismatches 164;	Indels 0;	Gaps 0;

QY	647	AAAGCTGTGAGAACTTGAACAAAGATGGAAGACGGTTTCTAAGATGTGTGACATACA	706
Db	125713	ACAGAGATTAACACCTGGGTTTAAATAAAGTACTAGCAAGACATCGCTTTCGTACATTAG	125655
QY	707	ATGCTGACCTTTTACTTCTGATGGAATAATGACAGCACACTTGACTTTCATGATTCATATG	766
Db	125653	ATAAAAATATTTGGTTATTTATTTGGATATTTAACCTAATTTCTAACCTTTAGGACCTTAAAA	125594
QY	767	TCAAGATCTGTATGTAGTAAGTCAGATGACATGCAGTGCAGACACAGTCCAAAGACTGGAA	826
Db	125593	CACAGATGGGGCTGTTTGTGAGGTATATTAACCTCCCATTCACGCCAAAGAAATTTAAGCA	125533
QY	827	ATGATGTTTTGGAATTTATCTCAAAATGTGATGATGATGATGATGATGATGATGATGATGATG	886
Db	125533	GAGTGTGGGTAGCCACTTTTTCGACCTCCCATTAATAAAAAATTTATCCCAATATGAGAAATACT	125474
QY	887	GGACATATGATTTATCCCAAGTATGAGAAGAGACTCTAACTAAATATAGAAATGAAATTAAG	946
Db	125473	TGACATAGTGTATTTCCAGAGCTAAGATGCTGTGTACACGACACATGTGGCGAAGCTACAG	125414
QY	947	GGGT 950	
Db	125413	GGGT 125410	

Search completed: August 10, 2003, 19:54:19  
Job time : 111.467 secs

Db 1306 CTTTTTAATACATTGAGAAAAGCTGTAGTAAATAAGGAGGCTAGAAAGACGAA 1365  
QY 666 CAAAAGATGAGAGAGCGTTCTGATGATGCGACATACATGCTGACCTTTTACTTCT 725  
Db 1366 TGGGGAAGATGAGAAAGAGTTTACACAGATGATGAGAAAGCCAGAGCTTTCAGGA 1425  
QY 726 GATGAAAATGAGAGACACTTGACTTTCATGCTTCTATGTCAGAAATCTGTATAGTAA 785  
Db 1426 AGTGAAGAAGAAAGAGATGAGATTCTCGATGAGCAGATGTCCTTCTTCAGAGCAT 1485  
QY 786 AGTCA 790  
Db 1486 GGACA 1490

RESULT 13  
US-10-286-897-452  
; Sequence 452, Application US/10286897  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq Inc  
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides  
; FILE REFERENCE: 784FLPCT  
; CURRENT APPLICATION NUMBER: US/10/286,897  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: US/09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US/09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: US/09/598,042  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: US/09/620,312  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: US/09/653,450  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: US/09/662,191  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: US/09/693,036  
; PRIOR FILING DATE: 2000-10-19  
; PRIOR APPLICATION NUMBER: US/09/727,344  
; PRIOR FILING DATE: 2000-11-29  
; NUMBER OF SEQ ID NOS: 7143  
; SOFTWARE: PL\_FL\_genes\_b Versions 1.0  
; SEQ ID NO 452  
; LENGTH: 3423  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (53)..(2800)  
US-10-286-897-452

Query Match 3.7%; Score 41.8; DB 6; Length 3423;  
Best Local Similarity 48.2%; Pred. No. 0.018; Indels 0; Gaps 0;  
Matches 118; Conservative 0; Mismatches 127;

QY 546 TCAAAAGCATTGAGATCACCACAGCTAAATCTGTGATGAAAGATAAACAC 605  
Db 1246 CTAAGAAATTTACAGAAAGCTCTTGAGATTAAGCTTTGTAGAGATAGATGAA 1305  
QY 606 CCAATTTGAGCTGTGGGAAAGAAATTCGCTACTTGAAGAAAGACTGGAGACTTGA 665  
Db 1306 CTTTATTAATACATGAGGAAAGAACTGTAGTAAATGAGAAAGCTAGAAAGACAGAA 1365  
QY 666 CAAAAGATGAGAAAGCGTTCTGATGATGTCGACATACATGCTGAGCTTTTACTTCT 725  
Db 1366 TGAGAAATGATGAAGAAAGCTTTTAGCCAGATATGATGAGAAAGCCAGAGCTTTGAGGA 1425  
QY 726 GATGAAAATGAGAGACACTTGACTTTCATGATTTCTATGTCAGAAATCTGTATAGTAA 785  
Db 1426 AGTGAAGAAGAAAGATGAGATTCTCGATGAGCAGATGTCCTTCTTCAGAGCAT 1485  
QY 786 AGTCA 790  
Db 1486 GGACA 1490

Db 1486 GGACA 1490

RESULT 14  
US-10-286-897-1473  
; Sequence 1473, Application US/10286897  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq Inc  
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides  
; FILE REFERENCE: 784FLPCT  
; CURRENT APPLICATION NUMBER: US/10/286,897  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: US/09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US/09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: US/09/598,042  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: US/09/620,312  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: US/09/653,450  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: US/09/662,191  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: US/09/693,036  
; PRIOR FILING DATE: 2000-10-19  
; PRIOR APPLICATION NUMBER: US/09/727,344  
; PRIOR FILING DATE: 2000-11-29  
; NUMBER OF SEQ ID NOS: 7143  
; SOFTWARE: PL\_FL\_genes\_b Versions 1.0  
; SEQ ID NO 1473  
; LENGTH: 11116  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (4532)..(11116)  
US-10-286-897-1473

Query Match 3.7%; Score 41.8; DB 6; Length 11116;  
Best Local Similarity 48.2%; Pred. No. 0.03;  
Matches 118; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 546 TCAAAAGCATTGAGATCACCACAGCTAAATCTGTGATGAAAGATAAACAC 605  
Db 10060 TCTAGAAATTTACAGAAAGCTCTTGAGATGAGCTTTGTAGTGAATGAAATC 10119  
QY 606 CCAATTTGAGCTGTGGGAAAGAAATTCGCTACTTGAAGAAAGACTGGAGACTTGA 665  
Db 10120 CTTTATTAATACATGAGGAAAGAACTGTAGTAAATGAGAAAGCTAGAAAGACAGAA 10179  
QY 666 CAAAAGATGAGAGAGCGTTTCTGATGATGTCGACATACATGCTGAGCTTTTACTTCT 725  
Db 10180 TGAGAAATGATGAAGAGAGTTTGTAGCAGATGATGATGAGAAAGCCAGAGCTTTCAGGA 10239  
QY 726 GATGAAAATGAGAGACACTTGACTTTCATGATTTCTATGTCAGAAATCTGTATAGTAA 785  
Db 10240 AGTGAAGAAGAAAGATGAGATTCTCGATGAGCAGATGTCCTTCTTCAGAGCAT 10299  
QY 786 AGTCA 790  
Db 10300 GGACA 10304

RESULT 15  
US-60-487-610-19897/c  
; Sequence 19897, Application US/60487610  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,  
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF



```

1  APPLICANT HUANG, Hongjin
2  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
3  TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS
4  TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
5  FILE REFERENCE: C0001469
6  CURRENT APPLICATION NUMBER US/60/487,610
7  CURRENT FILING DATE: 2003-07-17
8  NUMBER OF SEQ ID NOS: 9710
9  SOFTWARE: FastSeq for Windows Version 4.0
10 SEQ ID NO 42952
11 LENGTH: 201
12 TYPE: DNA
13 ORGANISM: Homo sapiens
14 US-60-487-610-42952

```

Query Match	4.88	Score 48.4	DB 7	Length 201
Best Local Similarity	56.28	Pred. No. 5.6e-05		
Matches 91, Conservative	0	Mismatches 71	Indels 0	Gaps 0

[illegible]

```

RESULT 7
US-60-487-610-42953
: Sequence 42953. Application US/60487610
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: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michels
: APPLICANT: HUANG, Hongjin
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-
: TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL0014469
: CURRENT APPLICATION NUMBER: US/60/487,610
: CURRENT FILING DATE: 2003-07-17
: NUMBER OF SEQ ID NOS: 97101
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 42953
: LENGTH: 201
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-60-487-610-42953

```

[illegible]

RESULT 8	
US-60-487-610-42923	
; Sequence 42923, Application	US/60487610
; GENERAL INFORMATION:	

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: APPLICANT: CARGILL, Michele
: APPLICANT: HUANG, Hongjin
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS
: TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C1001469
: CURRENT APPLICATION NUMBER: US/60/487,610
: CURRENT FILING DATE: 2003-07-17
: NUMBER OF SEQ. ID NOS: 97101
: SOFTWARE: FASTSEQ for windows Version 4.0
: SEQ. ID NO 42923
: LENGTH: 201
: TYPE: DNA
: ORGANISM: Homo sapiens
:
: US-60-487-610-42923

```

Query Match	4.2%	Score 48:	DB 7:	Length 201:
Best Local Similarity	55.6%	Pred.	No. 7.3e-05:	
Matches 90:	Conservative 1:	Mismatches 71:	Indels 0:	Gaps 0

[illegible]

```

RESULT 9
US-09-947-914-42
: Sequence 42, Application US/09947914
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig
: TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPS) LOCATED ON
: TITLE OF INVENTION: 21, METHODS OF DETECTION, AND USES THEREOF
: FILE REFERENCE: CLO01298
: CURRENT APPLICATION NUMBER: US/09/947, 914
: CURRENT FILING DATE: 2001-09-07
: NUMBER OF SEQ ID NOS: 75
: SEQ ID NO 42
: LENGTH: 1946141
: TYPE: DNA
: ORGANISM: HUMAN
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(1946141)
: OTHER INFORMATION: n = A,T,C or G
: US-09-947-914-42

```

	Query Match	Best Local Similarity	4.0% ; Score 45.2 ; DB 5 ; Length 1946141 ;
	Matches 161 ; Conservative	0 ; Mismatches 193 ; Indels	0 ; Gaps 0 ;
QY	603 CACCCATTGTAAGCTGTGGGAAGAATTCGGTAACTTAGAGAAAAGACTGGAACCTT	662	
Db	489963 CTCACATTGGAAACAATAAATAAATAATTTAAATAATTTATTAAGAAAAAATATCAACAG	490022	
QY	663 GAACAAAAAGATGGAAGACGGTCTTGATGTGTGGACATACATGCTGAGCTTTTAACT	722	
Db	490023 AGAAACCACAAACACAAATGATTTAAATTAATTAACAACAAACCATTAATGACTATAAAG	490082	
QY	723 TCTGATGGAAGATGAGAGACACTTGACTTTTCATGATCTCATTCAAGATCGTATAG	782	
Db	490083 ATTCTTTTAAAAAGGAGACACATTAATTAACCAATTGCCAATTCAGAAATAAATGTGA	490142	
QY	783 TAAAGTCAGAAATGCAGCTGAGAGACACCTGAAGAAGACTAGGAATAAGATGTTTTGAATT	842	
Db	490143 CATATACACTAATATATCTTTACCTACATCCAAGGCGCTATATAGAAAATATTTTCAGCAAAT	490202	

Db	1116	AAGGGTTTCTTGGAGGCTNTTGGTGGTTTCTTGGAAAGAGATGGGAAGCATATGTC	1175
QY	480	CGGTTGGTATGGATACATCACAGCAATGACACGGATCAGGGTATGCAGACAGAAAGA	539
Db	1176	AGGTGGCAGGATACATCTCATGAGACCATGAGATGGCAGTGGCAGCAGACCTTAA	1235
QY	540	ATCCACTCAAAAGCATTTGATGATCCACCACACAGTAAATTCGTGATTTGAAAAGAT	599
Db	1236	GAGTAGCAGAAGCATTAACACAGATTAACAAAAATCTCATTTCTTAAAGTACCTAGA	1295
QY	600	AAACACCAATTTGAAGCTGTGGGAAAGATTCGTAACCTAGAGAAAAAGACTGAGAA	659
Db	1296	AGTAAGATCTTCAAGACATAAGGGGTGCAATGATGAATCCACACAGAAATCTCGA	1355
QY	660	CTTGACAAAAAGATGGAAGCGGTTTCTAGATGTGTGCATATCAATGCTGACCTTTT	719
Db	1356	GCTGATGAGAAGTGTGATCTACAGCTGATCAATTAAGCTCCAAATAGACCTTGC	1415
QY	720	AGTTCTGATGAAAAATGAGAGACACTTGACTTTCATGATTTCAATGTCAAGATCTGA	779
Db	1416	AGCTCTGCTTCCACAGGAAGATAATTAACAGTAGAAGACATCTCTTGACACTTGA	1475
QY	780	TACTTAAGTCACATGCAAGCTGAGAGACACAGCTCAAGAACTAGGAATGGATGTTTGA	839
Db	1476	AAGAAACAGGAAGAAATGCTGGGCCCTCTGCTGTAGACATGAGGAATGGATGCTTGA	1535
QY	840	ATTTTTCCAAAATGTGATGTAATGATGAATAGTCAAAAAACGGGACATATGAT	897
Db	1536	AACCAACCAATCAACCAAGCTGTGCTAGAGAGATAGCTGTGGACCTTTAAT	1593

```

RESULT 5
US-60-487-610-19458
? Sequence 19458, Application US/60487610
? GENERAL INFORMATION:
? APPLICANT: CARGILL, Michele
? TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
? TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
? TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
? FILE REFERENCE: CU001469
? CURRENT APPLICATION NUMBER: US/60/487,610
? CURRENT FILING DATE: 2003-07-17
? NUMBER OF SEQ ID NOS: 97101
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 19458
? LENGTH: 124326
? TYPE: DNA
? ORGANISM: Homo sapiens
US-60-487-610-19458

Query Match          4.3%: Score 49.2; DB 7; Length 124326;
Best Local Similarity 55.6%; Pred. No. 0.00046;
Matches 90; Conservative 2; Mismatches 70; Indels 0; Gaps 0;

OY      849 CAAAATGCGATGATGATGCATGTAGTCTGAAAAAGGGACATATGATTATCCCAAGTA 908
        || |||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       93443 CACTTTTGAGCAGAGAGTTCAAAGCCSCCGGCCAACATGTGTAAAACCCTCATCTCATTTA 93502

OY      909 TGAAGAAGAGCTCTAAACTAATAATGAATCAAAATCAAAAGGGCTAAATTTGACGACATGGG 968
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       93503 AAAAAAAAAAATAAATAATATAATANAANNAANNAATAAAAAATAAAAAAGCTTGGCATGGT 93562

OY      969 GGTTTATCAAAATCCTTGCCATTATTCGTACAGTAGCAGGTTTC 1010
        || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       93563 GGCACATTGCTACTCCAGCCACTCCAGAGCKCTGAGCGAGGATCT 93604

```

RESULT 6  
US-60-487-610-42952  
; Sequence 42952, Application US/60487610  
; GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele

QY	583	TCTGATGATTGAAAATNTAAACACCCCAATTTGAAGCTGTGGGAAGAATTCGGTAACTTA	642
Db	1206	TGATCATTTAACAAATGACACACTAGTTTGAGCCGTTTGGAGAAGGAATTTATTAACCTTA	1265
QY	643	GAGAAAAGACTGGAGAACCTTGACAAAAAAGATGAAAGACGGGTTTCTAGATGTGGACA	702
Db	1266	GAAAGGAGAAATAGAGAAATTTAAACAAAGAAAATGGAAGACGGATTCCTAGATGTGGACT	1322
QY	703	TACAAATGCTGAGCTTTTAGTGTCTGATGGAAAATGAGACACTTGACTTTTCATATCT	762
Db	1336	TACAAATGCTGAACTTTGGTCTCTGAGAAAATGGAAGAACCTTCGACTTTTCATACCTCA	1385
QY	763	AATGTCAGAAATCTGTATAGTAAAGTCCAGAAATGCAGCTGAGACACACGTCACAAAGACTA	822
Db	1386	AATGTCAGAAACCTTTACGACAGAGTCCGACTACAGCTTAGGGATTAATGCCAAGGAACCTG	1444
QY	823	GGAATGAGATCTTTTGAATTTTATTCACAATGTGATGAATGCATGAATAGTGGAAA	882
Db	1446	GGTAAATGTTTCTTTCGAATTTCTATCCAAATGTGATGAATGATGAAGTGTAAAA	1505
QY	883	AACGGAGCATATGATATATCCACAGATGACAGAGAGAGTCAACTAATATGAATCAATC	942
Db	1506	AACGGAGCATGTGACTATCCCGCAGTATTCAGAGAGAGCAAGACTTAACAGAGAGGAATTA	1565
QY	943	AAAGGGGTAAATTTAGCAGCATGGGGGTTTATCAAAATCCTTGGCATTTATGCTACAGTA	1002
Db	1566	AGTGAGATAAATTTGGAATCAATGGGAGACTTACCAAAATATGTCATATTTATCAACAGT	1622
QY	1003	GCAGTCTATATCTATATGGCAATCATATATGCTGGAGATCTCTTTGGGTGTCTCCAAC	1066
Db	1626	GCGAGTTCCTCAGAGATGGCAATATCATGTGTACTGTCTATCTTTATGATGATGCTCCAAAT	1685
QY	1063	GGGTCTCTGCAGTGCAGGATCTGCATATGATTAAT	1096
Db	1686	GGATCGTTTACAAATCGAGAAATTTGCATTTAAATTT	1719
RESULT 2			
US-60-470-920-21			
Sequence 21, Application US/60470920			
GENERAL INFORMATION:			
APPLICANT: Luke, Catherine, J.			
APPLICANT: Vilalta, Adrian			
APPLICANT: Wiloch, Mary K.			
APPLICANT: Evans, Thomas S.			
APPLICANT: Geall, Andrew B.			
TITLE OF INVENTION: DNA Influenza Vaccine Compositions			
FILE REFERENCE: 1530 064000			
CURRENT APPLICATION NUMBER: US/60/470,920			
NUMBER OF SEQ ID NOS: 45			
SOFTWARE: PatentIn version 3.2			
SEQ ID NO 21			
LENGTH: 1714			
TYPE: DNA			
ORGANISM: Influenza A virus			
US-60-470-920-21			

	Query Match	29.4%	Score 333.6	DB 7	Length 1714
	Best Local Similarity	61.7%	Pred. No. 3.1e-91		
	Matches 531	Conservative	0	Mismatches 329	Indels 0
				Gaps 0	
QY	233 GGATCATGAAACAGAGAGACACTGTAGAACTGTGAGACCAATGCGCAATCTCTTTGG	292			
Db	855 GAATCTGAGAGACGATTAAAGGTGGTAATTTGTAGTGCATGTGCAGACTGAAAG	914			
QY	293 GAGCAATAATACACATTACCTTTTACAAATGTCACACCAGTACAAATAGTAGTGC	352			
Db	915 GTGCTTAAACAGTACATGTCATCCACAAATATACAGTAATATGCAATTTGGAACCTGCC	974			
QY	353 CCAATATGTAATAATCGGAGAAGTTGGTCTTAGCAGACGACTAAGAAATTTCTCCAGA	412			
Db	975 CCAATATGTAGAGCTTAATATGCTCAAAACCTGGAGTGGCTGTAGACACTGCTCTGTA	1034			

QY	413	TTGATCAACAGCAATGTTGGTGGGCAATAGCTGGTTTATGTAAGAGAGATGGCAAGAA	472
Db	1035	GATCAAGTAGAGGACTATTTGGACCCATGCTGATTATAGAAAGAGGTTGGCCAGAC	1094
QY	473	TGCTTGAACGGTTGTATGATATCCATCAACAGCAATGACACGGATCAGGTAATGCAGCAG	532
Db	1095	TAGTCGGCTGGGTATGCTTTCCAGCTATCCAAATGATCAAGGGGTTGGTATGGCTCGC	1154
QY	533	ACAAAGAAATCCATCCAAAAGGCATTTGATGTAATCACCAACAGGTAATCTGTGATTCG	592
Db	1155	ATAGGGAATTCACACTCAAAAGGCATTTGATTAATATACATCCAAAGGTGATATATATAGTCG	1214
QY	593	AAAAGATAACACCCCAATTTGAAAGCTGTTGGGAAAGAAATTCGTAATCTAAGAAAAGAC	652
Db	1215	ACAGATGAAACACCAATATATGTAATATTTGATCATGTAATTCAGTAGAGTTGAACCTACAC	1274
QY	653	TGGGAACCTTGACAAAAAAGATGGAAGAAGCGGTTTATGATGTGTGCACATACATGCTG	712
Db	1275	TCATATATGATCAATAATATATAGATTATGATGACCAAAATACCAAGACGTAATGGCATATATATGCAG	1334
QY	713	AGCTTTAGTTCCTATGATGGAAATATAGAGACACTGTGACTTTCATGATCTCTATATGCAGA	772
Db	1335	AATTCGTAGTACTACTTGAATAATCAAAAACACTCGATGATGACATGATGCCAAGTGAACA	1394
QY	773	ATCTGTATAGTAAAGTCAAGATGCACCTGAGACACACGTCACAAAGACTAGCAAAATGGAT	832
Db	1395	ATCTATATTAACAAAGGTGAAGAGGCGACCTGCCACTCCAAATGCTATGGAAAGATGGGAAAGGCT	1454
QY	833	GTTTGAATTTTATACAAATGATGATGTGAATGCATGAATAGTGTGAAGAAACGGAGACAT	892
Db	1455	GTTTCGAGCTATACCATTAATGTATGATGATCGATCGATCGAACAATTCGGAACGGGACCT	1514
QY	893	ATGATTTATCCCAAGTATGAGAGAGAGCTTAACTTAATTAGAATGAATCAAGAGGTTAA	952
Db	1515	ATAATATAGAGAAAGCTATAGAGAGGAATCAAGACTAGAAAGCCAAAGAAATAAGAGGGTTTA	1574
QY	953	AATTAGACACAGATGGGGTTTATCAAAATCCCTGTCATTTATGTATGTACAGTACAGGTTCTA	1012
Db	1575	AGCTGGAAATCTGAGGGAACCTTACAAAATCCCTCACCATTTTATTCGACATGTGCGCTTCATCTC	1634
QY	1013	TGTCACGTGGCAATCATGATGGCTGGGATCTCTTTCTGGGTGCTGCCAACGGGCTCTCGC	1072
Db	1635	TTTGAGCTTGCAAATGGGCTTTCCTCCCTCTGTTCTGGGCGATGTCCAAATGATCTTGCA	1694
QY	1073	AGTGCAGGATCTGCATATGA	1092
Db	1695	GATGCCAACATTTGTATATAA	1714

```

RESULT 3
US-60-470-920-17
: Sequence 17, Application US/60470920
: GENERAL INFORMATION:
: APPLICANT: Luke, Catherine, J.
: APPLICANT: Vialta, Adrian
: APPLICANT: Wlooch, Mary K.
: APPLICANT: Evans, Thomas G.
: APPLICANT: Geall, Andrew J.
: TITLE OF INVENTION: DNA Influenza Vaccine Compositions
: FILE REFERENCE: 1530.0640000
: CURRENT APPLICATION NUMBER: US/60/470,920
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 17
: LENGTH: 1220
: TYPE: DNA
: ORGANISM: Influenza A virus
: US-60-470-920-17

Query Match      17.9%      Score 203.6;  DB 7;  Length 1220;
Best Local Similarity  70.3%;  Pred. No. 8,4e-52;

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Db	792	GTCAAGATACAAGATTGATCTGTGATTTCTTTCATATCATGCTTTTGCTTG	851
QY	1008	TGTTGTTTGGCTGCTCATCATGTGGCTTGCAGAGAGCAACATTAGTGCAACAT	1067
Db	852	TGTTGTTTGGCTGCTCATCATGTGGCTTGCAGAGAGCAACATTAGTGCAACAT	911
QY	1068	TTGCATT	1074
Db	912	TTGCATT	918

Search completed: August 10, 2003, 18:58:45  
Job time : 2454.76 secs

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Db      252 TATGGGCAATATTCGGGGCAATAGCAGTTTCATAGAAAATGTTGGAGGAAATGATAGA 311
QY      468 CGGTGGTACGGTTTCAGGATCAAAATCTGTGGGACAGAGCAAGCAATCTTA 527
Db      312 CGGTGGTACGGTTTCAGGATCAAAATCTGTGGGACAGAGCAAGCAATCTTA 371
QY      528 AAGCACTCAAGCAGCCATGACCAAAATCAATGGGAATTAACAGGGTAAATCAGAGA 587
Db      372 AAGCACTCAAGCAGCCATGACCAAAATCAATGGGAATTAACAGGGTAAATCAGAGA 431
QY      588 GAACGAGAAATTCATCAAAATCGAAAAGAAATTCAGAGAATGAGAGGAATTCAGGA 647
Db      432 GAACGAGAAATTCATCAAAATCGAAAAGAAATTCAGAGAATGAGAGGAATTCAGGA 491
QY      648 CCTGAGAAATACGTTGAAGACATCAAAATAGATCTGCTTAAATGGGAGCTTCT 707
Db      492 CCTGAGAAATACGTTGAAGACATCAAAATAGATCTGCTTAAATGGGAGCTTCT 551
QY      708 TGTGCTCTGGAATCAACATACAAATGACCTGACTGCGAATGCAACAGCTGTT 767
Db      552 TGTGCTCTGGAATCAACATACAAATGACCTGACTGCGAATGCAACAGCTGTT 611
QY      768 TGAATAAACAGAGGCAACTGAGGAAAATGCTGAAGAGATGGCAATGTTGCTTCAA 827
Db      612 TGAATAAACAGAGGCAACTGAGGAAAATGCTGAAGAGATGGCAATGTTGCTTCAA 671
QY      828 AATATACCAAAATGAGCAACGCTTGACATGACAAATGCAAAATGACTATACCA 887
Db      672 AATATACCAAAATGAGCAACGCTTGACATGACAAATGCAAAATGACTATACCA 731
QY      888 TGATGTATACAGAGCAAGCAATTAACAACCGGTTTCAGATCAAAAGTGTTGAATGAA 947
Db      732 TGATGTATACAGAGCAAGCAATTAACAACCGGTTTCAGATCAAAAGTGTTGAATGAA 791
QY      948 GTCTGTATACAAAGACTGATCCTGTGATTTCTTTGCCATATCATGCTTTTGTGTTG 1007
Db      792 GTCAAGATACAAAGACTGATCCTGTGATTTCTTTGCCATATCATGCTTTTGTGTTG 851
QY      1008 TGTGTTTGTGCGGGTTCATGATGAGGCTGCGCAGAGAGCAACATTAAGTGCANAAT 1067
Db      852 TGTGTTTGTGCGGGTTCATGATGAGGCTGCGCAGAGAGCAACATTAAGTGCANAAT 911
QY      1068 TTGCATT 1074
Db      912 TTGCATT 918

```

RESULT 15

US-08-391-315-9

Sequence 9, Application US/08391315

GENERAL INFORMATION:

APPLICANT: Shatzman, Allan

APPLICANT: Scott, Miller, Allan

APPLICANT: Dillon, Susan B.

TITLE OF INVENTION: Vaccinal Polypeptides

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation - Corporate

STREET: U.S. Mailcode VW2220 - 709 Swedeland Road

CITY: King of Prussia

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19406-2799

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/391.315

FILING DATE:

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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/108, 914
FILING DATE:
APPLICATION NUMBER: US 837, 773
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 751, 896
FILING DATE: 30-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 387, 200
FILING DATE: 28-JUL-1989
ATTORNEY/AGENT INFORMATION:
NAME: Lentz, Edward T.
REGISTRATION NUMBER: 30,191
REFERENCE/DOCKET NUMBER: SBCL4224-8c1p
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-270-5013
TELEFAX: 215-270-5090
INFORMATION FOR SEQ. ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..918
US-08-391-315-9

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Query Match      57.8%; Score 641.4; DB 8; Length 918;
Best Local Similarity 97.6%; Pred. No. 5.4e-170;
Matches 651; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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QY      408 TAGAGGCTATTTCGGGCAATAGCAGTTTCATAGAAAATGTTGGAGGAATGATAGA 467
Db      252 TATGGGCAATATTCGGGGCAATAGCAGTTTCATAGAAAATGTTGGAGGAATGATAGA 311
QY      468 CGGTGGTACGGTTTCAGGATCAAAATCTGTGGGACAGAGCAAGCAATCTTA 527
Db      312 CGGTGGTACGGTTTCAGGATCAAAATCTGTGGGACAGAGCAAGCAATCTTA 371
QY      528 AAGCACTCAAGCAGCCATGACCAAAATCAATGGGAATTAACAGGGTAAATCAGAGA 587
Db      372 AAGCACTCAAGCAGCCATGACCAAAATCAATGGGAATTAACAGGGTAAATCAGAGA 431
QY      588 GAACGAGAAATTCATCAAAATCGAAAAGAAATTCAGAGAATGAGAGGAATTCAGGA 647
Db      432 GAACGAGAAATTCATCAAAATCGAAAAGAAATTCAGAGAATGAGAGGAATTCAGGA 491
QY      648 CCTGAGAAATACGTTGAAGACATCAAAATAGATCTGCTTAAATGGGAGCTTCT 707
Db      492 CCTGAGAAATACGTTGAAGACATCAAAATAGATCTGCTTAAATGGGAGCTTCT 551
QY      708 TGTGCTCTGGAATCAACATACAAATGACCTGACTGCTGCGAATGCAACAGCTGTT 767
Db      552 TGTGCTCTGGAATCAACATACAAATGACCTGACTGCTGCGAATGCAACAGCTGTT 611
QY      768 TGAATAAACAGAGGCAACTGAGGAAAATGCTGAAGAGATGGCAATGTTGCTTCAA 827
Db      612 TGAATAAACAGAGGCAACTGAGGAAAATGCTGAAGAGATGGCAATGTTGCTTCAA 671
QY      828 AATATACCAAAATGAGCAACGCTTGACATGACATCAAAATGCTTAAATGCTTAA 887
Db      672 AATATACCAAAATGAGCAACGCTTGACATGACATCAAAATGCTTAAATGCTTAA 731
QY      888 TGATGTATACAGAGCAAGCAATTAACAACCGGTTTCAGATCAAAAGTGTTGAATGAA 947
Db      732 TGATGTATACAGAGCAAGCAATTAACAACCGGTTTCAGATCAAAAGTGTTGAATGAA 791
QY      948 GTCTGTATACAAAGACTGATCCTGTGATTTCTTTGCCATATCATGCTTTTGTGTTG 1007

```

RESULT 13  
US-07-837-773-9  
Sequence 9, Application US/07837773  
GENERAL INFORMATION:  
APPLICANT: Shatzman, Allan  
APPLICANT: Scott, Miller  
APPLICANT: Dillon, Susan B.  
TITLE OF INVENTION: Vaccinal Polypeptides  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation - Corporate  
ADDRESS: Patents  
STREET: U.S. Mailcode  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/837,773  
FILING DATE: 19920218  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Canter, Carol G.  
REGISTRATION NUMBER: 81,151  
REFERENCE/DOCKET NUMBER: SHC14224-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-270-5013  
TELEFAX: 215-270-5090  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 918 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..918  
US-07-837-773-9  
Query Match 57.8%; Score 641.4; DB 4; Length 918;  
Best Local Similarity 97.6%; Pred. No. 5.4e-170;  
Matches 651; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 408 TAGAGGCTATTTCGGCCCAATAGCAGGTTTCATAGAAAATGGTTGGGAGGAATGATAGA 467  
DB 252 TATGGGATATTCGGCCGATAGCAGGTTTCATAGAAAATGGTTGGGAGGAATGATAGA 311  
QY 468 CGTTGGTACGGTTTCAGGCATCAAAATTCAGAGGCACAGACACAGATCTTAA 527  
DB 312 CGTTGGTACGGTTTCAGGCATCAAAATTCAGAGGCACAGACACAGATCTTAA 371  
QY 528 AAGACCTAAGCAGCCTATCGACCAATTCAGGAATTCGAAGGTTATTCGAGAGAC 587  
DB 372 AAGACCTAAGCAGCCTATCGACCAATTCAGGAATTCGAAGGTTATTCGAGAGAC 431  
QY 588 GAACGAGAATTCCTCAAAATCGAAAAGAAATTCAGAGTGAAGGAGAAATTCGGA 647  
DB 432 GAACGAGAATTCCTCAAAATCGAAAAGAAATTCAGAGTGAAGGAGAAATTCGGA 491  
QY 648 CCTCGAAGAAATAGCTTGAAGACACTAAATAGATCTCTGCTTCAATCGGAGCTTCT 707  
DB 492 CCTCGAAGAAATAGCTTGAAGACACTAAATAGATCTCTGCTTCAATCGGAGCTTCT 551  
QY 708 TGTGCGCTTGAGAGATCAACATACCAATTCGACTGACTGGAATTCGAACAGCTGT 767  
DB 552 TGTGCGCTTGAGAGATCAACATACCAATTCGACTGACTGGAATTCGAACAGCTGT 611

QY 768 TGAACAAAACAGAGCACTGAGGAAATGCTGAAGATGGCAATGTTCTTCAA 827  
DB 612 TGAACAAAACAGAGCACTGAGGAAATGCTGAAGATGGCAATGTTCTTCAA 671  
QY 828 AATATACCACAAATGTGACAAACGCTTCATAGACTCAATGAAATGTAATATGACCA 887  
DB 672 AATATACCACAAATGTGACAAATGCTTCATAGAGTCAATGAAATGTAATATGACCA 731  
QY 888 TGATGTATACGAGACGAGCATTTAAACACCGCTTCAGATCAAAAGTGTGACTGAA 947  
DB 732 TGATGTATACGAGACGAGCATTTAAACACCGCTTCAGATCAAAAGTGTGACTGAA 791  
QY 948 GTCTGATATACAAAGCTGATCCTGTGATTTCTTCCATATCATGCTTTTGTG 1007  
DB 792 GTCTGATATACAAAGCTGATCCTGTGATTTCTTCCATATCATGCTTTTGTG 851  
QY 1008 TGTGTTTGTGCTGGGTTTCATCATGTGGGCTGACAGAGCAACATTAAGTCAACAT 1067  
DB 852 TGTGTTTGTGCTGGGTTTCATCATGTGGGCTGACAGAGCAACATTAAGTCAACAT 911  
QY 1068 TTGCATT 1074  
DB 912 TTGCATT 918  
RESULT 14  
US-08-013-415-5  
Sequence 5, Application US/08013415  
GENERAL INFORMATION:  
APPLICANT: Shatzman, Allan  
APPLICANT: Kane, James  
TITLE OF INVENTION: Modified Influenza Sequences  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation - Corporate  
ADDRESS: Patents  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/013,415  
FILING DATE: 19930201  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Canter, Carol G.  
REGISTRATION NUMBER: 31,151  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5015  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 918 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..915  
US-08-013-415-5  
Query Match 57.8%; Score 641.4; DB 5; Length 918;  
Best Local Similarity 97.6%; Pred. No. 5.4e-170;  
Matches 651; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 408 TAGAGGCTATTTCGGCCCAATAGCAGGTTTCATAGAAAATGTTGGAGGAGATGATAGA 467



ADDRESSEE: Patents  
STREET: U.S. Mailcode VW2220 - 709 Swedeland Road  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA  
APPLICATION NUMBER: US/07/837,773  
FILING DATE: 19920218  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Canter, Carol G.  
REGISTRATION NUMBER: 31,151  
REFERENCE/DOCKET NUMBER: SBC14224-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-270-5013  
TELEFAX: 215-270-5090  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 666 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..663  
US-07-837-773-3

Query Match 57.8%; Score 642; DB 4; Length 666;  
Best Local Similarity 97.7%; Pred. No. 3.2e-170;  
Matches 651; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

412 GGCCATATCGGCCCATATGACAGGTTTCATGAAATGTTGGGAGGGAATGATAGACGGT 471  
1 GGCATATTCGGCCCATATGACAGGTTTCATGAAATGTTGGGAGGGAATGATAGACGGT 60

472 TGGTACGGTTTCAGGATATCAAAATTCAGAGGACAGAGACAGACAGATCTTAAAGC 531  
1 TGGTACGGTTTCAGGATATCAAAATTCAGAGGACAGAGACAGACAGATCTTAAAGC 120

61 TGGTACGGTTTCAGGATATCAAAATTCAGAGGACAGAGACAGACAGATCTTAAAGC 120

532 ACTCAAGCAGCCATCAACCAATCAATGGGAATTTGACAGGGTATTCGAAGACGAC 591  
1 ACTCAAGCAGCCATCAACCAATCAATGGGAATTTGACAGGGTATTCGAAGACGAC 180

121 ACTCAAGCAGCCATCAACCAATCAATGGGAATTTGACAGGGTATTCGAAGACGAC 180

592 GAGAAATTCATCAATTCGAAAAGGAATTCAGAAAGTACAGAGGGAATTCAGAGCCTC 651  
1 GAGAAATTCATCAATTCGAAAAGGAATTCAGAAAGTACAGAGGGAATTCAGAGCCTC 240

181 GAGAAATTCATCAATTCGAAAAGGAATTCAGAAAGTACAGAGGGAATTCAGAGCCTC 240

652 GAGAAATTCATCAATTCGAAAAGGAATTCAGAAAGTACAGAGGGAATTCAGAGCCTC 711  
1 GAGAAATTCATCAATTCGAAAAGGAATTCAGAAAGTACAGAGGGAATTCAGAGCCTC 300

241 GAGAAATTCATCAATTCGAAAAGGAATTCAGAAAGTACAGAGGGAATTCAGAGCCTC 300

712 GCCTCGAGAAATCAATATACAAATTCGACTGACTCGAATTCGAACAGCTGTTTGA 771  
1 GCCTCGAGAAATCAATATACAAATTCGACTGACTCGAATTCGAACAGCTGTTTGA 360

301 GCCTCGAGAAATCAATATACAAATTCGACTGACTCGAATTCGAACAGCTGTTTGA 360

772 AAAACAAGAGGCAATTCAGAGGAAATGCTGAGAGAGTGGCAATGTTCTTCAAAATA 831  
1 AAAACAAGAGGCAATTCAGAGGAAATGCTGAGAGAGTGGCAATGTTCTTCAAAATA 420

361 AAAACAAGAGGCAATTCAGAGGAAATGCTGAGAGAGTGGCAATGTTCTTCAAAATA 420

832 TACCACAATGTGACAAAGCTTCATAGAGTCAATCAGAAATGCTACTTATGACCATGAT 891  
1 TACCACAATGTGACAAAGCTTCATAGAGTCAATCAGAAATGCTACTTATGACCATGAT 480

421 TACCACAATGTGACAAAGCTTCATAGAGTCAATCAGAAATGCTACTTATGACCATGAT 480

892 GTTATCAGAGAGCAATCATTAACAACCGGTTTCAGATCAAAAGTGTGAACTGAAGTCT 951  
1 GTTATCAGAGAGCAATCATTAACAACCGGTTTCAGATCAAAAGTGTGAACTGAAGTCT 540

952 GGATCAAAAGACATGATCCTGTGATTTCTTTGCCATATCATGCTTTTGTGCTT 1011  
1 GGATCAAAAGACATGATCCTGTGATTTCTTTGCCATATCATGCTTTTGTGCTT 600

541 GGATCAAAAGACATGATCCTGTGATTTCTTTGCCATATCATGCTTTTGTGCTT 600

1012 GTTTTGTGCGGTTTCATCATATGATGGCCCTGCCAGAGGCAACATTAAGTCAACATTTGC 1071  
1 GTTTTGTGCGGTTTCATCATATGATGGCCCTGCCAGAGGCAACATTAAGTCAACATTTGC 660

601 GTTTTGTGCGGTTTCATCATATGATGGCCCTGCCAGAGGCAACATTAAGTCAACATTTGC 660

1072 ATTTGA 1077  
1 ATTTGA 666

661 ATTTGA 666

RESULT 11  
US-08-013-415-3  
Sequence 3, Application US/08013415  
GENERAL INFORMATION:  
APPLICANT: Shatzman, Allan  
APPLICANT: Kane, James  
TITLE OF INVENTION: Modified Influenza Sequences  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: SmithKline Beecham Corporation - Corporate  
ADDRESS: Patents  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/013,415  
FILING DATE: 19930201  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Canter, Carol G.  
REGISTRATION NUMBER: 31,151  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5015  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 666 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..663  
US-08-013-415-3

Query Match 57.8%; Score 642; DB 5; Length 666;  
Best Local Similarity 97.7%; Pred. No. 3.2e-170;  
Matches 651; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

412 GGCCATATCGGCCCATATGACAGGTTTCATGAAATGTTGGGAGGGAATGATAGACGGT 471  
1 GGCATATTCGGCCCATATGACAGGTTTCATGAAATGTTGGGAGGGAATGATAGACGGT 60

472 TGGTACGGTTTCAGGATATCAAAATTCAGAGGACAGAGACAGACAGATCTTAAAGC 531  
1 TGGTACGGTTTCAGGATATCAAAATTCAGAGGACAGAGACAGACAGATCTTAAAGC 120

61 TGGTACGGTTTCAGGATATCAAAATTCAGAGGACAGAGACAGACAGATCTTAAAGC 120

532 ACTCAAGCAGCCATCAACCAATCAATGGGAATTTGACAGGGTATTCGAAGACGAC 591  
1 ACTCAAGCAGCCATCAACCAATCAATGGGAATTTGACAGGGTATTCGAAGACGAC 180





```
Db 1256 TCAATCGAAGGAAATTCAGAGTAGAAGGAAATTCAGAGCTCGAAGAAATACGT 1315
QY 663 TGAAGACCTAAATAGATCTGTGTACATCGGAGCTTCTGTGCTGTGAGAA 722
Db 1316 TGAAGACCTAAATAGATCTGTGTACATCGGAGCTTCTGTGCTGTGAGAA 1375
QY 723 TCAACATCAATTTGACTGACTGACTGCGAAATGAACAAGCTGTTGAAAAACAAGAG 782
Db 1376 CCAACATCAATTTGACTGACTGACTGCGAAATGAACAAGCTGTTGAAAAACAAGAG 1435
QY 783 GCAACTGAGGAGAAATGCTGAAGATGGGCAATGCTTCAAAATATACCAAAATG 842
Db 1436 GCAACTGAGGAGAAATGCTGAAGATGGGCAATGCTTCAAAATATACCAAAATG 1495
QY 843 TGACAACTGCTGATAGATGATGAGAAATGCTTATGACATGATGATGATGAGAG 902
Db 1496 TGACAACTGCTGATAGATGATGAGAAATGCTTATGACATGATGATGATGAGAG 1555
QY 903 CGAAGCATTTAAACAACCGGTTTCAGATCAAAAGGTTGAAGTGAAGTGTGATACAAAG 962
Db 1556 CGAAGCATTTAAACAACCGGTTTCAGATCAAAAGGTTGAAGTGAAGTGTGATACAAAG 1615
QY 963 CTGATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1022
Db 1616 CTGATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1675
QY 1023 GTTATCATGATGAGGCTGCGAGAGAGCAACATTAAGTGCACATTTGATGATGAT 1082
Db 1676 GTTATCATGATGAGGCTGCGAGAGAGCAACATTAAGTGCACATTTGATGATGAT 1735
QY 1083 TTAGTAATTTAAACAACCGCTGTTTCT 1109
Db 1736 TTAGTAATTTAAACAACCGCTGTTTCT 1762
```

```
RESULT 6
US-10-311-581-21
; Sequence 21, Application US/10311581
; GENERAL INFORMATION:
; APPLICANT: American Cyanamid Company
; TITLE OF INVENTION: Nucleotide Sequence of Influenza A/udorn/72 (H3N2)
; TITLE OF INVENTION: Genome
; FILE REFERENCE: AM100289PCT
; CURRENT APPLICATION NUMBER: US/10/311,581
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/213,650
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Influenza A virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30)..(1727)
US-10-311-581-21
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Query Match 75.0%; Score 832; DB 50; Length 1764;
Best Local Similarity 97.7%; Freq. No. 8,36-224;
Matches 844; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
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QY 243 TATGATACCTGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATG 302
Db 896 TATGATACCTGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATG 955
QY 303 CTTTCAAAAGCTAAACAGATACATATGAGCATGCCCAAGTATGTTAAGCAAAACAC 362
Db 956 CTTTCAAAAGCTAAACAGATACATATGAGCATGCCCAAGTATGTTAAGCAAAACAC 1015
QY 363 CTTGAGCTTGGCAACAGGATGCGGAATGTACCAAGAAACAACTAGAGGCTTATCGG 422
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Db 1016 CCTGAAGTTGGCAACAGGATGCGGAATGTACCAAGAAACAACTAGAGGCTTATCGAG 1075
QY 423 CCGAATAGCAGGTTTCATAGAAATGCTTGGAGGAAATGATAGAGGTTGATGAGTT 482
Db 1076 CCGAATAGCAGGTTTCATAGAAATGCTTGGAGGAAATGATAGAGGTTGATGAGTT 1135
QY 483 CAGGATCAAAATTTCTGAGGCGACAGAGACACAGATCTTAAAGCACTCAACAGAGC 542
Db 1136 CAGGATCAAAATTTCTGAGGCGACAGAGACACAGATCTTAAAGCACTCAACAGAGC 1195
QY 543 CATGAGCAAAATTCAGGAAATGAAACAGGTTATTCAGAGAGAGAGAGAGAGAGAGAG 602
Db 1196 CATGAGCAAAATTCAGGAAATGAAACAGGTTATTCAGAGAGAGAGAGAGAGAGAGAG 1255
QY 603 TCAAAATCGAAGAAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 662
Db 1256 TCAAAATCGAAGAAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1315
QY 663 TGAAGACACTAAATATGATCTGTGCTTACATGCGGAGCTTCTTGTGCTGTGAGAGAA 722
Db 1316 TGAAGACACTAAATATGATCTGTGCTTACATGCGGAGCTTCTTGTGCTGTGAGAGAA 1375
QY 723 TCAACATCAATTTGACTGACTGACTGCGAAATGAACAAGCTGTTGAAAAACAAGAG 782
Db 1376 CCAACATCAATTTGACTGACTGACTGCGAAATGAACAAGCTGTTGAAAAACAAGAG 1435
QY 783 GCAACTGAGGAGAAATGCTGAAGATGGGCAATGCTTCAAAATATACCAAAATG 842
Db 1436 GCAACTGAGGAGAAATGCTGAAGATGGGCAATGCTTCAAAATATACCAAAATG 1495
QY 843 TGACAACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 902
Db 1496 TGACAACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1555
QY 903 CGAAGCATTTAAACAACCGGTTTCAGATCAAAAGGTTGAAGTGAAGTGTGATACAAAG 962
Db 1556 CGAAGCATTTAAACAACCGGTTTCAGATCAAAAGGTTGAAGTGAAGTGTGATACAAAG 1615
QY 963 CTGATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1022
Db 1616 CTGATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1675
QY 1023 GTTATCATGATGAGGCTGCGAGAGCAACATTAAGTGCACATTTGATGATGAT 1082
Db 1676 GTTATCATGATGAGGCTGCGAGAGCAACATTAAGTGCACATTTGATGATGAT 1735
QY 1083 TTAGTAATTTAAACAACCGCTGTTTCT 1106
Db 1736 TTAGTAATTTAAACAACCGCTGTTTCT 1759
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```
RESULT 7
US-07-837-773-1
; Sequence 1, Application US/07837773
; GENERAL INFORMATION:
; APPLICANT: Shatzman, Allan
; APPLICANT: Scott, Miller
; APPLICANT: Dillon, Susan B.
; TITLE OF INVENTION: Vaccinal Polypeptides
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corporate
; STREET: U.S. Mailcode VM2220 - 709 Swedeland Road
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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CELL LINE: <Unknown>  
ORGANELL: <Unknown>  
IMMEDIATE SOURCE:  
LIBRARY: <Unknown>  
CLONE: <Unknown>  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: <Unknown>  
MAP POSITION: <Unknown>  
UNITS: <Unknown>  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 54;  
US-09-918-568-54

Query Match 78.2%; Score 868; DB 38; Length 1777;  
Best Local Similarity 100.0%; Pred. No. 5,4e-234;  
Matches 868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 TATTGATACCTGTTATTTCTGTAATGATCACCCTCAATGGAAGCATTTCCCATGACAGCC 302  
DB 903 TATTGATACCTGTTATTTCTGTAATGATCACCCTCAATGGAAGCATTTCCCATGACAGCC 962  
QY 303 CTTTCAAAACGTAA/CAAGATCATATGAGCATGCCCAAGTATGTTAAGCAAAACAC 362  
DB 963 CTTTCAAAACGTAA/CAAGATCATATGAGCATGCCCAAGTATGTTAAGCAAAACAC 1022  
QY 363 CCTAAGTTGGCA/AGGATGCGGAATGTRACAGAAACAACTAGAGCCATTTCGG 422  
DB 1023 CCTAAGTTGGCA/AGGATGCGGAATGTRACAGAAACAACTAGAGCCATTTCGG 1082  
QY 423 CGCAATGACAGGTT/CTATGAAATGGTTGGAGGAGATGATAGCGTTGCTACGGTTT 482  
DB 1083 CGCAATGACAGGTT/CTATGAAATGGTTGGAGGAGATGATAGCGTTGCTACGGTTT 1142  
QY 483 CAGGCATCAAAATTTGAGGGCACAGACAGAGATCTTAAAGCACTCAAGAGC 542  
DB 1143 CAGGCATCAAAATTTGAGGGCACAGACAGAGATCTTAAAGCACTCAAGAGC 1202  
QY 543 CATGACCAATCA/TTGGGAATTTGAACAGGGTATTCGAGAAGACGAGAGAAATTTCA 602  
DB 1203 CATGACCAATCA/TTGGGAATTTGAACAGGGTATTCGAGAAGACGAGAGAAATTTCA 1262  
QY 603 TCAATGAGAAAGG/ATTTCTCAGAGTGAAGAGGAGATTCAGGACCTCCAGAAATTCGT 662  
DB 1263 TCAATGAGAAAGG/ATTTCTCAGAGTGAAGAGGAGATTCAGGACCTCCAGAAATTCGT 1322  
QY 663 TGAAGACACTAA/ATGATCTCTGGTTTACAAATGCGAGCTTCTTCCCTCGAGAA 722  
DB 1323 TGAAGACACTAA/ATGATCTCTGGTTTACAAATGCGAGCTTCTTCCCTCGAGAA 1382  
QY 723 TCAACATCAATTA/CTGACTGACTGGAATGAAATGACAGCTGTTTCAAAAACAGAG 782  
DB 1383 TCAACATCAATTA/CTGACTGACTGGAATGAAATGAAAGCTGTTTCAAAAACAGAG 1442  
QY 783 GCAACTGAGGAGAA/TTGCTGAAGAGATGGCAATGTTGCTCAAAATATACCAAAATG 842  
DB 1443 GCAACTGAGGAGAA/TTGCTGAAGAGATGGCAATGTTGCTCAAAATATACCAAAATG 1502

QY 843 TGACACGCTTGATAGATGATCAGAAATGTTACTATGACCATGATGTATACAGAGA 902  
DB 1503 TGACACGCTTGATAGATGATCAGAAATGTTACTATGACCATGATGTATACAGAGA 1562  
QY 903 CGAAGCATTTAAACAACCGGTTTCAGATCAAAAGTGTGAACTGAAAGTGTGATCAAGA 962  
DB 1563 CGAAGCATTTAAACAACCGGTTTCAGATCAAAAGTGTGAACTGAAAGTGTGATCAAGA 1622  
QY 963 CTGATCCTGTGATTTCTTCCATATATCATGCTTTTGTGTTGTTGCTGGG 1022  
DB 1623 CTGATCCTGTGATTTCTTCCATATATCATGCTTTTGTGTTGTTGCTGGG 1682  
QY 1023 GTTCATCATGTTGGGCTTGGCCAGAGAGCAACATTAGGCAACATTTGATGAGTA 1082  
DB 1683 GTTCATCATGTTGGGCTTGGCCAGAGAGCAACATTAGGCAACATTTGATGAGTA 1742  
QY 1083 TTAGTAATTTAAACACCCCTGTTTCTG 1110  
DB 1743 TTAGTAATTTAAACACCCCTGTTTCTG 1770

## RESULT 5

US-10-311-581-7  
Sequence 7, Application US/10311581  
GENERAL INFORMATION:  
APPLICANT: American Cyanamid Company  
TITLE OF INVENTION: Nucleotide Sequence of Influenza A/Usorn/72 (H3N2)  
TITLE OF INVENTION: Genome  
FILE REFERENCE: AM100289PCT  
CURRENT APPLICATION NUMBER: US/10/311,581  
CURRENT FILING DATE: 2002-12-16  
PRIOR APPLICATION NUMBER: 60/213,650  
PRIOR FILING DATE: 2000-06-23  
NUMBER OF SEQ ID NOS: 117  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 1765  
TYPE: DNA  
ORGANISM: Influenza A virus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (30)..(1727)  
US-10-311-581-7

Query Match 75.1%; Score 833.4; DB 50; Length 1765;  
Best Local Similarity 97.6%; Pred. No. 3.3e-224;  
Matches 846; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 243 TATTGATACCTGTTATTTCTGTAATGATCACCCTCAATGGAAGCATTTCCCATGACAGCC 302  
DB 896 TATTGATACCTGTTATTTCTGTAATGATCACCCTCAATGGAAGCATTTCCCATGACAGCC 955  
QY 303 CTTTCAAAACGTAA/CAAGATCATATGAGCATGCCCAAGTATGTTAAGCAAAACAC 362  
DB 956 CTTTCAAAACGTAA/CAAGATCATATGAGCATGCCCAAGTATGTTAAGCAAAACAC 1015  
QY 363 CCTAAGTTGGCA/AGGATGCGGAATGTRACAGAAACAACTAGAGCCATTTCGG 422  
DB 1016 CCTAAGTTGGCA/AGGATGCGGAATGTRACAGAAACAACTAGAGCCATTTCGG 1075  
QY 423 CGCAATGACAGGTT/CTATGAAATGGTTGGAGGAGATGATAGCGTTGCTACGGTTT 482  
DB 1076 CGCAATGACAGGTT/CTATGAAATGGTTGGAGGAGATGATAGCGTTGCTACGGTTT 1135  
QY 483 CAGGCATCAAAATTTGAGGGCACAGACAGAGATCTTAAAGCACTCAAGAGC 542  
DB 1136 CAGGCATCAAAATTTGAGGGCACAGACAGAGATCTTAAAGCACTCAAGAGC 1195  
QY 543 CATGACCAATCA/TTGGGAATTTGAACAGGGTATTCGAGAAGACGAGAGAAATTTCA 602  
DB 1196 CATGACCAATCA/TTGGGAATTTGAACAGGGTATTCGAGAAGACGAGAGAAATTTCA 1255  
QY 603 TCAATGAGAAAGG/ATTTCTCAGAGTGAAGAGGAGATTCAGGACCTCCAGAAATTCGT 662

CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
VOLUME:  
ISSUE:  
PAGES:  
DATE:  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-443-862-54

Query Match 78.2%; Score 868; DB 9; Length 1777;  
Best Local Similarity 100.0%; Pred. No. 5.4e-234;  
Matches 868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 TATTGATACCTGATTTCTGATGATCATCTCCAAATGAGAGCATTCCTCAATGACAAAGC 302  
|||||  
Db 903 TATTGATACCTGATTTCTGATGATCATCTCCAAATGAGAGCATTCCTCAATGACAAAGC 962  
QY 303 CTTTCAAAAGCTAAACAGATCACATATGAGCATGCCCAAGTATGTTAAGCAAAACAC 362  
|||||  
Db 963 CTTTCAAAAGCTAAACAGATCACATATGAGCATGCCCAAGTATGTTAAGCAAAACAC 1022  
QY 363 CCTGAGTTGGACAGGAGATGCGAATGTACCAAGAAACAAACAGAGGCGCTATTGGG 422  
|||||  
Db 1023 CCTGAGTTGGACAGGAGATGCGAATGTACCAAGAAACAAACAGAGGCGCTATTGGG 1082  
QY 423 CGCAATAGCAGGTTTCATAGAAATGTTGGAGGGAATGATAGAGGTTGTTACGCTTT 482  
|||||  
Db 1083 CGCAATAGCAGGTTTCATAGAAATGTTGGAGGGAATGATAGAGGTTGTTACGCTTT 1142  
QY 483 CAGGATCAAAATTTCTGAGGCGACAGACAGCAGATCTTAAAGCACTCAAGCAGC 542  
|||||  
Db 1143 CAGGATCAAAATTTCTGAGGCGACAGACAGCAGATCTTAAAGCACTCAAGCAGC 1202  
QY 543 CATGACCAATTCATGGAATTAACAGGTTATCGAAGAGCAAGCAAGCAAAATTCGA 602  
|||||  
Db 1203 CATGACCAATTCATGGAATTAACAGGTTATCGAAGAGCAAGCAAGCAAAATTCGA 1262  
QY 603 TCAATCGAAAGGAATTCAGAGTGAAGGGAATTCAGAGCTCGAGAAATACGT 662  
|||||  
Db 1263 TCAATCGAAAGGAATTCAGAGTGAAGGGAATTCAGAGCTCGAGAAATACGT 1322  
QY 663 TGAAGACACTAAATAGATCTCTGCTTCAATCGGAGCTTCTTGCTCTGAGAA 722  
|||||  
Db 1323 TGAAGACACTAAATAGATCTCTGCTTCAATCGGAGCTTCTTGCTCTGAGAA 1382  
QY 723 TCAACATCAATTTGACTGACTGATCGGAATGAACAAGCTGTTGAAAAACAAGAG 782  
|||||  
Db 1383 TCAACATCAATTTGACTGACTGATCGGAATGAACAAGCTGTTGAAAAACAAGAG 1442  
QY 783 GCAACTGAGGAAATGCTGAAGAGATGGCAATGTTGCTCAAAATATACCAAAATG 842  
|||||  
Db 1443 GCAACTGAGGAAATGCTGAAGAGATGGCAATGTTGCTCAAAATATACCAAAATG 1502  
QY 843 TGACACGCTTGATAGATGATCAATGAGAAATGTTACTTATGACATGATGTATACAGAG 902  
|||||  
Db 1503 TGACACGCTTGATAGATGATCAATGAGAAATGTTACTTATGACATGATGTATACAGAG 1562  
QY 903 CGAAGCATTAACAACCGGTTTCAGATCAAAAGGTGTTGACTGAAGTCTGAGTATACAGAG 962  
|||||  
Db 1563 CGAAGCATTAACAACCGGTTTCAGATCAAAAGGTGTTGACTGAAGTCTGAGTATACAGAG 1622

QY 963 CTGATCTCTGTGATTTCTCTTGCATATCATGCTTTTGTGCTTTGTGTTTCTGCG 1022  
|||||  
Db 1623 CTGATCTCTGTGATTTCTCTTGCATATCATGCTTTTGTGCTTTGTGTTTCTGCG 1682  
QY 1023 GTTCATCATGTGGGCTGCGACAGAGCAACATTTAGGCAACATTTGATTTAGTGA 1082  
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Db 1683 GTTCATCATGTGGGCTGCGACAGAGCAACATTTAGGCAACATTTGATTTAGTGA 1742  
QY 1083 TTGATTAATAAACAACCTGTTCTGTG 1110  
|||||  
Db 1743 TTGATTAATAAACAACCTGTTCTGTG 1770

RESULT 4  
US-09-918-568-54  
Sequence 54, Application US/09918568  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKUNO et al.  
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/918,568  
FILING DATE: 02-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/004,422  
FILING DATE: January 8, 1998  
APPLICATION NUMBER: 08/443,862  
FILING DATE: May 22, 1995  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/054,016  
FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1777 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL: <Unknown>  
ANTI-SENSE: <Unknown>  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
ORGANISM: A2/Aich1/2/68  
STRAIN: <Unknown>  
INDIVIDUAL ISOLATE: <Unknown>  
DEVELOPMENTAL STAGE: <Unknown>  
HAPLOTYPE: <Unknown>  
TISSUE TYPE: <Unknown>  
CELL TYPE: <Unknown>

PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
SEQUENCE DESCRIPTION: SEQ ID NO: 57:  
US-09-918-568-57

Query Match 100.0%; Score 1110; DB 38; Length 1110;  
Best Local Similarity 100.0%; Pred. No. 1.5e-302;  
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 61 ATTTCTGTGGCTCTGGCCAGACCTTCAGAAATGACACAGACGACGACGCTG 120
DB 61 ATTTCTGTGGCTCTGGCCAGACCTTCAGAAATGACACAGACGACGACGCTG 120
OY 121 TGCCCTGGACATCATGCGGTGCCAAAGCGAACTAGTGAAGCAATCAGATGATCAG 180
DB 121 TGCCCTGGACATCATGCGGTGCCAAAGCGAACTAGTGAAGCAATCAGATGATCAG 180
OY 181 ATTGAAGTACTAATGCTACTGAGCTAGTTCAGAGCTCTCAAGGGGAAATATGCAC 240
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OY 301 CCCTTTCAAAAGCTAACAGATCATATGAGGACATCCCAATGATATTAGCAAAAC 360
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OY 361 ACCCTGAAGTGGCTACAGGATGCGGATGTACAGAGAAACAACTAGAGGCTATTC 420
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OY 421 GGGCCAAATAGCAGGTTTCATAGAAATGTTGGAGGGAATGATAGAGCGTTGAGCGT 480
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OY 481 TTCAGGATCAAAATTCAGAGGCAAGGACAGACAGATCTTAAAGCAGCTCAAGCA 540
DB 481 TTCAGGATCAAAATTCAGAGGCAAGGACAGACAGATCTTAAAGCAGCTCAAGCA 540
OY 541 GCCATCGACCAATTAATGGAAATGGAAGGGAATGCGAGAGAGCAAGCAAAATTC 600
DB 541 GCCATCGACCAATTAATGGAAATGGAAGGGAATGCGAGAGAGCAAGCAAAATTC 600
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OY 661 GTTGAAGACACTAATATAGATCTCTGCTTACATCGGAGCTTCTTGTGCTCTGAG 720
DB 661 GTTGAAGACACTAATATAGATCTCTGCTTACATCGGAGCTTCTTGTGCTCTGAG 720
OY 721 AATCAACATACATGACTGACTGACTCGGAATGAACAAGCTGTTGAAAAAACAAG 780
DB 721 AATCAACATACATGACTGACTGACTCGGAATGAACAAGCTGTTGAAAAAACAAG 780
OY 781 AGGCACTGAGGGAATATGCTGAAGAGATGGCAATGTTGCTTCAAAATATACACAAA 840
DB 781 AGGCACTGAGGGAATATGCTGAAGAGATGGCAATGTTGCTTCAAAATATACACAAA 840
OY 841 TGTGACAAGCGTTGATAGAGTCAATGAAATGTACTATGACCATGATGATACAGA 900
DB 841 TGTGACAAGCGTTGATAGAGTCAATGAAATGTACTATGACCATGATGATACAGA 900
OY 901 GAGCAAGCATTAAGAACCGGTTTCAGATCAAAAGTGTAAAGTGAAGTCTGATACAA 960
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DB 1021 GGGTTTCATCATGTGGGCTGCGAGAGAGCAACATTTAGTCAACATTTGATGACTG 1080
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DB 1081 TATTAGTAAATTAACACCCCTGTTCTG 1110

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## RESULT 3

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US-08-443-862-54
; Sequence 54, Application US/08443862
; GENERAL INFORMATION:
; APPLICANT: Yoshinobu OKUNO et al.
; TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,862
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,781
; FILING DATE: April 19, 1994
; APPLICATION NUMBER: 08/054,016
; FILING DATE: April 29, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1777 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: A2/A1ch1/2/68
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:

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      241 AATATTGATACCTGATTTCTGATGATGATCACTCCAAATGGAAGCATTCCTCAATGCAAG 300
      301 CCCTTTCAAAACGTAAACAGATCAATATGAGAGCATGCCCAAGTATGTTAAAGCAAAAC 360
      301 CCCTTTCAAAACGTAAACAGATCAATATGAGAGCATGCCCAAGTATGTTAAAGCAAAAC 360
      361 ACCCTGAAGTTGGCAACAGGGATGGGGAATGTACCAAGAAACAACTAGAGCCATATTC 420
      361 ACCCTGAAGTTGGCAACAGGGATGGGGAATGTACCAAGAAACAACTAGAGCCATATTC 420
      421 GGGCAATAGCAGGTTTCTATAGAAATGGTTGGAGGGAATGATAGACGGTGGTACGGT 480
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      541 GCCATCGACCAATATGAGGGAATTTGAACAGGATATGAGAAGACGACGAGAAATTC 600
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      601 CATCAATTCGAAAAAGGAATTTCTCAGAGAGTAAAGAGGAGAAATTCAGAGCTCGAAGATC 660
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      721 AATCAACATACATTTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
      721 AATCAACATACATTTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
      781 AGGCAACATGAGGAAATGCTGAAGAGATGGGCAATGGTCTTCAAAATATACCAAA 840
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      841 TGTGACAAACGCTTGCATAGATGATCAGAAATGTACTATAGACATGATATACAGA 900
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      901 GACGACATTAACAAACCGGTTTCAATCAAAAGTGTGAAGTGTGATGATCAAA 960
      901 GACGACATTAACAAACCGGTTTCAATCAAAAGTGTGAAGTGTGATGATCAAA 960
      961 GACTGATCCTGTGATTTCTTCCATATCATGCTTTTCTTCTTCTTCTTCTTCTG 1020
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      1021 GGGTTTCATCATGTGGGCTTCCAGAGAGGCAACATTAAGTGCACATTTGAGTG 1080
      1021 GGGTTTCATCATGTGGGCTTCCAGAGAGGCAACATTAAGTGCACATTTGAGTG 1080
      1081 TATTAGTATTAATAAACCCCTGTGTTCTG 1110
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## RESULT 2

US-09-918-568-57

Sequence 57, Application us/09918568

GENERAL INFORMATION:

APPLICANT: Yoshinobu OKUNO et al.

TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING

NUMBER OF SEQUENCES: 58 ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind &amp; Ponack, L.L.P.

```

? STREET: 2033 K Street, N.W., #800
? City: Washington
? STATE: D.C.
? COUNTRY: U.S.A.
? ZIP: 20006
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: MS-DOS
? SOFTWARE: Nordperfect 5.1
?
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/918,568
? FILING DATE: 02-Aug-2001
? CLASSIFICATION: <Unknown>
?
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/004,422
? FILING DATE: January 8, 1998
? APPLICATION NUMBER: 08/443,862
? FILING DATE: May 22, 1995
? APPLICATION NUMBER: 08/229,781
? FILING DATE: April 19, 1994
? APPLICATION NUMBER: 08/054,016
? FILING DATE: April 29, 1993
?
? ATTORNEY/AGENT INFORMATION:
? NAME: Warren M. Cheek, Jr.
? REGISTRATION NUMBER: 33,367
? REFERENCE/DOCKET NUMBER: <Unknown>
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-721-8200
? TELEFAX: 202-721-8250
?
? INFORMATION FOR SEQ ID NO: 57:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1110 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
?
? MOLECULE TYPE: cDNA to genomic RNA
? HYPOTHETICAL: <Unknown>
? ANTI-SENSE: <Unknown>
? FRAGMENT TYPE: <Unknown>
?
? ORIGINAL SOURCE:
? ORGANISM: A2/Aich1/2/68
? STRAIN: <Unknown>
? INDIVIDUAL ISOLATE: <Unknown>
? DEVELOPMENTAL STAGE: <Unknown>
?
? HAPLOTYPE: <Unknown>
? TISSUE TYPE: <Unknown>
? CELL TYPE: <Unknown>
? CELL LINE: <Unknown>
? ORGANELL: <Unknown>
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? IMMEDIATE SOURCE:
? LIBRARY: <Unknown>
? CLONE: <Unknown>
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? CHROMOSOME/SEGMENT: <Unknown>
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? UNITS: <Unknown>
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? FEATURE:
? NAME/KEY:
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? PUBLICATION INFORMATION:
? AUTHORS:
? TITLE:
? JOURNAL:
? VOLUME:
? ISSUE:
? PAGES:
? DATE:
? DOCUMENT NUMBER:
? FILING DATE:

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5 833.4 75.1 1765 50 US-10-311-581-7 Sequence 7, Appl  
6 832 75.0 1764 50 US-10-311-581-21 Sequence 21, Appl  
7 645.2 58.1 666 4 US-07-837-773-1 Sequence 1, Appl  
8 645.2 58.1 666 5 US-08-013-415-1 Sequence 1, Appl  
9 645.2 58.1 666 4 US-08-391-315-1 Sequence 1, Appl  
10 642 57.8 666 4 US-07-837-773-3 Sequence 3, Appl  
11 642 57.8 666 5 US-08-013-415-3 Sequence 3, Appl  
12 642 57.8 666 8 US-08-391-315-3 Sequence 3, Appl  
13 641.4 57.8 918 4 US-07-837-773-9 Sequence 9, Appl  
14 641.4 57.8 918 5 US-08-013-415-5 Sequence 9, Appl  
15 641.4 57.8 918 8 US-08-391-315-9 Sequence 9, Appl  
16 631.8 56.9 918 8 US-08-013-415-7 Sequence 7, Appl  
17 631.8 56.9 918 8 US-08-391-315-58 Sequence 58, Appl  
18 630.2 56.8 670 4 US-07-837-773-7 Sequence 7, Appl  
19 630.2 56.8 670 8 US-08-391-315-7 Sequence 7, Appl  
20 605.2 54.5 1762 45 US-10-065-133A-10 Sequence 10, Appl  
21 603.6 54.4 1762 4 US-07-847-951A-284 Sequence 284, App  
22 603.6 54.4 1762 4 US-07-847-951A-300 Sequence 300, App  
23 602 54.2 1762 45 US-10-065-133A-7 Sequence 7, Appl  
24 582.8 52.5 1698 29 US-09-677-672A-3 Sequence 3, Appl  
25 579.8 52.2 1695 45 US-10-065-133A-12 Sequence 12, Appl  
26 576.6 51.9 1695 45 US-10-065-133A-9 Sequence 9, Appl  
27 576.4 51.9 1698 27 US-09-622-951-1 Sequence 1, Appl  
28 536.6 50.1 1698 29 US-09-677-672A-5 Sequence 5, Appl  
29 418.4 37.7 690 4 US-07-837-773-11 Sequence 11, Appl  
30 418.4 37.7 690 5 US-08-013-415-18 Sequence 18, Appl  
31 418.4 37.7 690 8 US-08-391-315-11 Sequence 11, Appl  
32 333.6 30.1 2005 38 US-09-914-658B-3 Sequence 3, Appl  
33 333.6 30.1 4930 38 US-09-914-658B-1 Sequence 1, Appl  
34 332.8 30.0 4610 38 US-09-914-658B-6 Sequence 6, Appl  
35 329 29.6 329 9 US-08-443-862-37 Sequence 37, Appl  
36 329 29.6 329 38 US-09-918-568-37 Sequence 37, Appl  
37 321 28.9 1711 45 US-10-099-619-1 Sequence 1, Appl  
38 311.6 28.1 334 9 US-08-443-862-38 Sequence 38, Appl  
39 306.2 27.6 1759 4 US-07-847-951A-279 Sequence 38, Appl  
40 305.2 27.5 334 9 US-08-443-862-40 Sequence 279, App  
41 305.2 27.5 334 38 US-09-918-568-40 Sequence 40, Appl  
42 301.8 27.2 329 9 US-08-443-862-39 Sequence 39, Appl  
43 301.8 27.2 329 38 US-09-918-568-39 Sequence 39, Appl  
44 295.4 26.6 329 9 US-08-443-862-41 Sequence 41, Appl

## ALIGNMENTS

RESULT 1  
US-08-443-862-57  
Sequence 57, Application US/08443862  
GENERAL INFORMATION:  
APPLICANT: Yoshinobu OKuno et al.  
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/443,862  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/229,781  
FILING DATE: April 19, 1994  
APPLICATION NUMBER: 08/034,016

FILING DATE: April 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1110 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORGANISM: A2/Aichi/2/68  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:  
LOCATION:  
IDENTIFICATION METHOD:  
OTHER INFORMATION:  
PUBLICATION INFORMATION:  
AUTHORS:  
TITLE:  
JOURNAL:  
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FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO:  
US-08-443-862-57  
Query Match 100.0%; Score 1110; DB 9; Length 1110;  
Best Local Similarity 100.0%; Pred. No.1.5e-302; Indels 0; Gaps 0;  
Matches 1110; Conservative 0; Mismatches 0;

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|||||  
Db 1 CTGAGACCAAGCAGGCGATATCTATTATCATGAAGACCATTCGCTTGAGCTAC 60  
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QY 61 ATTTTCTGTCTGCTTCGCGCAAGACCTTCGAGGAATGCAACACGACGACGCTG 120  
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Db 121 TGCCTGGACATCATGCGGTGCGCAAGGAACTAGTGAACCAATCACAGATGATCAG 180  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 10, 2003, 02:11:24 ; Search time 2451.76 Seconds  
(without alignments)  
14835.212 Million cell updates/sec

Title: US-09-918-568-57  
1110  
Perfect score: 1 CTAGACGCAAGACGAGCGAT.....TAAACACACCTTGTTCG 1110.  
Sequence:

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32997241 seqs, 16383922548 residues

Total number of hits satisfying chosen parameters: 65994482

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pending\_Patents\_NA\_Main:\*

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- 55: /cgn2\_6/ptodata/2/pna/US6001\_COMB.seq:\*
- 56: /cgn2\_6/ptodata/2/pna/US6002\_COMB.seq:\*
- 57: /cgn2\_6/ptodata/2/pna/US6003\_COMB.seq:\*
- 58: /cgn2\_6/ptodata/2/pna/US6004\_COMB.seq:\*
- 59: /cgn2\_6/ptodata/2/pna/US6005\_COMB.seq:\*
- 60: /cgn2\_6/ptodata/2/pna/US6006\_COMB.seq:\*
- 61: /cgn2\_6/ptodata/2/pna/US6007\_COMB.seq:\*
- 62: /cgn2\_6/ptodata/2/pna/US6008\_COMB.seq:\*
- 63: /cgn2\_6/ptodata/2/pna/US6009\_COMB.seq:\*
- 64: /cgn2\_6/ptodata/2/pna/US6010\_COMB.seq:\*
- 65: /cgn2\_6/ptodata/2/pna/US6011\_COMB.seq:\*
- 66: /cgn2\_6/ptodata/2/pna/US6012\_COMB.seq:\*
- 67: /cgn2\_6/ptodata/2/pna/US6013\_COMB.seq:\*
- 68: /cgn2\_6/ptodata/2/pna/US6014\_COMB.seq:\*
- 69: /cgn2\_6/ptodata/2/pna/US6015\_COMB.seq:\*
- 70: /cgn2\_6/ptodata/2/pna/US6016\_COMB.seq:\*
- 71: /cgn2\_6/ptodata/2/pna/US6017\_COMB.seq:\*
- 72: /cgn2\_6/ptodata/2/pna/US6018\_COMB.seq:\*
- 73: /cgn2\_6/ptodata/2/pna/US6019\_COMB.seq:\*
- 74: /cgn2\_6/ptodata/2/pna/US6020\_COMB.seq:\*
- 75: /cgn2\_6/ptodata/2/pna/US6021\_COMB.seq:\*
- 76: /cgn2\_6/ptodata/2/pna/US6022\_COMB.seq:\*
- 77: /cgn2\_6/ptodata/2/pna/US6023A\_COMB.seq:\*
- 78: /cgn2\_6/ptodata/2/pna/US6023B\_COMB.seq:\*
- 79: /cgn2\_6/ptodata/2/pna/US6024\_COMB.seq:\*
- 80: /cgn2\_6/ptodata/2/pna/US6025\_COMB.seq:\*
- 81: /cgn2\_6/ptodata/2/pna/US6026\_COMB.seq:\*
- 82: /cgn2\_6/ptodata/2/pna/US6027\_COMB.seq:\*
- 83: /cgn2\_6/ptodata/2/pna/US6028\_COMB.seq:\*
- 84: /cgn2\_6/ptodata/2/pna/US6029\_COMB.seq:\*
- 85: /cgn2\_6/ptodata/2/pna/US6030\_COMB.seq:\*
- 86: /cgn2\_6/ptodata/2/pna/US6031\_COMB.seq:\*
- 87: /cgn2\_6/ptodata/2/pna/US6032\_COMB.seq:\*
- 88: /cgn2\_6/ptodata/2/pna/US6033\_COMB.seq:\*
- 89: /cgn2\_6/ptodata/2/pna/US6034\_COMB.seq:\*
- 90: /cgn2\_6/ptodata/2/pna/US6035\_COMB.seq:\*
- 91: /cgn2\_6/ptodata/2/pna/US6036\_COMB.seq:\*
- 92: /cgn2\_6/ptodata/2/pna/US6037\_COMB.seq:\*
- 93: /cgn2\_6/ptodata/2/pna/US6038\_COMB.seq:\*
- 94: /cgn2\_6/ptodata/2/pna/US6039\_COMB.seq:\*
- 95: /cgn2\_6/ptodata/2/pna/US6040\_COMB.seq:\*
- 96: /cgn2\_6/ptodata/2/pna/US6041\_COMB.seq:\*
- 97: /cgn2\_6/ptodata/2/pna/US6042\_COMB.seq:\*
- 98: /cgn2\_6/ptodata/2/pna/US6043\_COMB.seq:\*
- 99: /cgn2\_6/ptodata/2/pna/US6044\_COMB.seq:\*
- 100: /cgn2\_6/ptodata/2/pna/US6045\_COMB.seq:\*
- 101: /cgn2\_6/ptodata/2/pna/US6046\_COMB.seq:\*
- 102: /cgn2\_6/ptodata/2/pna/US6047\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Score	Query	Match	Length	ID	Description
No.						
1	1110	100.0	1110	9	US-08-443-862-57	Sequence 57, Appl
2	1110	100.0	1110	38	US-09-918-568-57	Sequence 57, Appl
3	868	78.2	1777	9	US-08-443-862-54	Sequence 54, Appl
4	868	78.2	1777	38	US-09-918-568-54	Sequence 54, Appl

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Tue Aug 12 10:28:32 2003

Job time : 129.277 secs

us-09-918-568-57.rnpn

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Page 7





Matches	78:	Conservative	0:	Mismatches	64:	Indels	0:	Gaps	0:
QY	580	GAGAAAGCAGAACGAGAAATTCCATCAATCGAAANGAATTTCTCAGAGACTAGAGGAGA							639
Db	233	GAATATACGCAAGAGAACTCCGAAATTTCCAGAGGAGCGCCGAAATATGAACCTGAA							292
QY	640	ATTGAGGACCTCGAANAATACCTTGAAGACACTAAATAATGATCTCTGCTTACCATGCG							699
Db	293	TTGGGAGCGCAGACTCAACCAAAATTTAAACACAGAGACAGACCCTCTCTCGCAAAATAAC							352
QY	700	GAGCTTCTTGTGCTCTGAGAGA	721						
Db	353	CGCCTTCGATGAGACTGGAAA	374						

RESULT 10  
US-60-487-610-19808/C  
Sequence 19808, Application US/60487610

```

: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS
: TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL001469
: CURRENT APPLICATION NUMBER: US/60/487,610
: CURRENT FILING DATE: 2003-07-17
: NUMBER OF SEQ ID NOS: 97101
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 19808
: LENGTH: 83514
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-60-487-610-19808

```

Query Match	3.68;	Score 39.6;	DB 7;	Length 83514
Best Local Similarity	56.28;	Pred. No. 0.16;		
Matches 72: Conservative	1;	Mismatches 55;	Indels 0	

OY 550 CAAATCAATTGGAAATTTGAACAGGCTAATCAGAACAAGCAAGAAATTCATCAAATC 609  
| | | | | | | | | | | | | | | | | | | | |  
Db 14771 CCAAGCAGTGGGAAATTTGACATGGCGAATCAAGCACAGACAGACACATACATCATCTT 14712  
  
OY 610 GAAAAGCAATTCTCAGAGTAGAAGGAGAAATTCAGACCTCGAGAAATACGTGAAGAC 669  
| | | | | | | | | | | | | | | | : | | | | |  
Db 14711 CTGAAGGATACAGTAGACACAGAAAGAAGTAAARBCATAAAAAACAACCTTGCGGGA 14652  
  
OY 670 ACTAAAT 677  
| | | | |  
Db 14651 ATACCAAT 14644

```

RESULT 11
US-60-485-450-12200/C
: Sequence 12200, Application US/60485450
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C.
: TITLE OF INVENTION: VIRUS INFECTED SUBJECTS, METHODS OF DETECTION AND USES
: TITLE OF INVENTION: THERIOF
: FILE REFERENCE: CLO01470
: CURRENT APPLICATION NUMBER: US/60/485,450
: CURRENT FILING DATE: 2003-07-09
: NUMBER OF SEQ ID NOS: 47859
: SOFTWARE: fastSeq for Windows Version 4.0
: SEQ ID NO 12200
: LENGTH: 83514
: TYPE: DNA
: ORGANISM: Homo sapiens
US-60-485-450-12200

```

Query Match 3.6%; Score 39.6; DB 7; Length 83514;  
Best Local Similarity 56.2%; Pred. No. 0.16;  
Matches 72; Conservative 1; Mismatches 55; Indels 0; Gaps 0;

QY	670	ACTAAAT	677	.
		1	111	
Db	14651	ATACAAAT	14644	

RESULT 12  
US-10-293-244-2166

```

1  APPLICANT: Hyseq, Inc.
2  APPLICANT: Tang, Y. Tom et al
3  TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
4  FILE REFERENCE: 21272-029
5  CURRENT APPLICATION NUMBER: US/10/293,244
6  CURRENT FILING DATE: 2002-11-12
7  PRIOR APPLICATION NUMBER: Not Yet Assigned
8  PRIOR FILING DATE: 2001-01-30
9  PRIOR APPLICATION NUMBER: 09/728,422
10 PRIOR FILING DATE: 2000-11-30
11 PRIOR APPLICATION NUMBER: 09/693,325
12 PRIOR FILING DATE: 2000-10-20
13 PRIOR APPLICATION NUMBER: 09/663,561
14 PRIOR FILING DATE: 2000-09-15

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? PRIOR APPLICATION NUMBER: 09/654, 936
? PRIOR FILING DATE: 2000-09-01
? PRIOR APPLICATION NUMBER: 09/620, 325
? PRIOR FILING DATE: 2000-07-19
? PRIOR APPLICATION NUMBER: 09/598, 075
? PRIOR FILING DATE: 2000-06-20
? PRIOR APPLICATION NUMBER: 09/560, 875
? PRIOR FILING DATE: 2000-04-27
? PRIOR APPLICATION NUMBER: 08/496, 914
? PRIOR FILING DATE: 2000-02-03
? NUMBER OF SEQ ID NOS: 3960
? SOFTWARE: Custom
? SEQ ID NO: 2166
? LENGTH: 2795
? TYPE: DNA
? ORGANISM: Homo sapiens
? OS-10-293-244--2166

```

	Query Match	3.4%	Score 38.2:	DB 6:	Length 2795;
	Best Local Similarity .56.9%:	Pred. NO.0.1;			
	Matches 70; Conservative 0;	Mismatches 53;	Indels 0;	Gaps 0;	
QY	556 AATGGGAATTGAAACAGGGTAAATCGACAAGCAAGAATAATTCATCAATCGAANAAG	615               -			
Dd	2079 AAATCAAGACTGCAAAAAACCTTTAGAGACACGCATTAATAATCCACCATTTAGACAGT	2138 			
QY	616 GAAATTCAGAGTAGAAGGAGGAGGAATTCAGACCCTCGAANAATCGTTGAAGACACTAAA	675 			
Dd	2139 GAACGTACAGACTTAGAGATGGAATAATCAAACATTTGACAGAAAACCTAGAGACTAAAA	2198 			
QY	676 ATA 678				
Dd	2199 ATA 2201				

RESULT 13  
US-10-293-244-198  
Sequence 198, Application US/10293244

RESULT 13  
US-10-293-244-198  
; Sequence 198, Application US/10293244



```

Db      989  GGATGGCTACAGAGCTACGAACATTCATCTATTCCATCCAGGGGTCTATTGGAGCCA 1048
Oy      428  TAGCAGCTTTTCATAGAAAATGGTGGAGGAGATGATAGCGTTGGTACGGTTCAGGC 487
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1049  TTGGCGGTTTATTTGAGGGGGGATGACCTGGAATGATGATGATGATGATGATGATGATC 1108
Oy      488  ATCAAAATTTGAGGGGACAGACAGACAGACAGATCTTAAAGACTCAAGCAGCCATCG 547
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1109  ATCAAAATGACAGGATGAGGCTATGACGCGATCAAAAAGACACAAAATGCGCATTG 1168
Oy      548  ACCAAATGATGGGAATTTGACAGGCTATGAGAGACGAGACGAAATTT 599
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1169  ACGGATTACAAAACAAAGGTGTAATCTGTATGAGAAAATGAAACACCAATT 1220

```

## RESULT 4

```

PCT-US03-12728-94
; Sequence 94, Application PC/TUS0312728
; GENERAL INFORMATION:
; APPLICANT: Medimmune Vaccines, Inc.
; APPLICANT: Hoffman, Erich
; APPLICANT: Jin, Hong
; APPLICANT: Lu, Bin
; APPLICANT: Duke, George
; TITLE OF INVENTION: MULTI PLASMID SYSTEM FOR THE PRODUCTION OF INFLUENZA VIRUS
; FILE REFERENCE: 26-000270US/PC
; CURRENT FILING DATE: 2003-04-25
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/375,675
; PRIOR FILING DATE: 26-04-2002
; PRIOR APPLICATION NUMBER: 60/394,983
; PRIOR FILING DATE: 09-07-2002
; PRIOR APPLICATION NUMBER: 60/410,576
; PRIOR FILING DATE: 12-09-2002
; PRIOR APPLICATION NUMBER: 60/419,802
; PRIOR FILING DATE: 18-10-2002
; PRIOR APPLICATION NUMBER: 60/420,708
; PRIOR FILING DATE: 23-10-2002
; PRIOR APPLICATION NUMBER: 60/457,699
; PRIOR FILING DATE: 24-03-2003
; PRIOR APPLICATION NUMBER: 60/462,361
; PRIOR FILING DATE: 10-04-2003
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 1884
; TYPE: DNA
; ORGANISM: Influenza B virus
PCT-US03-12728-94

```

Query Match 9.6%; Score 106.4; DB 1; Length 1884;

Best Local Similarity 51.5%; Pred. No. 2.1e-23;

Matches 245; Conservative 0; Mismatches 231; Indels 0; Gaps 0;

```

Oy      409  AGAGGCTATTTCGGGCAATATGACGTTTCATAGAAAATGTTGGAGGGAATGATAGAC 468
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1117  AGGGGTTTCTTCGGAGTATTCCTGTTCTTGAAGAGGATGGGAAGATGATGGA 1176
Oy      469  GGTGGTACGTTTACGATCAAAATTTGAGGCGACAGCAAGCAGACAGATCTTAAA 528
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1177  GGTGGGACGATACATCTCATGAGACATGAGAGTGCGACAGTGCACAGACCTTAA 1236
Oy      529  AGCACTAAGGACGATGACCAATTCATGGAATTTGAACAGGTATGAGGAAGAGC 588
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1237  AGTACGCAAGAGCTATTAACAGATTAACAAAAATCTCAATTTCTTAAGTAGCTAGAA 1296
Oy      589  AACGGAATTCATCAATCGAAAGGAATTCAGAGATGAGAGGAGGAATTCAGGAC 648
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1297  GTAAGATCTTCAAGAGCTAAGCGGTGCAATGATGATGATGATGATGATGATGATG 1356
Oy      649  CTCGGAATATCGTTGAAGACACTAAATAGATCTCTGCTTTACATGCGGAGCTTCT 708
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

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Db      1357  CTGGATGAGAAAGTGTATGATCTCAGAGCTGATACAAATAGCTGCCAAATAGAGCTTCA 1416
Oy      709  GTGCTCTGAGAGATGACATCAATTTGACCTGACTGACTCGGAATGAAACAGCTGTTT 768
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1417  GTCTTCTCTTCCACCAAGGAATTAATTAACAGTGAAGATGAGACATCTCTTGCACTTGA 1476
Oy      769  GAAAACCAAGAGGAGCACTGAGGAAATGCTGAAGAGATGGGAATGTTGCTTCAAA 828
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1477  AGAAACATGAGAAATTTGCTGGGCCCCCTCTGCTGATGACATGAGGAATGATGATTCGAA 1536
Oy      829  ATATACCAATATGTACACAGCTTGCATAGATGATCAATGAAATGATGATGATGATG 884
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1537  ACCAAACAAAGATGCAACCAAGACTTCCCTAGACAGATAGCTGCTGACCTTTAA 1592

```

## RESULT 5

```

US-10-466-655-1
; Sequence 1, Application US/1046655
; GENERAL INFORMATION:
; APPLICANT: VILAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE VZW
; TITLE OF INVENTION: Recombinant oligomeric protein complexes with enhanced
; FILE REFERENCE: TDR/Tec/V078
; CURRENT FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: part of PACGCN4nas
; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION:
US-10-466-655-1

```

Query Match 5.0%; Score 55; DB 6; Length 1350;

Best Local Similarity 77.0%; Pred. No. 3.5e-07;

Matches 67; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

```

Oy      34  ATGAAGACCATCATGCTTTGAGCTACATATTTCTGCTGCTGCGCCAGACCTTCCA 93
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1  ATGAAGACTATCATGCTTTGAGCTACATATTTCTGCTGCTGCTGCGCCAGACCTTGC 60
Oy      94  GGAATGACACAGCAGCAACGCTG 120
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      61  GGTATGAACAACAAATGCAAGACCAAGCTG 87

```

## RESULT 6

```

US-60-487-610-74191/c
; Sequence 74191, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: C1001469
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74191
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-487-610-74191

```

Query Match 3.6%; Score 39.6; DB 7; Length 201;

Oy	601	CATCAAAAGGGAAGTAATTCTCAGAAGTAGAGGACAATTCAGACCTCGAATAATG	660
Dd	1235	GAAATTAATTGCATGAATTAATCGTAGGTGGAACTAACATCAATATGATATATAG	1294
Oy	661	GTGAGACACTAAAATGATCTCTGGTCTTACCATGGGAGACTCTTGCGCTGGAG	720
Dd	1295	ATTGATGACCAAATATCAAGAGCTATGGCATATATATGCAAGATTCTGTACTACTGAA	1354
Oy	721	AATCAACATTAATTTACCTGACGTACGTGCGAATGAAACAAGCTTTGAAAAAACAAG	780
Dd	1355	AATCAAAATAACACTCTGATGACCATGATGTCGAACGTGAACAATCTATATACAAAGGTGAAG	1414
Oy	781	AGGCACATGAGGAGAAATGCTGAAGAGATGGGCATGGTGTCTTCAAAATATACCAAA	840
Dd	1415	AGGCGACTGGGCTCCATGCTATGGAAGATGGAAAGGCTGTTTGACACTTATACCATYAA	1474
Oy	841	TGTGCAACAGCTTGCAATAGACTCAATCAAGAAATGCTACTATAGCAATGATGTATACAGA	900
Dd	1475	TGTATGATCACTGCAATGGAACCAATTCGGAAACGGACCTTAATATAGAGAAAGATATGA	1534
Oy	901	GACCAAGAGATTAAACAAACCGTTTTCAAGTCAAGSTGTGTAACGTAGACTCGATACAAA	960
Dd	1535	GAGCAATTCAGACTTAAGAAAGCACAAAAATAAAGGGGTTAAAGCTGGGAATCTGAGGGAAC	1594
Oy	961	GACTGAGATCCTGTGAT--TTCCTTGGCAATATACGCTTTTGGCTTGTGTGTTTG	1017
Dd	1595	TACAAATATCCACACATTATATTCACAGCTGCCCTCATCTCTTGAGCTTCGAATGGGGTTT	1654
Oy	1018	CTGGGGTCATCATGTGGGGCTTGGCAAGAGGCAACAATTAGTGTGCACATTTGCAATTGGA	1077
Dd	1655	GCTGCTTCTCTGTTCTGGGGCATGTGCCAANTGATCTTGCAAGATCAACATTTGATATATA	1714

```

RESULT 2
US-60-470-920-19
: Sequence 19, Application US/60470920
: GENERAL INFORMATION:
: APPLICANT: Luke, Catherine, J.
: APPLICANT: Vialta, Adrian
: APPLICANT: Wloch, Mary K.
: APPLICANT: Evans, Thomas G.
: APPLICANT: Geall, Andrew J.
: TITLE OF INVENTION: DNA Influenza Vaccine Compositions
: FILE REFERENCE: 1530.0640600
: CURRENT APPLICATION NUMBER: US/60/470,920
: CURRENT FILING DATE: 2003-05-16
: NUMBER OF SEQ. ID NOS: 45
: SOFTWARE: patentIn version 3.2
: SEQ. ID NO 19
: LENGTH: 1741
: TYPE: DNA
: ORGANISM: Influenza A virus
: US-60-470-920-19

```

	Query Match	20.38;	Score 225.2;	DB 7;	Length 1741;
	Best Local Similarity	56.88;	Pred. No. 4; 5e-61;		
	Matches 441; Conservatively	0;	Mismatches 323;	Indels 12;	Gaps 1;
OY	216 CTCTCAACGGGGAATAATGACAATATTGATACCTGTATTTCATGATGCATCAGTCC	275			
Db	839 CTTAAACATTATGTAAGAATGATGGATATGTGAATCGAACACCAGTGTCAAATGCC	898			
OY	276 AATGGAAGCATTCGCATGSCAAGCCCTTCAAAAGSTAAACAAGATCATNTGTGAG	335			
Db	899 AATGGGGGCATATACTCTAGTAGTATGTCATTCACACATATCACCCCCTCACCATGGGGA	958			
OY	336 ATGCCCCCAATGATTGAGCAAAACACCCTGAAGTTGGCAACAGGAGTATGCGATATACC	395			
Db	959 ATCCCCCAATATGTGAAATCAAACAGATAGTCTTGCGACGTGACTCGAANAATACCC	1018			
OY	396 AGAGAA-----ACAACTAGAGCCATATTGGGGCATATGACAGTTCATAGA	443			
Db	1019 TCAGAGGAGACGAATAGAGAAAAAGAGAGACATATTGGAGCTATACAGAGTTTTATAGA	1078			

QY	444	AAATGCTTGGGGGGAATGATAGACGGTGTGGTACCGTTTCAGGCGATCAAAATTTCTGAGG	503
Db	1079	GGGAGGATGGCAGGGCATGTAGATGGTTGGTATGGGTACCACCATACCAATGAGCAGGG	1138
QY	504	CACAGGACAGCAGCAGATCTTTAAAGCACTTCAGCAGCCATCGACCAATCAATGAGAA	563
Db	1139	GAGTGGATACCTGCGACAAAGATCCACTCAAAAGGCATATAGTGGATGCCAATTA	1198
QY	564	ATTGAAACGGGGTAATCGAGACGACAGCAAGAAATCCATCAATTCGAAAGGAATTC	623
Db	1139	GGTCACTCGATCATTTAAACAAATGATACACTCAGTTTGAAGCCGTTGGAAAGGAATTTAA	1258
QY	674	AGAACTAGAGGGAGAAATTCAGGACCTTCGAGAAATACGTTGAGACACATAAATATGATCT	683
Db	1259	TAACTTAGAAAGAGAGATAGAGAAATTTAAACAGAAATGGAAGACGATTCCTATGATGT	1318
QY	684	CTGGCTTACACANTGGGAGCTTCTTGTCGCTCTGAGATACATACATACATTTGAGCTCAG	743
Db	1319	CTGCACTTACATGCTGCACTTCTTGTTCTCATGGAAATATAGAGAACTCTCGACTTTC	1378
QY	744	TGACTCGAAATGAACAAGCTGTTTGAAGAAAAACAAGGACCACTGAGGAGAAATGCTGA	803
Db	1379	TGACCAAAATGTCAAGAACCTTTACGACAAAGTCCGACTACAGCTTAGGGATTAATGCAAA	1438
QY	804	AGAGATGGGCAATGGTTCCTCAAAATTTACCAAAATGTACCAACGTTTCATATAGATC	863
Db	1439	GGAACTGGGTATGGTTTCTTGCAATTTTATACCAAAATGTATATATGATATATAGGAAG	1498
QY	864	AATCAGAAATGTTACTTATGACCATGATGTATACAGAGCAGCAAGCATTTAAACACCGGTT	923
Db	1499	TGTAAAAAACGACGATGTGACTACCCGCACTATTTCAGAGAAAGCAAGACTAAACAGAGA	1558
QY	924	TCAGTCAAGAGGTGTGAACGTGAGTCTGATACAAAGACTGATCTCTGTGATTT	979
Db	1559	GGAATTAAGTGGAGTAAATGGAATCAGATGGAATTCCTCAAAATATCTCAATTT	1614

```

RESULT 3
US-60-470-920-17
: Sequence 17, Application US/60470920
: GENERAL INFORMATION:
: APPLICANT: Luke, Catherine, J.
: APPLICANT: Vialta, Adrian
: APPLICANT: Wlooch, Mary K.
: APPLICANT: Evans, Thomas G.
: APPLICANT: Geall, Andrew J.
: TITLE OF INVENTION: DNA Influenza Vaccine Compositions
: FILE REFERENCE: 1530.064000
: CURRENT APPLICATION NUMBER: US/60,470,920
: CURRENT FILING DATE: 2003-05-16
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: patentlin version 3.2
: SEQ ID NO 17
: LENGTH: 1220
: TYPE: DNA
: ORGANISM: Influenza A virus
: US-60-470-920-17

```

	Query Match	11.2%	Score 124.8;	DB: 7	Length 1220;
	Best Local Similarity	59.7%;	Pred. 2,56-29;		
	Matches 210;	Conservative 0;	Mismatches 142;	Indels 0;	Gaps 0;
OY	248	ATACCTGTATTTTGAATGATCATCTCCAAATGAGACATTC	307		
Db	869	ATGATTTTAAACAGCAAGTGTCAAAACACCCCATGTGCTTATAAACAGCAGTCTCCCTTTCC	928		
OY	308	AAAACGTAAACAGATACATATGAGACCATGCCCAAGTATGTTAAACCAAAACACCTGSA	367		
Db	929	AGAAATATRCATCCAGTACACATAGAGAGATGCCCAAAATATCGTCAGGAGTACCAAAATTGA	988		
OY	368	AGTTGGCAACAGGAGATCCGAATGTATACAGAAACAACTAGAGGCTTTCGGGCGCAA	427		

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 10, 2003, 06:17:35 ; Search time 97.2766 Seconds

(without alignments)  
7190.269 Million cell updates/sec

Title: US-09-918-568-57

Perfect score: 1110

Sequence: 1 CTGAGAGCAAGCAGGAGAT.....TAAAGACCCCTGTTCTG 1110

Sorting table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 646752 seqs, 315065167 residues

Total number of hits satisfying chosen parameters: 1293504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_NA\_New:\*  
1: /cgn2\_6/ptodata/1/pna/PCr\_NEW\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*  
7: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	251.2	22.6	1714	US-60-470-920-21	Sequence 21, Appl
2	225.2	20.3	1741	US-60-470-920-19	Sequence 19, Appl
3	124.8	11.2	1220	US-60-470-920-17	Sequence 17, Appl
4	106.4	9.6	1884	PCT-US03-12728-94	Sequence 94, Appl
5	55	5.0	1350	US-10-466-655-1	Sequence 1, Appl
6	39.6	3.6	201	US-60-487-610-74191	Sequence 74191, A
7	39.6	3.6	201	US-60-485-450-38314	Sequence 38314, A
8	39.6	3.6	2051	US-10-286-897-5262	Sequence 5262, Ap
9	39.6	3.6	2051	US-10-286-897-1690	Sequence 1690, Ap
10	39.6	3.6	83514	US-60-485-450-12200	Sequence 12200, A
11	39.6	3.6	83514	US-60-487-610-19808	Sequence 19808, A
12	38.2	3.4	2795	US-10-293-244-2166	Sequence 2166, Ap
13	38.2	3.4	3058	US-10-293-244-198	Sequence 198, Ap
14	37.4	3.4	4410	US-60-479-073-336	Sequence 336, Ap
15	37.4	3.4	1383163	US-09-947-914-41	Sequence 41, Appl
16	37.2	3.4	2079	US-10-603-113-2454	Sequence 2454, Ap
17	36	3.2	411	US-10-273-573-140	Sequence 140, App
18	36	3.2	411	US-10-273-573-483	Sequence 483, App
19	36	3.2	411	US-10-273-573-4994	Sequence 4994, Ap
20	36	3.2	20588	US-60-487-610-19871	Sequence 19871, A
21	36	3.2	20588	US-60-485-450-12234	Sequence 12234, A
22	35.8	3.2	3820	US-10-357-930-22140	Sequence 22140, A
23	35.8	3.2	3820	US-10-357-930-28002	Sequence 28002, A
24	35.8	3.2	3820	US-10-357-930-29182	Sequence 29182, A
25	35.8	3.2	26747	US-60-487-610-19407	Sequence 19407, A
26	35.6	3.2	74079	US-60-487-610-19261	Sequence 19261, A

C	27	35.2	3.2	2006	6	US-10-357-930-24237	Sequence 24237, A
C	28	35.2	3.2	13831263	5	US-09-947-914-41	Sequence 41, Appl
C	29	35	3.2	329132	7	US-60-487-610-19918	Sequence 19918, A
C	30	34.8	3.1	848	6	US-10-286-897-3697	Sequence 3697, Ap
C	31	34.8	3.1	955	6	US-10-286-897-125	Sequence 125, App
C	32	34.8	3.1	397027	7	US-60-487-610-19423	Sequence 19423, A
C	33	34.8	3.1	1946141	5	US-09-947-914-42	Sequence 42, Appl
C	34	34.6	3.1	1413	6	US-10-603-113-1908	Sequence 1908, Appl
C	35	34.6	3.1	113306	6	US-10-297-798-1007	Sequence 1007, Ap
C	36	34.4	3.1	2089	6	US-10-286-897-122	Sequence 122, App
C	37	34.4	3.1	2094	6	US-10-286-897-3694	Sequence 3694, App
C	38	34	3.1	20839	6	PCT-US03-21379-30	Sequence 30, Appl
C	39	33.8	3.0	1128	6	US-10-603-113-5231	Sequence 5231, Ap
C	40	33.8	3.0	280225	7	US-60-487-610-19457	Sequence 19457, A
C	41	33.8	3.0	1791310	5	US-09-947-914-46	Sequence 46, Appl
C	42	33.6	3.0	390	6	US-10-273-573-4913	Sequence 4913, Ap
C	43	33.6	3.0	122496	7	US-60-487-610-19283	Sequence 19283, A
C	44	33.6	3.0	122496	7	US-60-485-450-11884	Sequence 11884, A
C	45	33.6	3.0	4813087	5	US-09-947-914-75	Sequence 75, Appl

## ALIGNMENTS

RESULT 1

US-60-470-920-21

Sequence 21, Application US/60470920

GENERAL INFORMATION:

APPLICANT: Luke, Catherine, J.

APPLICANT: Villalta, Adrian

APPLICANT: Wloch, Mary K.

APPLICANT: Evans, Thomas G.

APPLICANT: Geall, Andrew J.

TITLE OF INVENTION: DNA Influenza Vaccine Compositions

FILE REFERENCE: 1530.0640000

CURRENT APPLICATION NUMBER: US/60/470.920

CURRENT FILING DATE: 2003-05-16

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatentIn version 3.2

SEQ ID NO 21

LENGTH: 1714

TYPE: DNA

ORGANISM: Influenza A virus

US-60-470-920-21

Query Match

Best Local Similarity

Matches 479; Conservative

Score 251.2; DB 7;

Pred. No. 2.5e-69;

Mismatches 358; Indels

Gaps: 1;

Length 1714;

Score 251.2; DB 7;

Pred. No. 2.5e-69;

Mismatches 358; Indels

Gaps: 1;

Length 1714;

Score 251.2; DB 7;

Pred. No. 2.5e-69;

Mismatches 358; Indels

Gaps: 1;

Length 1714;

Score 251.2; DB 7;

Pred. No. 2.5e-69;

Mismatches 358; Indels

Gaps: 1;

Length 1714;

Score 251.2; DB 7;

Pred. No. 2.5e-69;

Mismatches 358; Indels

Gaps: 1;

Length 1714;

Score 251.2; DB 7;

Pred. No. 2.5e-69;

Mismatches 358; Indels

Gaps: 1;